

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 06:14:03 ; Search time 7440 Seconds
(without alignments)
13361.329 Million cell updates/sec

Title: US-10-070-489A-1

Perfect score: 18937

Sequence: 1 ggatccgagtggaaggaatca.....cgtgcccgaggagcatggc 18937

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: N_Geneseq_23Sep04:*
- 2: Geneseq1980s:*
- 3: Geneseq1990s:*
- 4: Geneseq2000s:*
- 5: Geneseq2001as:*
- 6: Geneseq2001bs:*
- 7: Geneseq2002as:*
- 8: Geneseq2002bs:*
- 9: Geneseq2003as:*
- 10: Geneseq2003bs:*
- 11: Geneseq2003cs:*
- 12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	18914	99.9	18940	5	AAA91292	Aaa91292 Insectici
2	2368.8	12.5	37948	2	Aaz06831	Aaz06831 Photorhab
3	2357.8	12.5	110000	10	ACF67367_23	Continuation (24 o
C	2357.8	12.5	110000	10	ACF65386_5	Continuation (5 of
C	2283.6	12.1	110000	10	ACF65386_4	Continuation (5 of
6	1658.8	8.8	38258	2	AAV17876	AAV17876 Cloned to
7	1260.8	6.7	38258	2	AAV17876	AAV17876 Cloned to
8	1108.8	5.9	4431	6	ABS52584	ABS52584 P. lumine
9	1108.8	5.9	4434	12	ADN61378	Adn61378 Photorhab
10	1074	5.7	4431	10	ACF69437	ACF69437 Photorhab
11	1067.6	5.6	4428	10	ACF69428	ACF69428 Photorhab
12	1046.4	5.5	4425	12	ADN61379	Adn61379 Photorhab
13	1046.4	5.5	4425	12	ADP18621	Adp18621 Photorhab
14	969.8	5.1	4458	2	AAV29924	AAV29924 tcac gene
15	968.6	5.1	110000	10	ACF65385_0	ACF65385 Photorhab
16	968.6	5.1	110000	10	ACF67367_29	Continuation (30 o
17	967.8	5.1	4458	10	ACF69896	ACF69896 Photorhab
18	965	5.1	4458	2	AAT68840	Aat68840 Photorhab
19	962.8	5.1	37544	3	AAA50029	Aaa50029 Cosmid ch
20	915.6	4.8	6648	10	ACF69426	ACF69426 Photorhab
21	903.4	4.8	6005	2	AAT68837	Aat68837 Photorhab

22	901.8	4.8	6055	2	AAV29921	Aav29921 tcab gene
23	848.8	4.5	7551	4	AAFS8778	Aaf58778 Photorhab
24	848.8	4.5	7551	6	ABSS2583	Abss2583 P. lumine
25	848.8	4.5	7551	12	ADP18613	Adp18613 Photorhab
26	845.6	4.5	7551	2	AAV29928	Aav29928 tcda gene
27	832.8	4.4	7551	2	AAT68843	Aat68843 Photorhab
28	815.2	4.3	7577	4	AAFS8780	Aaf58780 Modified
29	815.2	4.3	7621	4	AAFS8783	Aaf58783 Tcda toxi
30	814	4.3	7578	10	ACF69436	ACf69436 Photorhab
31	797	4.2	4482	12	ADN61356	Adn61356 Xenorhab
32	781.2	4.1	7512	6	ABSS2586	Abss2586 P. lumine
33	781.2	4.1	7515	4	AAFS8779	Aaf58779 Photorhab
34	779.6	4.1	7515	2	AAV29985	Aav29985 tcba gene
35	776.4	4.1	7515	2	AAT68836	Aat68836 Photorhab
36	771.8	4.1	33521	12	ADN61337	Adn61337 Paenibaci
37	770.8	4.1	6534	12	ADP18617	Adp18617 Photorhab
38	764	4.0	7377	10	ACF69433	ACf69433 Photorhab
39	758.8	4.0	7500	12	ADP18615	Adp18615 Photorhab
40	755.6	4.0	3051	12	ADN61357	Adn61357 Xenorhab
41	748.6	4.0	7541	4	AAFS8781	Aaf58781 Modified
42	747.8	3.9	7335	10	ACF69427	ACf69427 Photorhab
43	732	3.9	7146	12	ADP18619	Adp18619 Photorhab
44	725	3.8	3132	2	AAT68850	Aat68850 Photorhab
45	725	3.8	3132	2	AAV29927	Aav29927 tccc gene

ALIGNMENTS

RESULT 1	
AAA91292	
ID AAA91292 standard; DNA; 18940 BP.	
XX	
AC AAA91292;	
XX	
DT 19-JUN-2001 (first entry)	
XX	
DE Insecticidal protein complex gene.	
XX	
KW Insecticidal protein complex; amber disease; insect; Coleoptera;	
KW pesticide; ds.	
XX	
XX Serratia sp.	
OS	
XX	
FH Key	Location/Qualifiers
FT CDS	1860..2295
FT	/*tag= a
FT	/product= "ORF1 protein"
FT	2416..9546
FT	/*tag= b
FT	/product= "SepA"
FT	9601..13887
FT	/*tag= c
FT	/product= "SepB"
FT	13911..14486
FT	/*tag= d
FT	/product= "ORF2 protein"
FT	14549..17470
FT	/*tag= e
FT	/product= "SepC"
XX	
PN WO200116305-A2.	
XX	
PD 08-MAR-2001.	
XX	
PF 04-SEP-2000; 2000WO-NZ000174.	
XX	
PR 02-SEP-1999; 99NZ-00337610.	
XX	
PA (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.	
XX	
PI Glare TR, Hurst MRH, Jackson TA;	
XX	

DR WPI; 2001-169009/17.
DR P-PSDB; AAP97692, AAP97693, AAP97694, AAP97695, AAP97696.
XX New nucleic acid encoding a polypeptide useful as a pesticide especially
PT for Coleoptera.
XX
XX Claim 1; Page 65-89; 109pp; English.
XX
CC This sequence represents the Serratia insecticidal protein complex gene
CC of the invention. The invention relates to a gene encoding an
CC insecticidal protein complex or a functional fragment, a neutral
CC mutation, or a homologue of the complex. The polypeptides and nucleotides
CC of the invention are used to induce amber diseases or like conditions in
CC insects, especially to those from the order comprising Coleoptera, useful
CC as a pesticide
XX
SQ Sequence 18940 BP; 4336 A; 4848 C; 5370 G; 4386 T; 0 U; 0 Other;

Query Match 99.9%; Score 18914; DB 5; Length 18940;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 18937; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

QY 1 GGATCCGAGTGAAGGAATCATCGCGCGCTTTATACGTTTCAGGGTGAATACGGTTGGCCG 60
DB 1 GGATCCGAGTGAAGGAATCATCGCGCGCTTTATACGTTTCAGGGTGAATACGGTTGGCCG 60

QY 61 CAACGTGGCAATCGATGTTGTTGTGTCGATATGAATCGCGCAACGTAATCGTGTCTCG 120
DB 61 CAACGTGGCAATCGATGTTGTTGTGTCGATATGAATCGCGCAACGTAATCGTGTCTCG 120

QY 121 ACATACCCAGTCCGATAAATCTGTGACGAACACTATCAAGATGTGTCGTCGACCTGA 180
DB 121 ACATACCCAGTCCGATAAATCTGTGACGAACACTATCAAGATGTGTCGTCGACCTGA 180

QY 181 AAGCAGGATTTATTTTACACCAATGTTGGTGGGCTTCCTTCTGAACTGGTGCATC 240
DB 181 AAGCAGGATTTATTTTACACCAATGTTGGTGGGCTTCCTTCTGAACTGGTGCATC 240

QY 241 ATTTAGCCGATCATCAAAAGATGATGGAATACAAATATCATATTTTACGACACCCA 300
DB 241 ATTTAGCCGATCATCAAAAGATGATGGAATACAAATATCATATTTTACGACACCCA 300

QY 301 AGTTGATGACCTCTCCGTGAGTTGAAATGCCAGCGGGGAAATCAGACGCTTTTCAAC 360
DB 301 AGTTGATGACCTCTCCGTGAGTTGAAATGCCAGCGGGGAAATCAGACGCTTTTCAAC 360

QY 361 TCATGAGCAGGGGAAATCAATCCTCAATAACCCGATGGATATCCTGCCAGTGTGA 420
DB 361 TCATGAGCAGGGGAAATCAATCCTCAATAACCCGATGGATATCCTGCCAGTGTGA 420

QY 421 TTTAAACCTTTTATGTTGTTTCTTAATATCCCAATCGTTGAATCGCTACATACGGCAGA 480
DB 421 TTTAAACCTTTTATGTTGTTTCTTAATATCCCAATCGTTGAATCGCTACATACGGCAGA 480

QY 481 CATTAGTATCTCACTTATCATCAAGATTAATCACAACCCGATGCTTAATTTTCAATAT 540
DB 481 CATTAGTATCTCACTTATCATCAAGATTAATCACAACCCGATGCTTAATTTTCAATAT 540

QY 541 GAAACGTTCCATTAATAATTTTACAGAACCTTAACACGGCAATTTTATGCTGATCAGTG 600
DB 541 GAAACGTTCCATTAATAATTTTACAGAACCTTAACACGGCAATTTTATGCTGATCAGTG 600

QY 601 AATTGATGTTTCTGAAATAATTAATTGCACTCTGCCACTTATCAGATATAAACAACCC 660
DB 601 AATTGATGTTTCTGAAATAATTAATTGCACTCTGCCACTTATCAGATATAAACAACCC 660

QY 661 ATCGGTAAGTATTTATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTT 720
DB 661 ATCGGTAAGTATTTATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTT 720

QY 721 TTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGATTT 780
DB 721 TTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGATTT 780

QY 781 TACTCAATTTAATGTTGGTATGACCATGTTTTAGATGAGTGGCAGGATTCATTATTGT 840
DB 781 TACTCAATTTAATGTTGGTATGACCATGTTTTAGATGAGTGGCAGGATTCATTATTGT 840

QY 841 AAAAAAGTATCTAAAACTTTAGCAGCAATCTTCTGAGGATGACCTCGACAGACTT 900
DB 841 AAAAAAGTATCTAAAACTTTAGCAGCAATCTTCTGAGGATGACCTCGACAGACTT 900

QY 901 GATTATGCAATTTTACGAAGGAGATGACGGGTGATAAATAATAAAAAACAAAAG 960
DB 901 GATTATGCAATTTTACGAAGGAGATGACGGGTGATAAATAATAAAAAACAAAAG 960

QY 961 TATAGCTTATAGTATCGCGGATTTACATCCAGTAACACTTTATTGACTTTTTTTACTTCTA 1020
DB 961 TATAGCTTATAGTATCGCGGATTTACATCCAGTAACACTTTATTGACTTTTTTTACTTCTA 1020

QY 1021 CCGTTAGCTATAAATATGATATTTAAATCTGTATTTTATAAACCAGTTTATCATGC 1080
DB 1021 CCGTTAGCTATAAATATGATATTTAAATCTGTATTTTATAAACCAGTTTATCATGC 1080

QY 1081 TGGATTGGTCATTAAGTCGTTATATGTCATCGTTATCTGTCAATGATTTGGTGTAAATC 1140
DB 1081 TGGATTGGTCATTAAGTCGTTATATGTCATCGTTATCTGTCAATGATTTGGTGTAAATC 1140

QY 1141 TTTTATTTCTCCAGTGAGGTTTCAGGGGAATGTTTGGTGAATCATCTCATGTCAATTT 1200
DB 1141 TTTTATTTCTCCAGTGAGGTTTCAGGGGAATGTTTGGTGAATCATCTCATGTCAATTT 1200

QY 1201 GTTGTCTTGATGTTAAATTAACGTGTTCAATTCATTATGTTTCTACTGTTGTTCTAATGTC 1260
DB 1201 GTTGTCTTGATGTTAAATTAACGTGTTCAATTCATTATGTTTCTACTGTTGTTCTAATGTC 1260

QY 1261 CGGAACGACCATAGAGACTGTCGCTATGTTAAATAGGAATTTTGAATGATTTATGCGGC 1320
DB 1261 CGGAACGACCATAGAGACTGTCGCTATGTTAAATAGGAATTTTGAATGATTTATGCGGC 1320

QY 1321 AAGGGTTATCGCTGCACTCTCTGGGCGATGTTTATTCATCATTCGCAAGATAAATTCAT 1380
DB 1321 AAGGGTTATCGCTGCACTCTCTGGGCGATGTTTATTCATCATTCGCAAGATAAATTCAT 1380

QY 1381 TGGTGTGACAGCGGGTATTGTTTGTCTCTTTTCTCTTTTCTCGGTTTCAATTTTCA 1440
DB 1381 TGGTGTGACAGCGGGTATTGTTTGTCTCTTTTCTCTTTTCTCGGTTTCAATTTTCA 1440

QY 1441 GACACAGCTTCCGTTATCACTTCTATATCCGAATGATATACATATAGGAATAAGACCT 1500
DB 1441 GACACAGCTTCCGTTATCACTTCTATATCCGAATGATATACATATAGGAATAAGACCT 1500

QY 1501 TGGTGCCTTTGTTTACAGCGCGTGAACGCTTTTCTTTTCTCATTTATGAGCAAGAT 1560
DB 1501 TGGTGCCTTTGTTTACAGCGCGTGAACGCTTTTCTTTTCTCATTTATGAGCAAGAT 1560

QY 1561 AGAGAGAAAATATCTTGGAGATAAACCGCATGTTCCAAATCATATCTTTAATGTTAAT 1620
DB 1561 AGAGAGAAAATATCTTGGAGATAAACCGCATGTTCCAAATCATATCTTTAATGTTAAT 1620

QY 1621 GCGGTGATTTGCTTGGCTATTGCGCTCAGATTATTCCTGCGGTATCAATCATAAATG 1680
DB 1621 GCGGTGATTTGCTTGGCTATTGCGCTCAGATTATTCCTGCGGTATCAATCATAAATG 1680

QY 1681 AAAAAATTTGCTCTCTTTTATTTGCTTTCTCATTTATACGCGCTGCGCGCTGCTCC 1740
DB 1681 AAAAAATTTGCTCTCTTTTATTTGCTTTCTCATTTATACGCGCTGCGCGCTGCTCC 1740

QY 1741 ATCAGAGCATGACGGGGAGTATTATCTATGCGGATTTGTCGAGACGATCAATTAACCTT 1800
DB 1741 ATCAGAGCATGACGGGGAGTATTATCTATGCGGATTTGTCGAGACGATCAATTAACCTT 1800

QY 1801 TCGCTTTTCTCTCTGTTTATATACGCAATGCGGAATCCTTCGGTGGGGGAG-AAAAA 1859
DB 1801 TCGCTTTTCTCTCTGTTTATATACGCAATGCGGAATCCTTCGGTGGGGGAGAAAAA 1860

Db 4021 GCTGAACGGCCAGCTGTTTTCTGCAGATGATACCCCTCGACTTACGCTCTGAAGCACC 4080
 Qy 4078 GGAGGATGCTTTCCGCTCTAGCGTACTGAACCGGCATTTAACTCAGCGCTTCGGGGCT 4137
 Db 4081 GGAGGATGCTTTCCGCTCTAGCGTACTGAACCGGCATTTAACTCAGCGCTTCGGGGCT 4140
 Qy 4138 TTCCAGGCTCTGGCAGTTGGCCAGCGGTGACAGCGCTGGGTTTGTAGTGTCTCTCTGA 4197
 Db 4141 TTCCAAGCTCTGGCAGTTGGCCAGCGGTGACAGCGCTGGGTTTGTAGTGTCTCTCTGA 4200
 Qy 4198 CAATAATCGCGCACTCTACCGAGTGAACCTCTGGCTGACATCCAGCACTTATCCGCTGG 4257
 Db 4201 CAATAATCGCGCACTCTACCGAGTGAACCTCTGGCTGACATCCAGCACTTATCCGCTGG 4260
 Qy 4258 TGAGCTGTCAATGTTGCTGCTCCCTCTCCCTTTTCAGGGGGTGGCCCGGCTCGCTGTC 4317
 Db 4261 TGAGCTGTCAATGTTGCTGCTCCCTCTCCCTTTTCAGGGGGTGGCCCGGCTCGCTGTC 4320
 Qy 4318 CGATAATGAGCTGACGCACTTTCTGTACAGACCAACCTGGCTCACGAGCAGGGCTG 4377
 Db 4321 CGATAATGAGCTGACGCACTTTCTGTACAGACCAACCTGGCTCACGAGCAGGGCTG 4380
 Qy 4378 GACGGTCAGCGATGTTTCTGTAGTGTGACGACGAGTACGGTACCCTGCTGACCCCGA 4437
 Db 4381 GACGGTCAGCGATGTTTCTGTAGTGTGACGACGAGTACGGTACCCTGCTGACCCCGA 4440
 Qy 4438 CATTTGAGAACCTGCTCGCTTCCCTCGCAACGCACTGTGGGGCGTGAGCTGTTCCCGA 4497
 Db 4441 CATTTGAGAACCTGCTCGCTTCCCTCGCAACGCACTGTGGGGCGTGAGCTGTTCCCGA 4500
 Qy 4498 AACGCTTCCCGCGGATGGGGCTCCCTTTATTTGCGCGCGCATCGAGCTGGAACCCACGGA 4557
 Db 4501 AACGCTTCCCGCGGATGGGGCTCCCTTTATTTGCGCGCGCATCGAGCTGGAACCCACGGA 4560
 Qy 4558 TAGCGGAAGGCGATGCTGTGATTTGGGGCGGACAGTTGAAGCCAGAGGGCTGACGCTGAC 4617
 Db 4561 TAGCGGAAGGCGATGCTGTGATTTGGGGCGGACAGTTGAAGCCAGAGGGCTGACGCTGAC 4620
 Qy 4618 GGAATTTATTTCTTTGATGATGAATCCGCCCCCAATGAGAGCGAGCGCGCCAGATGGC 4677
 Db 4621 GGAATTTATTTCTTTGATGATGAATCCGCCCCCAATGAGAGCGAGCGCGCCAGATGGC 4680
 Qy 4678 AGGTTTCTGCCAAGCCCTGTGGCACTGGCACTGATCATCCGCGAGCACCGGCTCAGCAC 4737
 Db 4681 AGGTTTCTGCCAAGCCCTGTGGCACTGGCACTGATCATCCGCGAGCACCGGCTCAGCAC 4740
 Qy 4738 GCGCGAGCTGACGCTGCTGGTACGACCGGAGCGCTTCCGACAGGATGGCACCATCT 4797
 Db 4741 GCGCGAGCTGACGCTGCTGGTACGACCGGAGCGCTTCCGACAGGATGGCACCATCT 4800
 Qy 4798 GCCCATGACCTGCGCGGCTTCGCGACATTAACCGCTTTTCATGCGCTGTTAAACCGCAG 4857
 Db 4801 GCCCATGACCTGCGCGGCTTCGCGACATTAACCGCTTTTCATGCGCTGTTAAACCGCAG 4860
 Qy 4858 CGGACGCCATGCGCGGGAGGTCTGTACCGCACTTGAGACCGGAGAACTGTCTGTCAGCCCT 4917
 Db 4861 CGGACGCCATGCGCGGGAGGTCTGTACCGCACTTGAGACCGGAGAACTGTCTGTCAGCCCT 4920
 Qy 4918 GCTGGCCCGGGCCCTGTCAAGAAATGAGCAGGATGACCGGGCCCTTGGCGAGGTGAG 4977
 Db 4921 GCTGGCCCGGGCCCTGTCAAGAAATGAGCAGGATGACCGGGCCCTTGGCGAGGTGAG 4980
 Qy 4978 GGGGGCCGGTGAACAGCAACAGCGTGTTCACCTCTGGGAAGAGGTGACAGGCTGA 5037
 Db 4981 GGGGGCCGGTGAACAGCAACAGCGTGTTCACCTCTGGGAAGAGGTGACAGGCTGA 5040
 Qy 5038 GCAGTGGCTGGACATGAGTGAACCTGTCATTAAGCCATCCGGCTGGCTAGCCCTGAT 5097
 Db 5041 GCAGTGGCTGGACATGAGTGAACCTGTCATTAAGCCATCCGGCTGGCTAGCCCTGAT 5100
 Qy 5098 TGCCCTTGAAGTACATCAATGTGTCCGATGACAGTGCACCGTTGTACAGCAGTGGCAGGT 5157
 Db 5101 TGCCCTTGAAGTACATCAATGTGTCCGATGACAGTGCACCGTTGTACAGCAGTGGCAGGT 5160

Qy 5158 GGTATCCGCTCTGCTGACGGCCGGCTGAAAGCAGCCAGAGCTCGGCGCTGCACGATTA 5217
 Db 5161 GGTATCCGCTCTGCTGACGGCCGGCTGAAAGCAGCCAGAGCTCGGCGCTGCACGATTA 5220
 Qy 5218 TCTGAGGAGGGGACACAGCAGCGCCCTTTGTGCGTATTAATCTGCGTAATCTGCGACCCGAA 5277
 Db 5221 TCTGAGGAGGGGACACAGCAGCGCCCTTTGTGCGTATTAATCTGCGTAATCTGCGACCCGAA 5280
 Qy 5278 CATGTTATCCGGGCGGATGACCTCTTCCGGTATCTGCTGCTGGATAATCAGGTGTTCAGC 5337
 Db 5281 CATGTTATCCGGGCGGATGACCTCTTCCGGTATCTGCTGCTGGATAATCAGGTGTTCAGC 5340
 Qy 5338 CAAGGTAAACCAACCCGATTTGCGAGGCAATCCGCGCATACGCTGTATATCAACCG 5397
 Db 5341 CAAGGTAAACCAACCCGATTTGCGAGGCAATCCGCGCATACGCTGTATATCAACCG 5400
 Qy 5398 GGCCTTTAACGGAATAGAACTCAGGCGCATGCGCAGAGGTGAGGGGCGTCAGTTTTTCAC 5457
 Db 5401 GGCCTTTAACGGAATAGAACTCAGGCGCATGCGCAGAGGTGAGGGGCGTCAGTTTTTCAC 5460
 Qy 5458 TGACTGGGATAGCTTCAACAAAGCTTACAGCACTTGGGGGGGCTCTCAGAGCTGTTTA 5517
 Db 5461 TGACTGGGATAGCTTCAACAAAGCTTACAGCACTTGGGGGGGCTCTCAGAGCTGTTTA 5520
 Qy 5518 CTATCCGGAATACTACCTCGACCCGCTCGTATCCGGGAGAGCCGGCATGATGAGAC 5577
 Db 5521 CTATCCGGAATACTACCTCGACCCGCTCGTATCCGGGAGAGCCGGCATGATGAGAC 5580
 Qy 5578 CTTGCTGACGTCTGTCAGCAGAGCAGTATCAACCCGATACCGTGGAGGATGCCTTTAA 5637
 Db 5581 CTTGCTGACGTCTGTCAGCAGAGCAGTATCAACCCGATACCGTGGAGGATGCCTTTAA 5640
 Qy 5638 AACCTATCTGACCAAGTTTGGAGCAGATTCGCAATCTGAACACTGTCCAGCGGATATCACGA 5697
 Db 5641 AACCTATCTGACCAAGTTTGGAGCAGATTCGCAATCTGAACACTGTCCAGCGGATATCACGA 5700
 Qy 5698 TAAACCCAGCATGAGCAGGGGACTACATGTTGTTGCTGCGCAGCATCACAGATCAGAC 5757
 Db 5701 TAAACCCAGCATGAGCAGGGGACTACATGTTGTTGCTGCGCAGCATCACAGATCAGAC 5760
 Qy 5758 TAACTGGTACTTGGCGAGCGCCCAACACAGCAAAATCCAAAGACTCAATGATCCCGCGAA 5817
 Db 5761 TAACTGGTACTTGGCGAGCGCCCAACACAGCAAAATCCAAAGACTCAATGATCCCGCGAA 5820
 Qy 5818 TGCCTGGACCGGATGGAACAAATTTAACTGCGGAATGAATCCGTGGTCAAGATCTTGTGTG 5877
 Db 5821 TGCCTGGACCGGATGGAACAAATTTAACTGCGGAATGAATCCGTGGTCAAGATCTTGTGTG 5880
 Qy 5878 CTCGGTGTTTTCAACAGTCCGCTTTATGCTGCTGGGTGGAAGAGAACTCAGTCTGCTGA 5937
 Db 5881 CTCGGTGTTTTCAACAGTCCGCTTTATGCTGCTGGGTGGAAGAGAACTCAGTCTGCTGA 5940
 Qy 5938 TACGAGGAGCAGAGCAGCAACACACGAGCAGAGCTACACGCTGAAACTGTGCTCCG 5997
 Db 5941 TACGAGGAGCAGAGCAGCAACACACGAGCAGAGCTACACGCTGAAACTGTGCTCCG 6000
 Qy 5998 GCGCTACGACGCTACATGGAGTTCCCGGTGCTTCCGATTAACCGGCAATCAGGCAATCGCAT 6057
 Db 6001 GCGCTACGACGCTACATGGAGTTCCCGGTGCTTCCGATTAACCGGCAATCAGGCAATCGCAT 6060
 Qy 6058 TCCGGAACCGCAGGGGATGATGTGACCTGTAATCCCTGACTGAGCAGCTCTATTGGCG 6117
 Db 6061 TCCGGAACCGCAGGGGATGATGTGACCTGTAATCCCTGACTGAGCAGCTCTATTGGCG 6120
 Qy 6118 GTTTTATCCCGTACACGACCGGACTTTGATAAAGCTCAGCTGATTTCTGTGATAA 6177
 Db 6121 GTTTTATCCCGTACACGACCGGACTTTGATAAAGCTCAGCTGATTTCTGTGATAA 6180
 Qy 6178 TGATATGAGCTTAAATGCTCATCTCAGATATAGGATTTTAAAGCGCTCAGTCAAGATT 6237
 Db 6181 TGATATGAGCTTAAATGCTCATCTCAGATATAGGATTTTAAAGCGCTCAGTCAAGATT 6240

Qy	10618	TTGCTGCACTACAGGGAAGTCTTTCACCTCAGTCTGCTCGAGAACGTGACACAGGTGGCT	10677
Db	10621	TTGCTGCACTACAGGGAAGTCTTTCACCTCAGTCTGCTCGAGAACGTGACACAGGTGGCT	10680
Qy	10678	TATGAGTCGGAACGGACGCTCTGCTGCTTCCGGCACCTGGCATTTGGGGTGGCAAACTTTT	10737
Db	10681	TATGAGTCGGAACGGACGCTCTGCTGCTTCCGGCACCTGGCATTTGGGGTGGCAAACTTTT	10740
Qy	10738	ACCCGCGCAGATGTGGCATCGCAGACGCGTGACGATATGGGCAAGTTGATTTGCTT	10797
Db	10741	ACCCGCGCAGATGTGGCATCGCAGACGCGTGACGATATGGGCAAGTTGATTTGCTT	10800
Qy	10798	CAACCTTATCAGCTTTAGACCTTAACGGCGAAGTGTGGTGATTCCTGTATCAGGAC	10857
Db	10801	CAACCTTATCAGCTTTAGACCTTAACGGCGAAGTGTGGTGATTCCTGTATCAGGAC	10860
Qy	10858	AGCGGTGCTGTGGTACCGTGAACCGGTACGCCAGTCCGGGGATGATCCGATGCTGTG	10917
Db	10861	AGCGGTGCTGTGGTACCGTGAACCGGTACGCCAGTCCGGGGATGATCCGATGCTGTG	10920
Qy	10918	ACTTGGGGGGCGCTCGCGCCCTCGCCGCAAAATGCCCGCTTTGCAATACAGCGGCATCCCTG	10977
Db	10921	ACTTGGGGGGCGCTCGCGCCCTCGCCGCAAAATGCCCGCTTTGCAATACAGCGGCATCCCTG	10980
Qy	10978	CGCGATCTTAATGGGGATGTGCGCTGGAGTGGGTGCTTACCGCCCCCGGTGTGGGGGG	11037
Db	10981	CGCGATCTTAATGGGGATGTGCGCTGGAGTGGGTGCTTACCGCCCCCGGTGTGGGGGG	11040
Qy	11038	ATGTATGATCGCACCCCGCGCGCACTGGTTGCATTTTCAACCCCGCTGCAGCCTTGCCC	11097
Db	11041	ATGTATGATCGCACCCCGCGCGCACTGGTTGCATTTTCAACCCCGCTGCAGCCTTGCCC	11100
Qy	11098	GTAGAATATCGCATCCAAAGCAGTCTCGCCGATATCCTTGGGGGCTGGTTAAACGGAC	11157
Db	11101	GTAGAATATCGCATCCAAAGCAGTCTCGCCGATATCCTTGGGGGCTGGTTAAACGGAC	11160
Qy	11158	ATGGTGTTATCGGGCGCGCAGTGTTCGCTCTATTTCCGGCAAAACGATGGTTGGAAT	11217
Db	11161	ATGGTGTTATCGGGCGCGCAGTGTTCGCTCTATTTCCGGCAAAACGATGGTTGGAAT	11220
Qy	11218	AAAGGGGAGACCTGCAGCAAAACGGAAGACTCACTCTCCCGTCCCGGGGTGACCCA	11277
Db	11221	AAAGGGGAGACCTGCAGCAAAACGGAAGACTCACTCTCCCGTCCCGGGGTGACCCA	11280
Qy	11278	CGTACCCCTCGTGGCGTTTCACTGATATGGTGGCAGTGGACAGCAGATTTGACGGAGGTG	11337
Db	11281	CGTACCCCTCGTGGCGTTTCACTGATATGGTGGCAGTGGACAGCAGATTTGACGGAGGTG	11340
Qy	11338	CGTGCTAAATGGAGTACGTTACTGGCAAAACCTGGGGCAACGCGTGTTCGGTCAGCCGGTG	11397
Db	11341	CGTGCTAAATGGAGTACGTTACTGGCAAAACCTGGGGCAACGCGTGTTCGGTCAGCCGGTG	11400
Qy	11398	AATATTTCCCGTTTTAGCCAGTCAGTACGTTTAAACCTGACCCAGATATGCTGGCC	11457
Db	11401	AATATTTCCCGTTTTAGCCAGTCAGTACGTTTAAACCTGACCCAGATATGCTGGCC	11460
Qy	11458	GATACCGACGGTTCCGGTACACCGGACCTGATTTATGCGATGAGTACCGGTTAGTCAAT	11517
Db	11461	GATACCGACGGTTCCGGTACACCGGACCTGATTTATGCGATGAGTACCGGTTAGTCAAT	11520
Qy	11518	TATTTCAACACAGAGTGTAAATTTTTCGGCGAGCCGATACGCTGCTTTTCGCGAAAGGT	11577
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XX Chen JS;
XX WFI; 1999-527479/44.
XX P-PSDB; AAY33728, AAY33729, AAY33730.
XX New nucleic acid from Photobacterium luminescens encoding insecticidal
XX toxins, used for making resistant transgenic plants.
XX Claim 1; Page 99-130; 148pp; English.
XX This sequence represents an approximately 38kb fragment of Photobacterium
XX luminescens DNA comprised in the plasmid pNOV2400 (NRRL B-30077). This
XX sequence contains 16 open reading frames (orfs) which encode three
XX insecticidal toxins. This sequence was isolated from a P. luminescens
XX cosmid library which had been screened for insecticidal activity. P.
XX luminescens is a member of the Enterobacteriaceae family and is a
XX symbiotic bacterium of nematodes of the genus Heterorhabditis. The
XX nematodes colonise insect larvae, kill them, and their offspring feed on
XX the dead larvae. However, the insecticidal agents are produced by P.

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CC luminescens rather than the nematodes. The toxins have activity against
CC Lepidopteran insects such as Cabbage Looper (Trichoplusia ni), European
CC Corn Borer (Ostrinia nubilalis) and Fall Armyworm (Spodoptera frugiperda)
CC and also against Coleopteran insects (e.g., Colorado Potato Beetle,
CC Leptinotarsa decimlineata). In addition the toxins are active against
CC strains resistant to known insecticides. This sequence can be used to
CC generate transgenic plants of various species that are resistant to
CC economically important insect pests and also for recombinant production
CC of toxins for use as insecticides
XX Sequence 37948 BP; 11822 A; 8637 C; 7661 G; 9828 T; 0 U; 0 Other;
SQ Query Match 12.5%; Score 2368.8; DB 2; Length 37948;
Best Local Similarity 54.0%; Pred. No. 0;
Matches 6358; Conservative 0; Mismatches 4747; Indels 671; Gaps 47;
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Db 15916 TAAACGGGAGCTGTTTAAACCTTAAAGAACCAACCGGAACAGTGTATCAGATCCCTGA 15975
QY 15354 CGTACTCGGCGCGGGAAAAAGTTGCGTGAAGAACACCGGCAACGCGGTGTTAACTCGT 15413
Db 15976 CTTATTCCGCGCGGCAAAAATACGGGAGGAACACGCGCAATGTGTGTTATCACCGAAT 16035
QY 15414 ATATTTACGAGCGGAAAAACACGCGCTGACGGGATTAAGAGGAACGTCGCTGCGG 15473
Db 16036 ACAGTTATGAACCGGAAACCAACAGCTTATCGGTACCAAAACCCACCGTCCGTAGAT- 16094
QY 15474 ACGTTCGGAGCAAAAGTGTCTGAGGACCTGCGCTATACGTATGACCGGTAGGCAAG 15533

Db 16095 -----GCCAAAGTGTTCAGAGTCTAGTTATGAGTATGACCCGGTAGGCAATG 16143
QY 15534 TACTCAGCGCTCAATTAACGATCGGAGAGACCCGCTTCTGGCGTAAACCAAGAAAGTGGTAC 15593
Db 16144 TCATCAGTATCCGTAAATGACGAGAACCCCGCTTCTGGCAATCAGAAAGTGGCGC 16203
QY 15594 CGGAGNATAGTACATCTACGACGCTGTACAGCTGTACAGCTGTGTCAGCGCCACAGGGCGTGA 15653
Db 16204 CGGAAAAACATTATACCTACGACTCCTTGTATCAGCTTATCAGCGCAACCGGCGCGGAGA 16263
QY 15654 TGGCCAAATCCCGCCAGCAGGCGCAAGACTTACCATCCGCTACAGCCCGCTTCTCTACAG 15713
Db 16264 TGGCGNATATAGGTGAGCAAAAGTAACCACTTCCTCC-----CTCACCTTCTCTG 16317
QY 15714 ACAGTCTCTCTACCAATTAACGCGCACTACCGTTATGACCGTGTGGCAACCTGA 15773
Db 16318 ATAAACAAACCTTACCACTATACCGTACTTATCTTATGACCGTGGCGGCAATTTGA 16377
QY 15774 CGCAGATGCGCCACAGTGCCTGCCAGAACAAATTAATATACGACAGACATCACGGTTA 15833
Db 16378 CTAAATCCAGCACAGTTTACC CGGCGACGCAAAACAACTACACCAAAACATCACGGTTT 16437
QY 15834 GTGACCGCAATAGGGCGGTACTGAGCACGTTGGCGGAAGTCCGTCAGATGTTGATA 15893
Db 16438 CTAAACCGAGCAATCGCGAGTACTCAGCACTCTGACCGAAGATCCGCGCAAGTAGATG 16497
QY 15894 TGCTGTTAGTGCAGAGGTCAACAGAACACTGTCAGCGCGGGGCAAGCACTGTGTGGA 15953
Db 16498 CTTTATTTGATGACGCGGACATCAGAACACCTGTATATCAGGACAAAACCTGAACTGGA 16557
QY 15954 CGCCAGTGGAGAACTGCAAAAGGTGACACCGTGTGTCGTATGGGGGGC---GGAGC 16010
Db 16558 ATACACCGCGTGAACATGACATGTCATTTGGTGAACCGGCAAGGGCGGCAATGATG 16617
QY 16011 ACAGCGAAAGCTTATCGGTATGATGGGCGAGTCAGCGTATTAATAAAACCGGACCGCG 16070
Db 16618 ATCCGGNATGGTATCGCTATAGTGTAGCGGAGAGGATATTAATAATCAATGACACG 16677
QY 16071 AAATGGGCAACAACTTCAGACACAGCGGTAGTGTACTGCGCGGGGCTGGAGTTACGTA 16130
Db 16678 AGACAGCAGCAACTCTCAAAACACAGAGAACTTATTTGCGGAGCTTAGAACTTCGTC 16737
QY 16131 TCATGCGAAATCGCGTGCAGGAAAGAAAGCTCAGCTTATACGTTGGCGGAGGCTG 16190
Db 16738 TAAACAAAACAGCAGATCAACCGAGATTTGCAAGTATCAAGTAGAGAGACGG 16797
QY 16191 GCGCGGCACAGTGGCGGTATTGCACTGGGAGATCGGCAAGCGGATGACCTCGATGAG 16250
Db 16798 GTCCGGCACAGGTACGAGTATTACATTGGGATAGCGGTCAACCGGAAGATATCGACAA 16857
QY 16251 ACTCGTGGTTTACAGTTACGATAACCTGGTGGCAGCAGCGCTGGAGCTGGACAGAG 16310
Db 16858 ATCAGTACGTTTATAGTACGATAATCTTATCGGTTCCAGTCACTTGAATTAGACAGA 16917
QY 16311 AGGGTTACCTTATAGTGGAGGAGTCTACCGGTATGGCGGAAACGCGTGTCTTGACCG 16370
Db 16918 AAGGAGAAATTAATAGTAGGAGAGTACTATCCCTATGGCGGACCGCATTTATGGGCA 16977
QY 16371 CCGCAAGTGGAGTTGAGGCTGATCAAAAACCTATCCGATCTCAGCAAGAGCGTGACG 16430
Db 16978 CAAGGAAGCGGACAGAACGAGTATATAAACCATCCGTTATTCAGTAAAGACGGGATG 17037
QY 16431 CGACGGGCTGAGTTATTAACGTTATCGGTATTAACAGCCATGGGCGGCGCTGCTCT 16490
Db 17038 CCACCGGACTATTAATTAACGTTTACCGGATATTAATCAGCTTTGGGTAGGACGATGGTTAA 17097
QY 16491 CCACGACCCCGCAGCAGCGTGGACGGCTGAACTGTTCCGCAATGGTGGCGGAAATAATC 16550
Db 17098 GTGCGGATCCGCGAGAACAGTAGATGGGTTGAAATTTATTCGGATGGTAAGGATATC 17157
QY 16551 CCGTCAACGCTGTTGA 16566
Db 17158 CGGTTACTCTGCTTGA 17173

Db 65478 GTCCGTGGCATCTCTACGGCCCTTCAAGCATCACATCTGGCAGCGCTGCATCTGATCTG 65537
Qy 8441 CTGCCCAATATTTACGGCTGGCGCTCGGGCTCCGGCTATCGGGCACTATTTAAAGCC 8500
Db 65538 GCCCCCAACATCTTGGCTTCGTGTAGTGTGGTATGGCCATTTGGGGGGCAATCGCCCAAGCC 65597
Qy 8501 ACCGCCATCGGCATCAGGTGTCTCCGATGCCACCGCATATCAGCGGACAAAATCAGC 8560
Db 65598 ACAGGTAAATGTGATGAGTTTTCGGCAGTGTCTATGAAACCCGAACGGATAAATATAGC 65657
Qy 8561 CAGTCGGAAGTATACCGCTTCGCCGGAGGAGTGGGAAATCCAGCGTATAGTGGCGAG 8620
Db 65658 CAGTCTGAAGCCTACCGTCGGCTGTCTCAGGAGTGGGAAATTCAGCGTAAATACGCGAG 65717
Qy 8621 TCTGACGTGGCGCAGATTAATGCCAGCTGGCGGCATGCGCAGTGGCGCGGAGGGCT 8680
Db 65718 ACAGAGCTGAAACAAATCGATGCTCACTTGGTTCGTGTAGTGGCGCGTGAAGCGCC 65777
Qy 8681 GAGCTGCAGAAAATTTACCTTTGAGACCCAGCAGACCCAGGCACAGCGCATTTGGCATTC 8740
Db 65778 GTGTTGGAGAAACCCAGCTGAAACGGCAACAGAACAGACTCATGCAAACTGACCTTC 65837
Qy 8741 CTCGAGAGTAAGTTCAACAAATACGGCTCTGTACAGCTGGCTCGCGGCGCAGGTTGTCCGCC 8800
Db 65838 CTACAAACATAAGTTACGAATCAAGCTTTGTACAACCTGGCTGGCTGGCTGTCCGCC 65897
Qy 8801 ATTTATACAGTTCTATGACCTGGCAGTATCCGCTGCGCTGATGCGGCAACAGGCTGG 8860
Db 65898 ATTTATCTTCAGTTCTATGATTTAAACAGTAGCTCGCTGTTTGTATGCTGAAATGGCCTAT 65957
Qy 8861 CAGTGGGATAAATTCAGAGCTAGGTC---GTTTATCCAGCCGGGGCCCTGGATGGGGCA 8917
Db 65958 CGCTGGGAGACTAACGATGCCGAGCAGCAGCTTTTATCAAGCCGGTGCCTGGCAGGAAAC 66017
Qy 8918 AATGCCGCTGTCTGGCCGGGAAACCTGATGCTGAAATCTGGCGCAGATGGAGCAGGCC 8977
Db 66018 CATGCCGCTTGTCTGGCAGGAGAAACCTTAATGCTGAATCTGGCACAATTTGGAAGACGG 66077
Qy 8978 TGCTCAGCGGGATGAGCGGCAATAGAGGTGACCGGACGCTGCTGCTGTCGGAGTTC 9037
Db 66078 CATCTGAAACAGAGACACCGCTACTGGAAGTAGAAGCTACCGCTTTCACCTGGCAAAATATC 66137
Qy 9038 TATACAGCCTCGCGGAGTATCGGCATCTCTCTGGCCGACAAAGGTGGTGGAACTGGTC 9097
Db 66138 TATAAA-----GAGAAAGTCAATTTCCCTGACTGAGAAATTCGAGAACTGATG 66188
Qy 9098 AGTAACGTTTCGGGAGTGGGGTACGAAAGCAACGGATTAACAGATGGAT-----9148
Db 66189 AAGAATAAATTAGTCACTGCCGCTAGCGGAAATAACACCTGAAGTTTGGTACCGGAAAT 66248
Qy 9149 ---CAACAGCAACTCGAGGCCCTGAAACTGGCTGACCTCGGTATCGGCACGATTAC 9205
Db 66249 GCCCAAACGCTCTGCAAGCATCCATTTGCTGTAGCTGACTACAAATTCGTACCGATTAC 66308
Qy 9206 CCGGCTCTCC-----TTGGCACCATGAGCGGCATCAACAAATAAGCGTCAAGCTCCCG 9259
Db 66309 CCAAGAAAACAGTGGAGTGGTACGTTTCGCCGGATTTAAACAGATCATGTCTACCCCTGCCA 66368
Qy 9260 GCGCTGGTCGGCCCTTATCAGGACGTCGCTGGCGGTTCTCAGCTACCGCGGAAAGTATG---9316
Db 66369 GCACTGTTAGTGTCCCTATCAGGATGTGCAGGCGATTTCTGTCTTACAGCGGAGATGTCACT 66428
Qy 9317 GTCATGCCCGGGTTGCAGCGCTGGCGGTCTCACCGGATGAACGACGCGCCAA 9376
Db 66429 GGATGGCTGAAAGTTGCAAAATCGTTGGCGGTTTCTCATGGGATGAATGACAGCGGCCAG 66488
Qy 9377 TTCCAACTGGATTTCAATGACCCGCGTTACCTCGCGTTTGAAGGACTTCCAGTTGATGAC 9436
Db 66489 TTCCAACTGGATTTCAACGATGCAAAATTCCTGCCAATTTGAAGGAATCGACATTTGAT---66545
Qy 9437 ACAGGACCCCTGACACTGAGCTTCCCGGATGC-----TGACGGCAAA 9478

Db 66546 AAAGGTACGCTGACATGAGCTTCCAAATGCAATTTGGTGAAGAGCAAGAAAGCAAA 66605
Qy 9479 CAACAGGCGATGCTCTCAGTCTGAGCGACATCATCTCGCATATCGGTTACACCAATTATC 9538
Db 66606 CAAAACCAATGCTGGAGAGTCTAAGCGACATCATTTCTGCATATTCTGCTACCACTTCGC 66665
Qy 9539 AGCTGATAGTATCAACATAGCGCA---GGCCCCCGAAGAGGGGCTTCGAGGAGACTG 9594
Db 66666 CAATAACGATTTCAATTAAGTCTAAACAGGCGCTTAATGGGCTCTCAAGGAGTCT- 66724
Qy 9595 AGCATGCAAAATCATCAAGCATGCGCATTTACTGCCCCCAGCTTGTCTTCGCGGGCGGT 9654
Db 66725 TTCTGCAAAATTTCAAGATTTTAGTATTAAGAACTATCATTTGCCAAAGAGGAGGCG 66784
Qy 9655 GCGGTACCGGGCTCAAGGGTGTATTCGCGGCGGACAGGCGGATGCTGGGCGACCTG 9714
Db 66785 GGTATACGCGGAATGGGGGAAGCGTTAACCCCCCGCGGACCGATGTTATGCGCGCTA 66844
Qy 9715 AGTATTTCCCTTCCGCTTACGCCCGGTGAGCGCGGTACGCCCCCACTGGGGCACTTAATTTAT 9774
Db 66845 TCTCTACCATTAATCTATTTCTGCGGGCGGGTATGCCCCGCTCACTCGCTTAACTAC 66904
Qy 9775 CACAGCGGTTCGGGAAACGGCCCCCTTTGGCATTTGGCTGGGGTATCGCGGTGCTGTC 9834
Db 66905 AACAGCGGTCCCGTAACACTCCATTTGGTCTGGGTGGGATTGCAACGTTATGACCATC 66964
Qy 9835 CAGCGTCTGACGCGCAACGGAGCACTTACGATGATGATGATGATGATGATGATGATGATG 9894
Db 66965 CCGCGCGGACCCATTTTGGTGTCCCCCATTAACGAACCGATACCTTTCTTGGGCGG 67024
Qy 9895 GACGCTGAGGTCTGTGTCGGCACTACGCGTGTGGCACCACCAAGAACGCGGAGGCC 9954
Db 67025 GAAGCGAAGTACTGT-----AGTCGCGGATCAACCGGTGATGAA 67066
Qy 9955 ACTCACTACTGGGATAAACCCAGCGGAAAGCTTCAAGTTCAAGTTTACGTTTACGTTAC 10014
Db 67067 TCGCATTTACAGGTATCAACCTAGCGCTACTTTTACCGGTTACCGGATACGCTTCCCT 67126
Qy 10015 ACAGGAGGTAGTCTCAGCGCTTTCAGCGTTCGCTGCGCGCGGACGAGACAGAAACG 10074
Db 67127 CTGGAAGTCAATTCAGCGGATTTGGAATTTGGAGCCCAACAGCAACAGGCAAAACAG 67186
Qy 10075 TTTTGGGTGTTATATACCCCTGACGAGAGGTGGTCTGCTGGCGGAAATCGCAGGCT 10134
Db 67187 TTTTGGTGTATATAGCCAGATGGCAGGTACATTTATTGGTAAATCACCGCAAGCA 67246
Qy 10135 CGCATCAGCAACCCACAGCCCAACACAGCGGGGTTGGCTGATGAGTCTCGGTA 10194
Db 67247 CGGATCAGCAACCCATCCAAACGACACAAACAGCAACATGGTTGCTGGAAGCTTCTG 67306
Qy 10195 TCACCTTACCGGGAACAGATGTTTACCAATACCGTGGGGAAGATGATGACGTTGTCGAC 10254
Db 67307 TCACCAATGTTGGAGCAATTTATTCAGTACCGGCGGGAAGATACTTAGATTGTGAA 67366
Qy 10255 GAGGCGGAGCGGACCGCACCCGAGCGCGCGCCCAACGTTATCCGCTGGCGGTCTCG 10314
Db 67367 ACTAATGAAATTAACGCTCCATCCAGGSCCAGACACAGCTTATTACATATAGTAT 67426
Qy 10315 TATGTTAACCGTACGCGGCTCGGACGCTACCGGCGCTG---GTGTCGACACATCAATG 10371
Db 67427 TACGGCAACCGGACCGCAGCGAAACGTTTACCGGCTGTAATGGTGGCGCCCATCACAA 67486
Qy 10372 GATAGTGGCTGTTTATCTGTTGTTTATGTTATGTTAGCTGAGCTCGGTGCTGTCGAA 10431
Db 67487 GCAGTGTGTTTCTTACCTGTTATTTGATTAAGGGAACGAGTAAACCTCTGAAATG 67546
Qy 10432 GCGCGCGCTGCAACACACAGGAAGTGGGAGTGGCTGTGTGTGTCAGGATTTGTTTCC 10491
Db 67547 CCACGAGC-----ATTTACAGCAACGGGTAACTGGCTTGTGTCGACGACCGGTTTCC 67600
Qy 10492 GGGTATGAGTTTGGTTTAACTCGGACTCGCGCTGTCGGCTGAGGTTTGTGTTTC 10551
Db 67601 CGTTATGAATATGGCTTTGCAATTACGTTACTCGCCGCTTATGCGCTGAGTACTGATG 67660

QY	7364	GTGTTCCAGCGGTTGTTGTCAGGAAACAGCACTTCCCGGAAGCCACCGCGTGGCTGCAGTAT	7423	8441	CTGCCCAATAATTTACGGCTGGCGCTCGGGGGCTCCCGCTATCGGGCACTATTTAAAGCC	8500
DB	34153	ATTGCTCAGCGTTTGTCTGACGAACAACAACTTCGATGAAGCTAAACCGTTGGCTGAAATAT	34094	33088	GCCCCCAACATCTTTTGGCTTCGTGTATGGTGTAGCCATTTGGGGGGCAATTCGCCCAAGCC	33029
QY	7424	GTCTGNAACCCGCGCGGGGACGTGTAAACGGGGTCTCGAGAT---	7430	8501	ACCGCCATCGCATCCAGGTGTCTCTCGATGCCACCGCATATCAGCGGACAAATCAGC	8560
DB	34093	GTCTGGAACCCATCAGGCCATATGTCACATATGTTCAAAAGCAGTATCCCCACACTTGGAT	34034	33028	ACAGGTAAATCATGTGAGTTTTCGCCAGTGTCTATGAACACCGAAGCGGATATAATATGAC	32969
QY	7481	GTCCGTCCGCTGGAGAGGACACCGCTGGAACGACTCGCCGCTGGACTCCATTTGACCCC	7540	8561	CAGTCGGAAGTGTATCCCGCGTFCGCGGGAGAGTGGGAAATTCAGACGTGTATGTGCCAG	8620
DB	34033	GTTCGCCCATTAACAGAGGACACAGTTGGAACGATCCGTTGGGTTCAITGATCCC	33974	32968	CAGTCGAAGCTTACCGCTCGCGGTCTCAGAGAGTGGGAAATTCAGCGTAAATAACCGCCGAG	32909
QY	7541	GATGCAATAGCCAGTACGACCCCATGCAATTAACAGGTGCGCCACCTTTATGTCTGACCTC	7600	8621	TCTGACGTGGCGCAGATTGATCCCGACGTGCGGCCCATGCGAGTGCGCCGGGAAGGGCT	8680
DB	33973	GATGCCATAGCGCAATATGATCCAAATGCACTACAAAGTCGCTTCTTTATGCGCACCTTT	33914	32908	ACAGAGCTGAACAAATCGATGCTCAACTTGGTTCGTGTGTAGTGCGCCGTGAAGCCGCC	32849
QY	7601	GACCTGCTGATTCGCCCGGTGATGCGCTACCGCGTCTCGAGCGGACACCTTTAAC	7660	8681	GAGCTGCAGAAAACTTACCTTTGAGACCCAGCAGACCAGGCACAGCGCGCAGTTGGCAATTC	8740
DB	33913	GATCTGTTGATCGAACAGGAGATTACGCTCTATCGCAATTTGAGCGGACACACTCGCC	33854	32848	GTGTTGCAAAAAACCCAGCTGAAAAACGAAACAGGAACAGACTCATGCACAACTGACCTTC	32789
QY	7661	GAGGCCGAGTGTGTAGCTGCAGGCCCTGAACTTCTTGGGCGACGAGCCCTATATTTCC	7720	8741	CTGCAGAGTAAGTTCAACNATACGGCTCTGTACAGCTGCGTGGGGCAGGTTGTCCGCC	8800
DB	33853	GAAGCCAAATGTGTATATGCAAGCATTTGCATCTCTTGGGTGATAAACCTCATTTATCA	33794	32788	CTACAAACATAAGTTTCAAGCTTTGTACAACTTGGCTGCGTGTGCGCTGCTCCGCC	32729
QY	7721	TTTGACCGCACTGGTCGGCGTTGACCCCTGGGTGACGACGACGAGTGTACGACGC	7780	8801	ATTTATTACCAAGTTCTATGACCTGGCAGTATCCCGCTGCCTGTATGGCGCAACAGGCCCTGG	8860
DB	33793	CTCAGTTCAACATGGAATGATTCAGAACTAGAAAGCCCGCAGATCTTGAGAAAAAAG	33734	32728	ATTTACTTCCAGTTCTATGATTTAAACAGTAGCTCGCTGTTGATGGCTGAAATGGCCTAT	32669
QY	7781	GATTACCAAGAGGCCCTGCTGGCGGTGCGCGGTGTGGTGCCTCCCGACACAGGAGC	7840	8861	CAGTGGGATAAATTCGAGACTAGGTG---GTTTATCCAGCGGGGGCTGTATGGGGCA	8917
DB	33733	ACATATCCAAAGCAGTAGCAGATTTACGACAGGCCAGTCT-----TACA	33689	32668	CGCTGGGAGACTAAACGATGCGCGACGACGCTTTATCAAGCCCGGTGCTGGCAGGAAACC	32609
QY	7841	CGCAATTCCTGACGGCACTGTTCTCCCGCAGCAGAACGAGGTGCTCAAGGCTACTGG	7900	8918	AATCGCGTCTGCTGGCGGGGAAACCTGATGCTGAATCTGGCGCAGATGGAGCAGCGCC	8977
DB	33688	GGTGGAAAGCAACACAGATCTTTTCTGCGCACAGGTCAATGAAGTGTGTGAGCTATTGG	33629	32608	CATGCCGTTTCTGCGCAGGAGAAACCTTAATGTGTAATCTGGCAAAATGGAAGACGCG	32549
QY	7901	CAAACTTTGGCAGCGGCTCCATAACCTTCGCGCACAACTCTCCATTCAGCGCAGCGC	7960	8978	TGCTGACCGGGGATGACGCGGCAATAGAGTACGCGGACGCTGCTGCTGCGGAGGTC	9037
DB	33628	CAGAACTGNAACACGCTGTATTAACCTGCGGCNTAACCTCTCTATTGATGTCAACT	33569	32548	CATCTGAAACAGGACACGCGTACTTGAAGTAGAAAGCTACCGTTTCACTGGCAAAATATC	32489
QY	7961	CTTTCCCTGTCCGTCTACGCGACGCGCTCGAAACCGTCCGCCCTGCAGAGTGCCTGCTC	8020	9038	TATACCGCTCTCGGAGGATGCGGCATTTCTCTGCGCCGACAGGTGGTGGAACTCGTC	9097
DB	33568	TTACATTGCTATTTTCGAAACACCAACAGCGCATCCAAAAGCGTGTCTACGCGCGCTGC	33509	32488	TATATA-----GAGAAAGGTCAATTTTCCCTGACTGAGAAATTTGCNAGAACTGATG	32438
QY	8021	AACAGCGCAGGGTGTGCAGCACTCCGCGCGCGGTGATGCGCTTTTACGTTTCCCG	8080	9098	AGTAACGGTTCCGGCAGTGCGGGTACGAAAAGCAACCGATTTACAGATGGAT-----	9148
DB	33508	GCCAGTTCAACAGGTGGAATAATCTTCCGTGACGGTTTATATCAGTTTGGCGTTCCCA	33449	32437	AAGATAAATTAGTCACTTCCCGTAGCGGAAATAACACCCCTGAAGTTTGTGTACCGGAAAT	32378
QY	8081	GTCACTGTGGAGAACCGCCGGGGATGTTGAGCTGTGACCGGGTTCCGCAACACACTG	8140	9149	---GAAACGCAACTCGAGGCCACCTTGAAACTGCTGACCTCGGTATCGGCAACGATTAC	9205
DB	33448	CACATGTGGAAACCGCCGAGTATGTTGTCAGTCAACTCACTCCAAATTTGGCTCCAGTTA	33389	32377	GCCCAACGCTCTCTGCAAGCATTCATTTCTGTTAGTGTACTTACAAATTCGTCAGATTAC	32318
QY	8141	CTCGTATTACGAGCTCAGGATGCGAGCGCGTGCCTGAACTGCTGACAGCCAGGGC	8200	9206	CCGCTCTCCC-----TTGGCAACATAGGCGCATCAAAACAAATAAGCGTCACTCCCG	9259
DB	33388	CAAAATATATTGAAACGTCAAGGATGCGGAGGCAATTAACACGCTGTTTGCAGAAATCAGGG	33329	32317	CCAGAAAAACAGTGGAGTCCGTTAAAGTTCCGCCGATTTAAACAGATCAGTGTCACTTGCCA	32258
QY	8201	AGTGAATGTATACGCCAGGGCTTTGCGCAGCAGGATTAACCTCTCGAGGAAATCGATGCG	8260	9260	GCGCTGTGCGCCCTTATCAGGACGTCCGTGCGGTTCTCAGCTACGCGCGGAAGTATG---	9316
DB	33328	GCGGAACTGGTATTGACCAATCTCAGCATACAGGACAAACCAATTGAAGCTGGATGTT	33269	32257	GCACCTGTTAGTCCCTATCAGGATGTGAGGCGATTTCTGTCTTACGCGGAGATGTCACT	32198
QY	8261	GATATTGCGCCCTTGAGAGAGAGCCGCGCGCGCGAGATGCGTTTGAAGCTTACAA	8320	9317	GTCAATGCCCCGGGTTGACGCGCTGCGCGTCTCACACGGAATTAACACAGCGGGCCAA	9376
DB	33268	GAAAAAATGTGCTAGAAAAAACCGCGCGCGGGCCCAATCACGTTTGTATAGCTACAGC	33209	32197	GAATTTGGCTGAAAGTTGCAATCTGTTGGCGTTTCTCATGGATGAATGACAGCGGCCAG	32138
QY	8321	GTGTTGTACGAGGGCGCTCAACACCGCGGAAAAACAGCGCATGGAATTTGTACCTCAGT	8380	9377	TTTCCAACTGGATTTCAATGACCCCGTTTACTGCGGTTTGAAGGACTTCCAGTTGATGAC	9436
DB	33208	AAATTTCTAATGAAGACATCAACGAGGTGAAAAACAGGCAATGGCTTTCGAGCTCC	33149	32137	TTTCCAACTGGATTTCAACGATGGCAAAATTCCTGCTCATTTGAAGGAATCGACATTGAT---	32081
QY						

Db	32020	CAAAAAACCATGCTGGAGAGTCTAAGCGACATCATTTCTGCATATTCCTACACCATTCGC	31961
Qy	9539	AGCTGATAGTATCAACATAGCGCA-----GGCCCCGAACGAGGGCTCGGAGGACTG	9594
Db	31960	CAATAACGATTTCAATTAAGTGCTAAACAGGCCCCCTAAATGGGGCTCGCAAGAGTCT-	31902
Qy	9595	AGCATGCAAAATCATCAAGACATGGCCATTTACTCCCCCACCAGTTTGCCTTCGGGGGGCGT	9654
Db	31901	TTCAATGCAAAATTCACAAAGATTTTAGTATTACAGAACTATCATTTGCCAAAGAGGAGGC	31842
Qy	9655	GGGTCACCGGGCTCAAGGGTGATATCGCGCGGCGAGGGCGGATGTGGCGGACCCCTG	9714
Db	31841	GCTATCACGGGAATGGGGGAGCGCTTAACCCCCCGCGGACCGGATGTATGGCGCGCTA	31782
Qy	9715	AGTATTCCTTTGCCGGTTAGCCCCGGTCGGGGTTACGCCCCCACTGGGGGACATTAATAT	9774
Db	31781	TCCTCAATTAACCTATTCTCGCGGGCGGGTTATCCCCCGTCACTCGCCCTTAAACTAC	31722
Qy	9775	CACAGCCGGTCGGGGAACGGCCCCCTTTGGCAITTTGGCTGGGGTATCGGGCGTGTCTGTGTC	9834
Db	31721	AACAGCGGTGCCGTACACTCCATTTGGTCTGGTTGGATTGCCAACGTTATGACCATC	31662
Qy	9835	CAGGTCGTACGGCGAACGGAGCACCTACCTACGATGATCTGATGAATTCACCGTCCG	9894
Db	31661	CGCGCGCACCCATTTTGGTGTCCCCCATTTATAACGAAACCGATACTTTCTTGGGCGC	31602
Qy	9895	GAGGTCAGGTGCTGTGGCGGCACTCACGGCTCTGGCACCCCAAGAGCACGGCAGGCC	9954
Db	31601	GAGGCGAAGTACTGTGT-----AGTCGCGGATCAACCGCGTGATGAA	31560
Qy	9955	ACCTCACTACTGGGGATAAACCCAGCGGAAGCTTCAACGTTACAGGTTTACCCTGTACAGT	10014
Db	31559	TCGACATTCAGGGTATCACTTAGCGCTACCTTACCGTTACCGGATACCGTTCCCGT	31500
Qy	10015	ACGAGAGGTAGTCTACCGCGCTTGACGCTTGGCTGCCCCCGGACGAGACAGAAACGAA	10074
Db	31499	CTGGAAAGTCATTTACGCCGATTTGGAAATATGGCAGCCCCAAGACAAACAGGCAAAACAGAT	31440
Qy	10075	TTTTGGGTGTATATACCCCTGACGACAGGTGCTCTGCTGGCGCCGAAATGCGCAGCT	10134
Db	31439	TTTTGGCTGATATATAGCCAGATGGCGAGTACATTTATGGGTAAATCACCAGCAAGCA	31380
Qy	10135	CGATCAGCAACCCACAGCGCCCAACACACAGCGCGGTTTGGCTGATGGAGTCTCTCGGTA	10194
Db	31379	CGGTCAGCAACCCATCCCAACGACACAAACAGCACAAATGGTTGCTGGAGCTTCTGTA	31320
Qy	10195	TCATTTACCGGCGAACAGATGTATTACCAATACCGTCGGGAAGATGATGACGTTGTGAC	10254
Db	31319	TCACCATAGTGGTAGCAAAATTTATATCAAGTACCGGCGCAAGATACTTTAGATTGTGA	31260
Qy	10255	GAGGCGAGCGGACGCGCAACCGCGAGCTACCGCGCTG---GTGTCGACACCATCAATG	10314
Db	31259	ACTAATGAATATAGCTTCCATCCACAGGCCACAGCAACGTTATTACATATAGTGTAT	31200
Qy	10315	TATGGTAAACCGTCAGGCGGCTCGAGCCTACCGCGCTG---GTGTCGACACCATCAATG	10371
Db	31199	TACGGCAACCGGACAGCGGAAACGTTACCCGGTCTGAATGGTCGCGCCCATCACAA	31140
Qy	10372	GATAGCTGGCTGTTTATCTGGTGTGTGATTTATGGTGAGCGTACGTCGTCGTCTGTA	10431
Db	31139	GCAGACTGGTTGTTCTACCTGGTATTGATTATCGGCGAAGCGAGTAACACCTGAAATG	31080
Qy	10432	GCSCCGCTGGCAACACAGGAGTGGGGAGTGGCTGTGTCGTCAGGATGTTTTC	10491
Db	31079	CCACCAGC-----ATTTCAGCAACCGGGTAACTGGGCTTTGTCGTCAGGACCGTTTTC	31026
Qy	10492	GGGTATCAGTTTGGTTTTTAACCTCGCGACTCGCGCCTGTGGCTGAGGTTTGTGATCTTC	10551
Db	31025	CGTTATGAAATATGGCTTTGATACGTACTCTGCGGCTTATGCGCTCAGATCTGATGAT	30966
Qy	10552	CATTACCTAGGTGTCTGGCGGGAGTTCCGGAGCGGAATGATCGCCAGCATTTGATTTCT	10611
Db	30965	CACTGCTGCAAGCGCTGGATAATAAGATAAAAGAACACAAACGCAACCAACGCTGGTTTCA	30906
Qy	10612	CGCTGCTGCTGACTACAGGGAAGTCTTCTACTCAGTCTGCTCGAGAACGTCACACGAG	10671
Db	30905	CGCTGATACTCAATTTATGAAGAAAGCGCAATCGCCAGCACGCTGGTATTCTGTCGTCGA	30846
Qy	10672	GTGGCTTATAGTTCGAGCGGACGCTTTGTGCTTCCGCACTGGCGCACTGGCATTTGGGGTGGCAA	10731
Db	30845	GTAGGACATGAGCAAGCGGTACTGCGGTACCTGCCACCATTAGAATTTGGGCTATCAA	30786
Qy	10732	ACCTTTACCCCGCCGACATTTGTCCGCAATGGCAGACGCGTGACGATATGGGCAAGTTGAGT	10791
Db	30785	GATTTTTCACCGCAACATAACTGACTGGCAACCGATGATGTGTGGCAAACTTCAAT	30726
Qy	10792	TTGCTTCAACCCCTATCAGCTTTAGACCTTAAACGCGAGAGGTGTGTGGGTATCTCTGAT	10851
Db	30725	GCAATTCAGCGCTGGCAGCTAGTTCGATCTAAAGGCGAAGGATTACCCGCGCTGCTATAT	30666
Qy	10852	CAGACAGCGGTGCTTGTGGTACCGGTGAACCGGTACCGCAGTCGGGGGATGATCCGGAT	10911
Db	30665	CAGGATAAAACCGCTTGTGGTACCGTTCGACACAGGCTCGGGTGAATTTGGCTCAGAT	30606
Qy	10912	GCTGTGACCTGGGGGGCGCTCGGCGCTGCCGACAAATGCCCGCTTTGCAATAACAGCGGC	10971
Db	30605	ACCGTCACTTTGGGAAAAAATACAGCCCTTTGTCTGTATTCCTTCTTGCAGAACGACGCC	30546
Qy	10972	ATCTCGCGGATCTTAATGGGATGCTCGGCTGGAGTGGGTGCTTACCGCCCCCGGTGTG	11031
Db	30545	TCGCTGGTGATATCAACGAGAGACGGCAACTTGTATGGGTATATCACCGGACCGGGATTA	30486
Qy	11032	CGGGGATGTATGATCGCACCCCGCGCGCACTGGTGTGATTTTCAACCCCTGTTCAGCC	11091
Db	30485	CGGGGATATCATAGTCAACGTCAGATGGCAGTTGGACAGGTTTATACCCCACTCAATGCT	30426
Qy	11092	TTGCCGCTAGATATCGGCAATCCAAAGCAGTCTCGCCGATATCTTGGGGCTGGGTTA	11151
Db	30425	CTGCCGCTGAAATATATCTCATCCAGTGGCGCACTCGCCGATTTAATATGGGAGCGGGCTC	30366
Qy	11152	ACGGACATGGTCTTATCGGCGCGCGAGTGTTCGCTCTATTCGCGCAAAACGATGCT	11211
Db	30365	TCGTATTTAGTGTGATGGCGCTTAATAGTGTGCTTTATATGCCAATATCTCGTGACGGC	30306
Qy	11212	TGGAATAAAGGGGAGACCGTGCAGCAAAACGGAAGACTCACTCTGCGGCTCCCGGGGCTT	11271
Db	30305	TTGCCCAAGGAAAAAGATGTGGTGCAATCCGGTGATGTCAOGTGCAGTACCGGGTGCC	30246
Qy	11272	GACCCAGTACCTCTGTGGGTTTCACTGATATGGCTGGGAGTGGACAGCAGATTTGACG	11331
Db	30245	GATCCGCTAAGCTGGTGGGCTTTAGTGTATGTATTGGGTTCCGCTCAGGCACATCTGTT	30186
Qy	11332	GAGGTCGTGCTAATCGAGTACGTTACTGCGCAAAACCTGGGCGACGCTCGTTTCGGTCAG	11391
Db	30185	GAGTGAGGCGCAACTAAAGTCACTGCTGGCTTAATCTGGGGCATGGACGCTTTTGGTCAA	30126
Qy	11392	CCGGTCAATATTTCCCGTTTTAGCCAGTCACTGACTACGTTTAAACCTGCACCAAGATTTG	11451
Db	30125	CCCATTTACCTTCGCGGATTCAGCCAGCCAGAGGCTATATTAAACCGGCTCAAGTTAT	30066
Qy	11452	CTGGCGGATACCGAGCGGTTCCGGTACACGAGCTGATTTATGCGATGATGACCGGTTA	11511
Db	30065	CTGGCGGATCTGATGGCAGCGGCCCAAGCGGATCTGATTTATGTTTACACCAACCGCTC	30006
Qy	11512	GTCAATTTATCAACAGAGTGTATTTATTTTCGCGGACCGCATACGCTGCTTTCGCG	11571
Db	30005	GACATCTTCTGAATAAAGTGGCAACCGGTTTTCGCGCACCGATGATATTCGCTTCCCA	29946
Qy	11572	AAAGTGTGCGCTATGATCGCACCTCAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGG	11631
Db	29945	GAAGGCTTGGTTTGGACCATACCTGTGATGATGAGTGGCGGATATACAAAGGGTAGGT	29886
Qy	11632	GTGCCGTAGCTGTACTGAGGTCGCCCATGTCCGCCCTCATCATCTGGGTGTGCCATTTA	11691
Db	29885	GTGCCAGGCTGATACTGAGCGTGCCACATATGACCCCCCATCTCACTGGCGCTTGTGATCTA	29826

QY	11692	TGGCAGACAAACCCCTGGTGTGTAATGATGCATGAACAAACAATATGGGGCCCGGATGCA	11751	12766	GGTCAGCAGCAAGTCTGGTATCTGATTCACAAGACGTTGGCCACCGTGGCTCCGGCA	12825	
DB	29825	ACACGCGCAAAACCGGTGTTACTACGGAATGAACAAACAATATGGGAGCCCAACACACC	29766	DB	28754	GGCAGAAAAAACAATTTATACCAATGGGAAAATATGAGCCGATTCACAAACGCCAAGC	28695
QY	11752	CTGCATATCGCAGTTCGGTGCAGTTCCTGGCTGGATGAGAAAAGCCGAGCACTGGCGGCA	11811	QY	12826	CTCCCCCCCAAGGTAGCTTTTATCGAAAACGGCGTGTGGATGAGGGGTATGGTCAATTCA	12885
DB	29765	TTGGCTTACCGAGTTCCTCCAGTTCCTGGCTGGATGAGAAAAGCCGCGCACTGGTTGCC	29706	DB	28694	CGACAAGCGCTAGTTGGCTTTACCGAGACAACGGTATTTAGTCAATCCACACTATCAGCG	28635
QY	11812	GGCAGTTCCTCCCTGCTGCTACCTGCAATTTACATGTCATACCTGTGGGTTCGGTGGTG	11871	QY	12886	CTGGCTGCTCTACATTTGTGGATGAACAT-----CTCGAGCAAGCCGGTTACCGG	12933
DB	29705	GGACAAACACCGGTTTGTATCTCCCTTCCCGGTACACACCTATGGCAACCGAAACA	29646	DB	28634	TTTGATGGGAGCATCCCACTGCTCAATTTGTCAACGACGCTGGAAACAAGCCGGATACCAA	28575
QY	11872	CAGGATGAGATCACCGGTAAACGCTGTGGTCAGCGAGCTGCTTTATCGCCACCGCTCTGG	11931	QY	12934	CAATCCGGATACCTTTTCCCTCGAGCGAGGGAAGCAGAACAGCAATTTGTGACCCAGTGT	12993
DB	29645	GCGGATGAATCAGCGGCAACAAATTAGTCAACAACACTGCGTTATGCTCGTGGCGCTTGG	29586	DB	28574	CAAAACAATTATCTATTTCTCGCAC-----GGAGAAGATAAATCTGGGTAGCTCAT	28521
QY	11932	GACGGCAGGAACCGCAGTTCGGGGGTTTGGGTTTGTGAGATCAGGAGTACCGATACC	11991	QY	12994	CAGGATATGTTTACCTATGCGCGGCGCAGAGCAATTTCTGGTACCCTATCTTTCTGGGAC	13053
DB	29585	GATGGGGTGAACGGGAATTTCCGGATTTGGTTATGTTGAGCAGACAGACAGCCATCAA	29526	DB	28520	CATGGTTATACCGATTACGGTACAGCCGACAGTTCTGGCGCCGCAAAAACAGAGCAAC	28461
QY	11992	TTGGCAAGCGAGGTACGGGACGGAACTGAGTATGCTTCTGTGTGAGCCGGAACCTGGTAT	12051	QY	13054	AGTATGTTGACCGGCCCACTTACCGTACGCGTGAACGCTGACGCTGATCGTCTCATCGCAG	13113
DB	29525	CTGGC---CCAGGCAACCGGTGAGAACGCCACCCACCGCGATGACCAAAAACCTGGTAT	29469	DB	28460	ACCCAACTCACGGGCAAAATTACACTCTTGGGATGCAACTATTTGGTGTGTACACAA	28401
QY	12052	GCCACCGGGTACCGGCTAGACGAGCGTCTGCCGGAGACGTATTTGGCAAAAACGATGCC	12111	QY	13114	TGGCAGGATGCCGAGGATTTGTACACAGCCGACTATGACTGGCGCTTCTCTGACGCC	13173
DB	29468	GCCACCGGGTACCGGTATAGATAACAATATCAACAGAGATTTGGGTGTGTATAT	29409	DB	28400	ACCCGAGATGCTGCTGGGCTGACAACTCAGCAATATGACTGGCGTTTCTGACCCCT	28341
QY	12112	GCCGCTTTTGGCCATTTCCGACCCGTTTCACTGTGCTGTTTTCAGGAGAGGATGACGAGCA	12171	QY	13174	GTCCGGGTGACGGACCCCAATGATTAATCTGCACTGCTGCTCTCTGATGCTCTGGGCCGG	13233
DB	29408	CAGGCTTTTGGCGTTTTCACCACGCTTTACGACTTGGCAAGATGCAAGATATCTG	29349	DB	28340	GTGCAACTCACAGATATCAATGACAATCAGCACCTTATCATGCTGGATGCACTGGGCCGG	28281
QY	12172	TATACTCCG---GACGACAGCAAGACATTTCTGTTGAGGAGCCCTGAAAGCATCTCG	12228	QY	13234	GTGACCCCTCGGATTTCTGGGGCACGGAGATGTTATTTGCCACCGTTTACAGT-----	13287
DB	29348	TTAACACCGGAAGATATACAGCCAGTATTTGCTTAAACCGGGCACTGAAAGGTCAACTG	29289	DB	28280	CCAACTCACACTCGCTTTTGGGAACTGAAACGCAAGATGACCGTTACTTCTCACCG	28221
QY	12229	CTCGCAGTGAAGTTATACGGTCCGATGGCAGCAGCCAGCCGATATCTCTTACACGCTC	12288	QY	13288	---GATGCCACGTTGCTCGTTCCGGACGGCGCAGACGCGCTCTGCGGTTGACGGCGCC	13344
DB	29288	CTAGTATGAGTGTACGGATTGGACGACAGTACAATAAACAACAGCTTCCCTATCTGTC	29229	DB	28220	GAAAAGCACCGTTTTCTCCACCGTCCGATGTGAATCCGCTATTGAGTTAAAAAACCG	28161
QY	12289	ACTGAGTCTCGCCCGCAGGTACGGC---TAGTTGAAGCGAATGAGACTACCGGTGGTG	12345	QY	13345	CTACAGTAGACAGTGTCTGTTATGTCACGGACAGTGGGGAGATGACGACATGAG	13404
DB	29228	ACTGAATTTCTGTCACAGGTACGTCGATTACAGCAGCAGATAAACCAATACCGGTACTT	29169	DB	28160	CTCCCTGTAGCAGAGTCAAGTTTACGCCACCAAGCTGGATGCGCAGTATTAAGTCAG	28101
QY	12346	TGSCCGATGGCGGGAAGCGTACGTAGTTTGAACGGTACCAATGATGATCTCAA	12405	QY	13405	AAAAATGCCCCCGCACGTTGCTGCTGCTACCGTACCGTATGACAGT---GATACCCG	13460
DB	29168	TGCTCATCTGTAGTTGAAGCCGACGTATCATTTACGAGCGTATCGCCAGCGACCCACAA	29109	DB	28100	AAAGCCCTCAATAGGCTGSCAGCAAGATCCGCCAAAAGTTATACAATACCCGATCATC	28041
QY	12406	TGCCAACAGCAGCGGTACTCCTCAGTGAATGATACGGTTTCCACTGCGTCAGTCAGT	12465	QY	13461	ACAGCAGGTCCGCCAACAGGTGACATTCAGTGACCGTGGGCTGGGCTGAGTTGGAATCGGC	13520
DB	29108	TGCAGCCAGATATTACGCTATCAGTGATCTATTGGCCCAACCGCTAAACAGGTTTCG	29049	DB	28040	ACCGAAGACGGCGCATATGTACTGGCTATCGCCACTGCTCAAAAAGTCAAAAAGGCA	27981
QY	12466	GTCAATTTATCCAGACGCCCTCCGTCCGGCGGAACAATCCATATCCGGCGTCTTTACCGGG	12525	QY	13521	AAACCGGAGCGGAGGGCAACGCTTGCAACAGGACGGACGGCAACACTGGTGAACGGC	13580
DB	29048	GTACAGTATCCAGCCGAAAAGCAACAGCAATCAGTCCGTTATCTGTATACGCTGCTGAT	28989	DB	27980	ACCCC-----TCAACTACTAGCTGTTTAAACAACGGGCCCACTTTACCCCTCACAGC	27927
QY	12526	ACGCTGTTCCCAACAGTTATGACGAGCAGCAGCAGATATTACGCTGGGGTTGCAACAG	12585	QY	13581	CAGTGACGGAATTCGCGTCACTGTAGCAACGAATTTCCCTGGGCGGTCAACGGGAGGCG	13640
DB	28988	GAATTTGTAGCCAACAGCTATGATGAACAGCAACGCAATTTACGGTCACTTATCAACAA	28929	DB	27926	CTCAATTCACCTACCGATCGTTATGATCAGATCTCTGACCAACAGATCCGTCAACAGGTA	27867
QY	12586	AGCAGTGCAATCACCTTGTGTTCACTGCTGAGGGGCATTTGTTTGGGGTTTGGGGAG	12645	QY	13641	GGAGTAGTACAATAAAGGCTCGCTGTTCCGGTTTATACGCGGTATTTCTGGAAGAGTTG	13700
DB	28928	TCCAGTTGGCATCATCTGACTGACATAACCG-----TTCCGGGTGTAGGATTTACCGAT	28875	DB	27866	GTATTCAGTGATGGCTTTGGTGGCTTACTGTCAAGCGCTGCGCGACATGAACGAGTATG	27807
QY	12646	CGCTCGGGGACGATGATTCAGTACTCTGCGGACAACTGCGGGAAGGGGTCTGACG	12705	QY	13701	GCNAATGTCAGTGATGACAGTGCCTCCGAGGACCTGTATGCGACACGCACTTTTACGA	13760
DB	28874	AGTACCCGCGAGTGATATCTTCACTTATGAAGCTAAATAATGACTGCTGCTGTTTAAAT	28815	DB	27806	GCTTGGCAACGCAATAAAGGGTCTCTGTATGATGAAGTGTCAAGCTACTGAGATCGT	27747
QY	12706	CTGGAACACTGTTGGCGCCGAAAGCTGCTCGGATAGTCAGGTCGCTGACGCTGGCG	12765	QY	13761	TCCGACGGCAGCGGAATGCGAGTTTATTACGGCAAAAGGTGAACGGCGCAGGTGCTGTA	13820
DB	28814	CTGGAACACTGATTAAGAATAGCTGATTTGCGGATTAATAAACCGGTGATATCTC	28755	DB	27746	TGGGCAGTGACTGGACGAACGGAATAT---GACAAATAAGGGAACGCGGATACGCACCTAT	27690
				QY	13821	TACCCCGTGGTGTGGTCAGTGAAGACGAGATGATACCGTTGGGCTAAACGACGCATC	13880

Db 27689 CAGCCCTATTTCCTCAATGACTGGCGATACGTTAGCAATGACATGTC - CGGCGAGGAAA 27632
Qy 13981 CTGACTGGAGAGGGGGGACCGGTGATGAGTCGCTCGCCCTGACAGCGCGTCCGCTG 13940
Db 27631 AAGAACTTATGACAGATACCCATGCTATGATCCCGTTGTCGAGAAATCAAGGTTATCA 27572
Qy 13941 ATGAGACAAAGATAGAAATACACTATCAGGTTGCGGCGGTGTCGACAGGTTGTTATG 14000
Db 27571 CCGCAAAAGTTGTTACCGCGAACCTTGTTCACTCCTGGTTTACTGTCAATGAGGATG 27512
Qy 14001 GTTTGGGGGCTTTCCCATGTCGGTTACACCGTCGGTTACACCGCGGAGATACTCAATGG 14060
Db 27511 AAAATGACACCGCTGCTGAGGTGAATGAGGTGAATATGTAATGATCAATCCGCGCTGC 27452
Qy 14061 CAACACCGCCAGGCGGACAGAAAGGCGGATCGGTTGGCCCTCCTCGGACGAGAAACC 14120
Db 27451 CTAACGCGGGAACAGAGATGAGGTGAAGGTGTTGTCATAATACCCTCAGATACT 27392
Qy 14121 CGGAAAGAAAGTGGGAGCAGCAACGACACTGACATGAACAAGGTGGCTATACATGCT 14180
Db 27391 CAACCTTATCTGTTGATCATTTGTTTATTTCGGCCTGGGCGGCTCGTAAGGTAC 27332
Qy 14181 GAAGAAGACTGGCTGCTGCGGTGACGCTGCCCTGATGCTCAGCGCATGTCAGCGC 14240
Db 27331 CTCATTGATATGCAAAACAAACATAATAAATGAGGTTGGATCAACGTTATTCTGTCAACTC 27272
Qy 14241 CTGACGACACCGTTTACCACCTCCAGCGCACTTCCAGTGTGTAACCCGCGCTT 14300
Db 27271 ATCATCTCTGCTTTTACCGGTGTTACTAGGAGGATTTGCTGAGTTTGAAGTGGCGCAGT 27212
Qy 14301 TCC-----GCAGCTACCGCTATCGGTACAGACCACTCGAGAGCCAAACCGCGGTTTG 14354
Db 27211 ATCTATATGACTTTTGCNAATTGCAGTTTATTTCGGCAACACAGGAAGTACCGNACTGAAC 27152
Qy 14355 TTTGCCGAACTGTTCCGCGCGTGCACAGAGCGGAGAGTGGCAGCGTATGCTGAC 14414
Db 27151 TGGCTCTGGCGCGCCCTCATTTACGTATCATCATGATCATGAGGAAGCAATTAAGGCCCC 27092
Qy 14415 AGGACAGAGTGAATGGCGGCTCGGCGCGCTTATCAGGCGGCTACGACGAGCA 14474
Db 27091 ACTGCCCAATAAACCACTAGTCTTAGTTAACTGCAAAATTTATCGACTACACTATCGA 27032
Qy 14475 GAAAAATAAGCGGATTTAGCGTTTAAAGAAAGTGAAGGTTTTCGCGATTAAATATAA 14534
Db 27031 CTATCGTTAAGAAACTAACATACAGACAACTATTCGATTCGAAAGGATTACACAA 26972
Qy 14535 -----CAGGAGTACATGACGACATCCTTGTTCAGTAGCACCC 14573
Db 26971 CAACCCAAACAGAGTAACTCATGAAAAAACATTGTATCCAAACTTTTATCAAAAGACTCC 26912
Qy 14574 CGTCGTTGCGGTGCTCGACNACCGCGCTGTTGGTGGGAGCTCGAGTACTACCGC 14633
Db 26911 CGTC-GTCAATGTCACAGAACCGGGTTCGAAATCCGTAACATCGATTTTTCACCG-- 26855
Qy 14634 ATCCGATACACCGGAGAGACGACGAGCGTATCACTGCGATCAGCAGATGAGCGG 14693
Db 26854 -TACCACTGCAACCGGTGATACCGATACCGGTATTACTGCGATCAATACACTACTCAG 26796
Qy 14694 GCAGCTTGTCAAAAGCCGACCCCGGTTACACGCGCGGCTGTCACAAATTTTCAG- 14752
Db 26795 GACACCTTAAGTCAAAAGCATCGATCCACGCTATATGATGAGGCAAGAAACCAAGTAGTACGA 26736
Qy 14753 ---TACCTGAATAGCTGACCGGACAGTACTGACAGCGCTCAGCGCGATGCGGTACG 14809
Db 26735 TCAACCCCAATTTTCTCTGCGAGTATGATCTGACCGGCAATTCCTTACGTACAGAGACGA 26676
Qy 14810 TCGCTGAACTGAGCGATGCGCGCGGCGGCTTCTGCGCGTCAACGG--GGCTGGGA 14867
Db 26675 TTGATGAGGTGCGCACTGTCACTTGAATGATATGAGGCGGCTCCCTGCTGACGTTGA 26616
Qy 14868 CGGAAGACGCGGTCAACCGCACTTGGCAATATGAAGACGATPACCTTCCGCGCGCCCGC 14927

Db 26615 CGGCAACAGGTGTATACAAACCCGCGCAATATGAAACTTCTTCCCTCCGCGCGCTCTGT 26556
Qy 14928 TGAGCATACCGAGCAGGTTTACCGGTG---AAGCGCCCAAAATTACCGAAGGTTCTGTGT 14984
Db 26555 TATCTGTTACCGAACAACACCCAGAGAAAAACATCCCGTACACCGAGCGCTGATTT 26496
Qy 14985 ACGCTGCAATACGGATGCGGAGAAGATTCTCAATCTGGCTGGCCAGTGTGTCTAGTCAATT 15044
Db 26495 GGGCGGCAATACCGAAGCAGAGAAAGACCATTAACCTTGGCGGCAAGTGTGCGCCACT 26436
Qy 15045 ACGATACCGCGGACTGTTGTCAGACGACAGCATGCGCCTTGAGCGGCTGCCGCTCCCG 15104
Db 26435 ATGACACGCGCGGAGTTACCGGATTGGAGAGTTCTGTCACCTGACCGTACTGTTTATCGC 26376
Qy 15105 TCACGCGGAGTTGTCGCCGACGCGCGGGGCGCACTGGAATGGGTGAGATGCTCTCGG 15164
Db 26375 AATCCAGCCAACTCTTGTCTCGACACTCAAGCAGCTAACTGGACAGGTGATAACGAAACCG 26316
Qy 15165 CTTGGAATGACCTGCTGGATGGGAGACGTTCTTACCCAGAGCCACGCTGATGCGACCG 15224
Db 26315 GCTGGCAAAACATGCTGGCTGCTGACATCTACACCATCTCTGAGCACCTTCGATGCGCACCG 26256
Qy 15225 GCGCGTCTGAGCATCACCGATGCAAAAGGTAATCTGACGCTGTGGCATATGATGTGG 15284
Db 26255 GCGCTTTACTGACTCAGACCGATCGAAAGGCAACATTCAGAGGCTAGCCTATGATGTGG 26196
Qy 15285 CTGGCTGCTATCGGCGAGTTGTTGACGCTGAAGNAGCGCACGAGCAGGTCATCTCTGG 15344
Db 26195 CCGGCGAGCTAAACCGGAGCGGTTAACTAAAGGTTCAGACGGAACAAGTAAATATCA 26136
Qy 15345 CTTCCCTGACGTACTCTGGCGCGCGGAAAAAAGTTGCGTGAAGAACACGCGCAACCGCTGG 15404
Db 26135 AATCCCTGACCTATTCTGCTGCGCGACNAAAATTCGAGAGAACACGCGCAATGCTGTA 26076
Qy 15405 TAACTCTGATATTTACGAGCCGAAACACAGCGCTGACGGGATTAATAACGGAACGTC 15464
Db 26075 TCACCGAATACAGTTATGACGAGGAAACCCAAAGGTTATCGGTATCAAAACCCGCGGTT 26016
Qy 15465 CGTCTGGCAGGTTGCGCGAG---CAAAAGTGTGAGGACCTCGGCTATACGTATGACC 15521
Db 26015 CGTTAGACACCAATCCGTGACAGACCAAAAGTTGCAAGACTTACGCTATGAGTATGACC 25956
Qy 15522 CGGTAGCAACGCTACTCAGCGTCAATAACGATCGGAAGAGACCGCTTCTGGCGTAACC 15581
Db 25955 CGGTAGCAATGTCTCATGATATCCGTAAACGATCGGNAAGCCACCGCTTTGGCACAAACC 25896
Qy 15582 AGAAAGTGTATCCGAGAAATACGTATCATCTACAGACGCTGTACCACTGGTGTGAGCGCCA 15641
Db 25895 AAAAAAGTGTGCGGAAAGTACTTATATCTACGACTCCCTGTATCAGCTTATCAGCGCCA 25836
Qy 15642 CAGGCGTGAATGCGCAATGCGCGCAGCGGCAACGACTTACCNTCCGCTACAGCCC 15701
Db 25835 CCGGCGGAGATGGCGAATATAGGTCAACAAAGTCAACCCATTTCCCTCC-----CGG 25782
Qy 15702 CCCTTCTTACAGACAGCTCTGCTTACACCAATTTACAGCGCACCTACCGTTATGACCGGTG 15761
Db 25781 CTCTACTTCTGATAACACACCTTACACCACTATACCCGTACTTATATGACCGGAG 25722
Qy 15762 GTGGCACTGACGAGATGCGCCACAGTGCCTGCGACGAAACAATAATATACGACAG 15821
Db 25721 GCGGCAATCTGAATAAAATCCAGACAGTTTACCGGCGACGCAAAACAACTACACCAAA 25662
Qy 15822 ACATACGTTAGTACCGCAGCAATAGGCGGTACTGAGCAGCTTGGCGGAGTGCCTG 15881
Db 25661 ACATACGTTTCTCACAGAGCAATCGCGCAGTACTCAGCACACTGACCGAAGATCCGA 25602
Qy 15882 CAGATGTTGATATGCTGTTTCAAGTGAAGGTCACAGAGGTCCTGACGCGCGGCAAG 15941
Db 25601 CACAAGTAGATGCTTATTTGACGCGAGCGGCGCACAGAACACAGTTGATAGCAGGACAA 25542
Qy 15942 CACTGTGTGACCGCACCGTGGAGAACTGCAAAAGGTGACACCGGTGTGCTGATGGGG 16001
Db 25541 ACCTGAACTTGGAATCCACGCGGTGAACCTACAAAGTGACATTTGGTGAACCGGACAAAGA 25482

Db	101775	AGGACAAATACCGTCATCTCACTGCGCCACCACTGGAGTGGCTTACCAAGCCTTTTGAGC	101716
Qy	10742	CGCGCAATGTGGGATGGGAGACCGGTGACGATATGGGCAAGTTGATGTTGCTTCAAC	10801
Db	101715	CAGAAACAAAGACACGCTGGCAATCAATGATGATGATGCAATTTTCAACGCAATTCAC	101656
Qy	10802	CCTATCAGCTTGTAGACCTTAAAGGCAAGGTGTGGTATCCCTGATATCAGGACAGCG	10861
Db	101655	GCTGGCACTGCTTGAACCTTGAAGAGAAAGGGTACCCGGTGTCTATATCAGGATAGAA	101596
Qy	10862	GTGCTGTGTGTACCGTAAACCGGTACGCGAGTTCGGGGGATGATCCGGATGCTGTGACCT	10921
Db	101595	ATGGCTGGTGGTATCGATCTGCCAACGTCAGGCGGGGAAGATGAATGCGGTCACT	101536
Qy	10922	GGGGGGGGTGGGGCCCTGCGGACAAATGCCCGCTTTTGATTAACAGCGGCATCTGGCGG	10981
Db	101535	GGGGGAAAAATGCAACTCTCTTCTATCACGCCAGCTTTGCAGGATTAACGCTCACTGATGG	101476
Qy	10982	ATCTTAATGGGATGTGCGCTGGAGTGGGTGCTTACCGCCCGCGGTGGGGGATGT	11041
Db	101475	ATATTAACCGTGACGGGCAACTGGACTGGGTATACCGGACCGGGTTAAGGGGTATC	101416
Qy	11042	ATGATCGCAACCCCGCGCGACTGGTTGCTATTTCAACCCCTGTGAGCCTTTCGCCGTAG	11101
Db	101415	ACAGCCAAACCGGATGGTAGCTGGACACGCTTTACACCAATTAGATGCTTGGCGATAG	101356
Qy	11102	AATATCGGATCAAAAGACGTGCTCGCGATATCTGGGGGTGGGTTAAAGGACATGG	11161
Db	101355	AATATTTCTATCCCGTGTCAACTTGGCGATTTAATGGGGCGGGCTGTCCGATTTAG	101296
Qy	11162	TGCTTATCGGGCGCGAGTGTTCGCTCTATTTCCGGCAAAACAGATGTTGGAATAAG	11221
Db	101295	TACTGATGGCCCCAAAGTGTACGCTTGTATGCTAATTAACCGTGAAGTTTTTACCAAG	101236
Qy	11222	GGGAGACCGGTGACGAAACGGAAGACTCACTCTGCCGCTCCGGGGGTGACCCACGTA	11281
Db	101235	GGCGGATGTGTGCAATCCGGTGATATCACTCTGCCGTTACCGGGTGGCGATG	101176
Qy	11282	CCCTGTGGGTTGAGTGATATGGCTGGCAGTGAGGACAGACGATTTGACGGAGTGGCTG	11341
Db	101175	AGTTAGTGGCATTTAGTGACGTACTCGGTTTCGGGCCAAGCACATCTGGTTGAAGTTAGT	101116
Qy	11342	CTAATCGAGTACGTTACTGSCAAACCTGGGCAACGCTGTTTCGGTCAAGCGGTGAATA	11401
Db	101115	CAACTCAAGTCACTGTGGCCAAATCTGGGACATGCGGTTTTGTTGACGCCAATTAAT	101056
Qy	11402	TTCCCGGTTTTAGCCAGTCACTGACGTTTAAACCTGACCAAGATATTTGCTGGCCGATA	11461
Db	101055	TGCGGGATTCAGCCAACTCTGCCGACAACTTTAATCCGACCGAGTTTCATCTGGCCGATC	100996
Qy	11462	CCGACGGTTCGGTACCAAGGACCTGATTTATCGGATGAGTACCGGTTAGTCAATTAAT	11521
Db	100995	TGATGGCAGTGGTCTCGCGATTTGATTAATGTTTCATCTGACCGCTGGAGATTTTCA	100936
Qy	11522	TCAACAGAGTGTAAATTTTCCCGAGCGGCATACGCTGCTTTGCCGAAAGGTGTC	11581
Db	100935	AGATGAAGTGTAAACAGCTTTGCAAAACCATTCACATCCGTTTTCTGACGGCTGCTG	100876
Qy	11582	GCTATGATCGCACTGCAAGTGTGCAAGTGGCGGATATCCAGGGGCTGGGGGTGCCPAGCC	11641
Db	100875	GTTTTGATGATATCTGACGACTACAGTGGCTGATGTTCAAGGGATTAAGGGCTGTGAGCC	100816
Qy	11642	TGTTACTGACGGTTCGCCATGTGCGGCTCATCTGAGGTGTGCAATTTATCGGACAGA	11701
Db	100815	TGATCTGACGTACCGCATATGGCGCCATCATTTGGCGCTGCGATCTGACCAATGCGGA	100756
Qy	11702	AACCTGGTGTGTAATGGCATCAACAAATATGGGGCCCGGCATGCACTGCACTATC	11761
Db	100755	AACCGTGGTGTCTCAGTGAATGAACAAATATGGGCGCTCATCACACCTGCAATTACC	100696
Qy	11762	GCAGTTCCGTGTGAGTTCTGCTCGATGAGAAAGCCGAGGCACCTGGCGGACGGCAGTTCCC	11821

Db	100695	GTAGTCTCTCCAGTTCTTGGCTGGATGACAAAGCCCGACGCTTGGCGACCGGACAAACAC	100636
Qy	11822	CTGCCCTGTACTGCAATTTACATTTGCATACCTGTGGGTTCCGTTGGTGAGGATGAGA	11881
Db	100635	CGGTCTGTACTGCTTCCCGGTCCATCTCTGTGGCAACAGAGACCCGAGGATGAAA	100576
Qy	11882	TCACCGGTAAACCGTCTGCTGACGACGCTTTATCGCCACCGGCTCTGGGACGGGACGG	11941
Db	100575	TCAGCGGCATATAAATATGTGACACGTTACGTTAGCTCACGGCCTGGGATGACGCTG	100516
Qy	11942	AAACGAGTTTCGGGGTTTGGTTTGTAGATCAGGGAATACGATACCTTTGGCAAGCC	12001
Db	100515	AACGGAAATTTCTGGCTTTGGTTATGTGACAGACAGACAGCCATCAACTCGC---TC	100459
Qy	12002	AGGTTACGGCAGCAATGTAGTATGCCCTTCTGTGAGCGGAACTGTGTATGCAACCGGG	12061
Db	100458	AAGGCAATGCCCCGAAACGACACACCGGCACTCAACAAACATGGTATGCAACCGGAG	100399
Qy	12062	TACCGGAGTAGACGAGGCTCTGCCGGAGACGATTTGGCMAAACGATGCGCGCTTTTG	12121
Db	100398	TCGCCGAGGTAGACAATACGCTATCTGCCGGTATTTGGGCTGGTATAAACAGGCTTCA	100339
Qy	12122	CCGATTTCCGACCCCGTTTCACTGTGCTTCAAGGATGAGGATGAGCAGACATATATCTCCG	12181
Db	100338	CGGTTTTACGCGACGCTTACTCTGCTGGAAGAGGGCAAGATGTTCCGGCGACACCGG	100279
Qy	12182	---ACGACAGCAAGACATCTGTTGACGAGCCCTGAAAGGCATCTCTGCTGCCAGTG	12238
Db	100278	AAAATGATGATTAATCTGACTGTTCAACCGGCACTAAAGGTCAGTCTACTGCTGAGTG	100219
Qy	12239	AGTTATACGGTCCGATGGCAGCAGCGCCGATATCCCTTACAGCGTCACTGAGTCTC	12298
Db	100218	AGCTCTACGGCTGTGATGACAGCAACAGCAAAATATCCCTATACAGTACTGTAATCTC	100159
Qy	12299	GCCCGAGGTACGGTAGTTGAAGCG--AATGGAGACTACCCGGTGGTGGCGGATGG	12355
Db	100158	GTCCCAAGTGGCCAAATACAGATGGCACTACCGCTTCCCGGTCTTGGGCGCTCGG	100099
Qy	12356	GCGCGAAGCCGTACGTAGTTTATGACGTTACCAATGATCCTCAATGCCAACAC	12415
Db	100098	TCGTGGAAAAACGTTAGTTATCACTATGAACTGATTTATCGGTGATCTCTAGTCAATCAG	100039
Qy	12416	AGCGGTACTCTCTAGTGATGAATACGGTTTCCCACTGCGTCAGGTCAAGTGTCAATATTC	12475
Db	100038	ATATTAAGTGTGTCAGGACCAATTCGGCAACCTCTGAAACAGGTTTCAATGCAATATC	99979
Qy	12476	CAGACGCCCTCGTGGCGGACATTCATTCGCGCTCTTACGGCGACGCTGTTCCG	12535
Db	99978	CCCGCGCAATCAACCAACCAATCCGTATCCGATACACTACCGGATACGCTATTTG	99919
Qy	12536	CCAACAGTTTACGACGACGACAGATATTACGCTGGGTTGCAACAGAGCAGTGAC	12595
Db	99918	CAGACGTTATACGATCAACCAACCTATTCGATTAACCTGCGACGAATCAGTTGCG	99859
Qy	12596	ATCACCTGTTTCACTGTCTGAGGGCATTTGTTGGGGTTGGCGGAGGCGTCCGCGG	12655
Db	99858	ACCATCT-----AACCGGTAATGAATCAGAGTGTGCGGATTTACCGGATGTGACACGA	99805
Qy	12656	ACGATGTTTACAGTACTCTCGGACACAGTCCGGAAGGGGTCTGACGCTGGAACACC	12715
Db	99804	GTGATGCTTCTTACGATGCAACAGGTCCTGTTGATGCTTTAAATCTGGAAGCCC	99745
Qy	12716	TGTTGGCGCCGAAAGCCCTGCTCGGATGATGAGTCAAGTCCGCTGCGGTGACGACG	12775
Db	99744	TATGTGCTGAAATAGTCTGATTCGATGCAAAACCGCGAATACCTTAATCAGCAAA	99685
Qy	12776	AAGTCTGTGATCTGGAATCAAGACGTTGCCACCGTCCGCTCCGCTCCGCCCA	12835
Db	99684	GAAGGTTCTATACCGATGGGAAAAACCAAGCGCCATTTGGAATAACGACACCAAGCTT	99625
Qy	12836	AGTGTCTTTTATCGAAACCGCGCTGCTGGATGAGGGTATGCTGAGTCTACTGGCTGCCT	12895
Db	99624	TAATCGCTTTTACCGAAACGGCGGTATTAAACGAATCTCTGTTATCCGCAATTTGATGGCG	99565

PT animals - contains pesticidal material from *Xenorhabdus* species
PT optionally synergised with *Bacillus thuringiensis* toxin.

XX

PS Claim 2; Fig 2; 46pp; English.

XY

55

CC This is a toxin gene sequence cloned from a *Xenorhabdus* strain NCIMB
CC 40887. This has insecticidal activity and can be used in an insecticidal
CC composition for oral delivery to an insect. The composition includes
CC material encoded by *Xenorhabdus* strains NCIMB 40886 and 40887,

CC particularly it contains *Xenorhabdus* cells or culture supernatant. It may
CC also include active materials from other sources, especially *Bacillus*
CC *thuringiensis* or delta-endotoxins, and is formulated with a carrier,
CC especially an edible material for the pest. Pesticidal agents isolated
CC from *Xenorhabdus* species, especially *X. nematophilus* have oral activity
CC against pig *Brassicacae* or rapae, *Plutella xylostella* and are heat-
CC stable at 55 deg. C. They are resistant to proteolysis by trypsin and
CC proteinase K, and are inactivated by sodium dodecylsulphate or acetone,
CC and by heating to 80 deg. C. The compositions are used to kill *Diptera*
CC and *Lepidoptera*, particularly *P. brassicae* or rapae, *P. xylostella* and
CC *Culex quinquefasciatus*, e.g. for crop or animal protection, also for
CC vector control. The isolated pesticidal agent may be expressed in
CC transformed plants to impart protection. *Xenorhabdus* materials show
CC synergistic effects when formulated with *Bacillus thuringiensis* toxins

Sequence 38258 BP; 10486 A; 8248 C; 8871 G; 10630 T; 0 U; 23 Other; XX SQ

Query Match	8.8%	Score 1658.8	DB 2	Length 38258
Best Local Similarity	53.1%	Pred. No. 0		
Matches 4978	Conservative	0	Mismatches 3802	Indels 598
				Gaps 44

Qy	7301	ATGGACTTCTCCGGAGCCAATGCCCTCTATTCTCGGAGCTGTCTATTACACGCCGATG	7360
Db	10859	ATGGATTTCAATAGTCGACGCCCTCTATTACTGGGA-ATGTTCTATTACACGCCCGATG	10917

Qy 7361 ATGGTGTTCCAGCGGTTGTCAGGAACAGCACCTCCCGGAAGCCACCGCTGGCTGCAG 7420

[illegible]

DB	1103AC
10978	TACGCTATTAATCCCGCCGGCTATATCGTTAAACGAGAAATCGCCCCCTGGATCTGGAAC
7481	GTCCGTC CGTGGAGGAGGCACCGGCTGGAA CGACTCGCGCCTGGACTCCATTGACCCC
QY	7540

DB 11038 TGCCGCCCGCTGGAAAGAG--ACATCTCTGGAATGCCAATCCGTTGGATGCCAATTGATCCG 11093

QY 7541 GATGCAATAGCCCGCAGTACGACGCCCCCATGCATTACAAGGTCGCCACCTTTATGTGCTACCTC 7600

Accession	Gene	Protein	Accession	Gene	Protein
11096	GATCCGTCGACAAATATGACCGGACACTATAAAGTTGCCACTTTATGCGCCTGTG	11155	7601	GACCTGCTGATTGCCGCGGTGATGCGCGCTACGCGTGTCTCGACGGGACACCTTAAC	7660
Db			Qy		

Db	11156	GATCAACTTATCTTCGGCGGCGATATGGCCCTATCGGAACTGACCCCGCATCGTTGAAT	11215
Qy	7661	GAGGCCCGGATGTGTGATCGTCCAGGCCCTGAACCTTCTGGCGCAGCAGGCCCTATATTTC	7720

Db 11216 GAAGCCAAGATGTGTATGTTCGGTCTTTGCAATTCCTGGTGATGAGCGGAGGATTAC 11275

Db 11276 GGCAGCAACAGTGGCGCACCGTCTCTTTCCGTGGCGGCACCACTGTGCAAGC 11335

[illegible]

Qy	7841	11396	Db
	GCGAATTCCTGACGACACTGTTCTCTCCGACAGACAGAGGTCTCAAGAGGTACTGG	GCTAACTCGTTGGTGG-TTTGGTCTGCGCGGAATATAACCCGGAATCAACCGATTACTGG	7900

Qy	7901	CAAACCTTGGCACAGCGGCTCCATAACCTTGGGCCAACCTCTCATTTGACGGCCAGCGG	7960
D _b	11455	CAAAC-C-TGGCTTTGGCGCTTGGTTAACTTGGGCCATAATCTCTTCCA-TGACGGGCCAAGG	11512

Db	14745	TTAGCGCTTATCGGCGCAATAGTGTACGTGTCTGGTCAATAATATCCGCGAGATGGGAT	14804
Qy	11218	AAAGGGAGACCGTGCAGCAAAACGGAAGAACTCACTCTGCGGTCCCGGGGTGACCCA	11277
Db	14805	CGCGCTCAGGATGTTATTCATTGTCAATAGCCACTGCGGTCCCGGCAAAATAAG	14864
Qy	11278	CGTACCCCTCGTGGCGTTCACTGATATCGCTGGCGATGAGCAGCAGCATTTTGAACGAGGTG	11337
Db	14865	CGTCACTCTGTCGCAATCAGTGATATGACAGGCTCCGGCAATCACATCTGGTGGAGTT	14924
Qy	11338	CGTGTAAATCGAGTACGTTACTGGCCAAACCTGGGGCAGCGTCTGTTGCGTACCGCGTG	11397
Db	14925	ACGGCAATAGCGTCCCTACTGCGCAACCTGGGGCATGGAAATTTGGTGAACCTCTG	14984
Qy	11398	AAATATCCCGGTTTTAGCCAGTCACTGACTACGTTTAAACCTGACCAAGATATTGCTGGCC	11457
Db	14985	ATGATAACAGG-CTTCCAAATACGGGGAACGTTTAAACCCCAACAGACTGTATATGGTA	15043
Qy	11458	GATACCGACGGTTCGGTACCA-CGGACCTGATTTATGCGATGAGTGACCGGTTAGTCAT	11516
Db	15044	GACCTAAATGGCTCAGGCACACCCGATTTTATTTATGCGCGCAATACTTTACCTTGAAC	15103
Qy	11517	TTATTTCAACAGAGTGGTAAATTTTCGCGGAGCCCATACGCTGCTCTTGGCGAAGG	11576
Db	15104	CTATGCCAATGAAGCGGCAATCATCTCTGCTGAACCTCAGCGTATTGATCTGCGCGATGG	15163
Qy	11577	TGTGCGCTATGATCGCACTCGAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGTGCC	11636
Db	15164	GGTACGTTTTGATGATCTTGTGCTTACAAATAGCGGATACAAAGGATTAGGAGCTGC	15223
Qy	11637	TAGCTGTATTACTGACGGTCCCGCATGTCGCGCCTCATCACTGGGTGTGCCATTTATCGGC	11696
Db	15224	CAGCATTTTTCAGATCCCGCATATGAAGTGCAGCACTGGCGATTGATATGACCAT	15283
Qy	11697	AGACAAACCTCGTTGTTGATGGCATGAACAACATATGGGGCCCGGCGATGCACTGCA	11756
Db	15284	ATTCAAGCCTTGGCTGCTGAATCCGCTCAATAACAATATGGGAACCAACCACTGTGA	15343
Qy	11757	CTATCGCAGTTCCGTGTCAGTTCTGGCTGGATGAGAAACCGAGCACTGGCGCAGCAG	11816
Db	15344	TTATCGCAGCTCTGCCAGTTCTGGCTGGATGAGAAATACAGGCTTCTGAATCCGGAT	15403
Qy	11817	TTCCCTTGCCTGCTACCTGCCATTTACATTCGATACCCCTGTCGGTTCGGTGGTGCAGGA	11876
Db	15404	GACGGTGTGAGCTACTTACCGTTCCCGGTGCATGTGTGTCGCGCACGGAAGTCTGGA	15463
Qy	11877	TGAGTACACCGGTAAACGCTGTGTCAGCAGTGTCTTTATCGCCACCGGCTCTGGGACGG	11936
Db	15464	TGAAATTTCCGGTAAACCGATTGACCGCCATTATCATTAATCTCACTGCTGGGATGG	15523
Qy	11937	GCAGGAACGAGTTTCGGGGTTTGGTTTGTGATCAGGATACCGATACCTTTGGC	11996
Db	15524	TCGTGAACGGGAGTTTCGTGGTTTGGCGGGTGCACCAACTGATATTGATTCACGGGC	15583
Qy	11997	AAG-----CCAGGATACGGCGACGGAACCTGAGTATGCTTCTGTGAGCGCGAACTGGTA	12050
Db	15584	GAGTGCACACAGGGACACATGCTGAACCCACCGCACCTTCGCGCACGGTTAATTGGTA	15643
Qy	12051	TGCCACCGGGTACCGCGATGACGAGCGTCTGCGGAGACGATTTGGCAAAACGATGC	12110
Db	15644	CGGCACCTGGCGGTACGGGAAGTCGATATCTCTTCTGCCACCGAATATTGGCAGGGGATCA	15703
Qy	12111	CGCGCTTTTTCGATTTCCGGACCGGCTTTCAC-----TGTGGTTTCAGGAGGATGA	12164
Db	15704	ACAGGCATTTCCCAATTTTACCCCAACCGCTTTACCCGTTATGACGAAAAATCCCGGTGTA	15763
Qy	12165	GCAGACATATACTCCGACACAGCAAGACATTTCTGTTGTCAGCGGACCGCTCGAAAGGCAT	12224
Db	15764	TATGACCGTCAACCGGACGACAGGAGAACTACTGTTTACATCGACCTTAAAGGACA	15823
Qy	12225	CTGCTCGCAGTGAATTAACGGTGGCGGATGGCAGCAGCGCGCCGATATCCCTTACAG	12284
Db	15824	ACGTTTACGCGAGTGTATGGGATGATGATTCTATATCTGCGCGGTACGCGCTTATTC	15883
Qy	12285	CGTCACTGAGTCTCGCCCGCAGGTAAGGCTAGTGTGAAGCGAAATGGA-----GACTACCCGGT	12341
Db	15884	AGTGGATGAATCCGCGACCAAGTACGTTTGTGTTTACCGTGATGATTCGACGCTGCTGC	15943
Qy	12342	GGTGTGCGCATGGGCGCGGAAAGCGGTACGTTAGTTCAGTTTATGAACGCTGACCAATGA-TC	12400
Db	15944	GGTACTGGTTTCGGTGGCGAATCCCGCAATACCGCATATGAAGGGGTGTTTACCGATTTC	16003
Qy	12401	CTCAATGCCAACAGCAGCGGTACTCTCAGTCATGAATACGTTTCCCACTCGGTGAGG	12460
Db	16004	CACAGTGCAGCCAAAAGATTGCTTAAATATGATGCTTAGGATTTCGCGAGCAATC	16063
Qy	12461	TCAGTGTCAATTTTCCACGACGCGCTCCGTCGCGGACAAATCCATATCCCGCGCTCTTAC	12520
Db	16064	TTGAGATTGGCTATTTCGAGACGCTCCACAGCTGAGTTCTCGCTTATCCGGATACCTGCG	16123
Qy	12521	CGCGCAGCTGTTCGCAACAGTTATGAAGCAGCAGCAGATATTAACGCTCGGGTTTC	12580
Db	16124	CCGAAACACTTTTTCACGACGTTTCGACGACAGATGTTCTCTCGTCT---GACAC	16180
Qy	12581	AACAGACGATGACACATCACTTGTTCAGTCTCTGAGGGCATTTGTTGTTGGGTGG	12640
Db	16181	GCAGCGTTTTCTTATCACCATCTGAATCATGATGATAAATACGTGATCACAGGGCTTA	16240
Qy	12641	CGAGCGCTCGCGGACGATGATTTCAGGTACTCTCGGACAAAGCTGTCGGAAGGGGTC	12700
Db	16241	TGATACCTCACGACGACGACGATTTTATCAAGCCGATAAAGTCCGCGACGCTGAT	16300
Qy	12701	TGACGCTGGAACACCTGTTTGGCGCCGAAAGCTGCTCGGATAGTCAGGTGCGTACGC	12760
Db	16301	TTTTCCCTTGAATGGTTTTCTGC-----CACAGTGCAGGACGATTTGTTGCTGC	16351
Qy	12761	TGCGGGTCAAGCAGTCTGATCTGATTTCAAGAGCTTGCACCGTGCCTGCTC	12820
Db	16352	ATGCCGACCGGATTATTCGGGACATCAGCGTGTAGCATATACCGTCCGAGAGAGCAAC	16411
Qy	12821	CGCACCTCCCGCCCAAGTAGCTTTTATCGAAACGGCGTGGTGGATGAGGGTATGCTCA	12880
Db	16412	CCGCTATTCTCGCTGGTGGCATACATTGAAACCGCAGAGTTTGTATGACGATCGTTGG	16471
Qy	12881	GTTTCACTGGCTGCTACATTTGTGA-----TGAAACATCTCGAGCAAGCCGGTTACCG	12932
Db	16472	CGGCTTTTGAAGGAGTGTGATGAGCAGGAGCTGACAAAACAGCTGAATGATCGGGCT	16531
Qy	12933	GCAATCGGATACCTTTTCCCTCGAGCGGGAAGCAGACAGGATTTGGACCCAGT	12992
Db	16532	GGAAATCGGCAAAAGTGCCTTCAGTGAAGA--CAGATTTCCATGCTGCGGTGGGACA	16589
Qy	12993	TCAGGATATGTTTACCTATGCGCGCGCAGAGCATTTCTGGCTACCGCTATCCTTTCCGGA	13052
Db	16590	AAAGGAATTTACAGATATGCGGTGCGACGAGGATTTCTATCGGCCATTGGTGCNAACGGA	16649
Qy	13053	CAGTATTTTGAACCGGCCCCAGTTTACCGTACCGGTGACGGGTAAGCTGCTGATACGCA	13112
Db	16650	AAACAAAGCTTACAGGTCAAACGACGATGACGTGGGATAGCCATTACTGTGTTATCACCGC	16709
Qy	13113	GTGGCAGGATGCGCGAGGATTTGTCAACAGCGGATATGATGCGGCTTCCTGACGCC	13172
Db	16710	AAACAGGATGCGGCTGCGCTTGCATGCAAGCGCATTTACGATTTATCGATTTATGTTGTTG	16769
Qy	13173	CGTCCGGTGAACGCGCCCAATGATTAATCTGAGTCCGCTCACTCTGATGCTCTGGGCGG	13232
Db	16770	GGATAACACCAAGATATCAATGATTAATCTATCACCGTGACGTTTGTATGACACTGGGAC	16829
Qy	13233	GGTACACCCCTCGGATTTTGGGGCAGCGGAAATGGTATTTGCCACCGGTTACAGTGTG	13292
Db	16830	GGTAAACAGCTTCCGTTTCTGGGGGACTGAAACCGGTGAAACAAAGGATATACCCCTGC	16889
Qy	13293	CAGTTGTCCGTTCCGACGCGCGCAGCGCTCTGGCGGTGACGCGGCCCTTACCAGT	13352
Db	16890	G-----GAAATGAACACTGTCCCTTTATTTGTCGCCCAACACCGGT	16928

Db 18651 AGAAAAATTTTACAAAACCTCGTTATGAATATGATCTCTCGGAAATGTCTGAAATCAA 18710
QY 15546 ATAACGATCGGAAGAGACCCGCTTCTGGCGTAAACAGAAAGTGGTACCGGAGATACGT 15605
Db 18711 CTAATGATGTGAATTAACCGCTTTTGGCGACACAGAAATTTGATCCGGAATACTT 18770
QY 15606 ACATCTACGACGCTGTACAGCTGTGTAGCGCCACAGCGCGTGAGATGCCAAATGCCG 15665
Db 18771 ACACCTATGACAGCTGTACAGCTGTGTTCGGTCACTGGCGGTGAATGGCGAATATTG 18830
QY 15666 GCCAGCAGGCGACGACTTACCATCCGCTACAGCCGCCCTTCTCTACAGACAGCTGCGCT 15725
Db 18831 GCCGACAAAACACAGTTAC-----CCATCCCGCTCTGATTTGATGAATACTT 18881
QY 15726 ACACCAATTAACGCGCACCTACCGTTATGACCGTGTGTGCAACCTGACGACAGTGGCC 15785
Db 18882 ATAGCAATTACTCTGCGACCTTACGACTATGATCGTGGGGAATCTGACGAGATCGATA 18941
QY 15786 ACAGTGCCTCCGCAACGAAATAATTAATACGACAGATCACGGTTAGTGACCGCAGCA 15845
Db 18942 A-----TTACAGATCACCGGTAATACTATACAAACGACATGACCGTTTCAGATCACAGCA 18997
QY 15846 ATAGGCGGTACTGACGACGCTTGGCGGAAGTGGCGTCAATGATGATCTGCTGTGAGT 15905
Db 18998 ACCGGGCTGACTGGAAGAGCTGGCGCAAGATCCCACTCAGGTGGATATGTTGTTCAACC 19057
QY 15906 CAGGAGTCAACAGAACCTCTGACCGCGGCGCAAGCACTGCTGTGACGCCACGCTGGAG 15965
Db 19058 CCGCGGGCATCAGACCGGCTGTGTCGGTCAAGATCTTTCTGGACACCCCGGTGACG 19117
QY 15966 AACTGCAAAAGGTGACACCGGTGTGTGATGGGGGGCGGACGACAGCGAAAGCTATC 16025
Db 19118 AATTGCAACAGTGATATGTTCAATAGGAAATACGACGCTGATCAGGATTTCTACC 19177
QY 16026 GGTATGATGCGGGAGTACGCTTATTAACAAACCGGCGACGCGGCAAACTGGCAACAG 16085
Db 19178 GTTATGATGACAGCTGACGCTGTCTAATTAAGACTCATATTCAGACAGCAGGTAACAGT 19237
QY 16086 TTACAGACAGCGGTAGTGTACTCGCGGGGTGGATTAATCTATCATGCGCAATGGCG 16145
Db 19238 AGCAATACAGCAACATTAATTTGCGAGCTGGAATGGCGACGACATATAGCGGCA 19297
QY 16146 TGACGGAAGAAAGCTCAGCTTATTAACGGTGGCGAGGTGGCGGGCAACAAGTGC 16205
Db 19298 ATACATTAAGAGTTTTTTCAGGTCATCACTGCTGCGTGAAGCGGTGACGCAAGTGC 19357
QY 16206 GCGTATGCTACTGGGATCGGACGCGGATGACCTCGATGAGGACTCGGTGGTTACA 16265
Db 19358 GGGTGTCTGCAATGGGAACAGGCAACCGCGGATATCAGCAATGATCAGCTGGCTACA 19417
QY 16266 GTTACGATACCTGTGGGACGACGCGCTGGAGCT--GGACAGAGGGGTACCTTATC 16324
Db 19418 GTTATGGCAACCTGATTGGCAGTAGCGGGCTGGAATGGGACAGTACGGCGAGATCAT 19477
QY 16325 AGTGAGGAGGAGTTTACCCGTTATGGCGGAACCGCTGTTCTGACGGCGCGGAAGTGGGTT 16384
Db 19478 AGTCAGGAAGATATTACCCCTATTGGGGGAACCGCGG--TGTGGGCAACCGAATCAGTCA 19536
QY 16385 GAGGCTGACTACAAACTATCTCGATACAGCAAGGAGCGTGACGCGAGCGGGCTGGAT 16444
Db 19537 GAAGCTGATTACAAAGCGCGGTTATTTCTGGCAAGAGCGGGATGCAACAGGGTTGTAT 19596
QY 16445 TATTACGGTTATCGGTATTACAGCCATGGCGAGGGCGCTGGCTCTCCAGGACCCGGCA 16504
Db 19597 TACTACGGCTATCGTTATTAATCAATCTGTGACAGGGCGATGGTTGAGTGTAGATTCCTGCC 19656
QY 16505 GGACGCTGACGGGCTGAACCTGTTCCGATGGTGGGAATAATCCCGTCAAGCTGTTTT 16564
Db 19657 GGTGAGGCCGATGCTCTCAATTTGTTCCGAATGTGCAGGAATAACCCATCGTTTTCT 19716
QY 16565 GACAGCAACGGCGGATC 16582
Db 19717 GATTCTGATGGTCTTTC 19734

RESULT 7

AAV17876/c

AAV17876 standard; DNA; 38258 BP.

XX

AC AAV17876;

XX

DT 23-JUL-1998 (first entry)

XX

DE Cloned toxin gene sequence from *Xenorhabdus* strain NCIMB 40887.

XX

KW *Xenorhabdus*; toxin; insecticidal; protection; *Pieris brassicae*; crop;KW *Pieris rapae*; *Plutella xylostella*; *Lepidoptera*; Diptera; animal; ss.

XX

OS *Xenorhabdus* sp.

XX

FN WO9808388-A1.

XX

PD 05-MAR-1998.

XX

PF 27-AUG-1997; 97WO-GB002284.

XX

PR 29-AUG-1996; 96GB-00018083.

XX

(UKAG-) UK MIN AGRIC FISHERIES & FOOD.

XX

PI Jarrett P, Ellis DJ, Morgan JAW;

XX

DR WPI; 1998-179074/16.

XX

PT Orally active insecticidal composition, used for protection of crops or

PT animals - contains pesticidal material from *Xenorhabdus* speciesPT optionally synergised with *Bacillus thuringiensis* toxin.

XX

PS Claim 2; Fig 2; 46pp; English.

XX

This is a toxin gene sequence cloned from a *Xenorhabdus* strain NCIMB 40887. This has insecticidal activity and can be used in an insecticidal composition for oral delivery to an insect. The composition includes material encoded by *Xenorhabdus* strains NCIMB 40886 and 40887, particularly it contains *Xenorhabdus* cells or culture supernatant. It may also include active materials from other sources, especially *Bacillus thuringiensis* or delta-endotoxins, and is formulated with a carrier, especially an edible material for the pest. Pesticidal agents isolated from *Xenorhabdus* species, especially *X. nematophilus* have oral activity against *Pieris brassicae* or *rapae*, *Plutella xylostella* and are heat-stable at 55 deg. C. They are resistant to proteolysis by trypsin and proteinase K, and are inactivated by sodium dodecylsulphate or acetone, and by heating to 80 deg. C. The compositions are used to kill Diptera and *Lepidoptera*, particularly *P. brassicae* or *rapae*, *P. xylostella* and *Culex quinquefasciatus*, e.g. for crop or animal protection, also for vector control. The isolated pesticidal agent may be expressed in transformed plants to impart protection. *Xenorhabdus* materials show synergistic effects when formulated with *Bacillus thuringiensis* toxins

XX

SQ Sequence 38258 BP; 10486 A; 8248 C; 8871 G; 10630 T; 0 U; 23 Other;

Query Match

Best Local Similarity 6.7%; Score 1260.8; DB 2; Length 38258;

Matches 3921; Conservative 0; Mismatches 3082; Indels 541; Gaps 27;

QY 2511 TGACGGAATTTATCTCGCGTTCTGTTTCCGAGGTCAAAAATCACTGGCGACAGCTGT 2570

Db 28349 TGACAAACATTTCTGTTTATGTTCTTTTCAGCGAATTTCTGTCATAGCAAGTGGAACTCTGA 28290

QY 2571 CATGGGCGAGGCTCTCTATCTGTACAGTCAGGCGAGCACGACAGAAAGAAAACCGCGC 2630

Db 28289 CGTGGCGAGAAACAGACTTTTATATCAACAGGCTCATCAGGANTCAAAACAGAAATAAC 28230

QY 2631 TCACGGAATCCCGTATTTCTGGCCCGGCGAATCCCTACTGTGTAATGCGGTTGCGCTGG 2690

Db 28229 TTGAAGAACTGGCGCATTTTGTCCCGTGCTAATCCACAACTGGGCTAATATCACTAAACCTTA 28170

QY	2691	GAATACGGAGGAGCGCGGAGCTGCGAGCTATGATGACTGGTTTGGCTCCCGCGAGACC	2750	3761	CTTAATAATAAAGTTATCCGCTATACAAGGCCACGGCATGACCACCGCGGAATA	3820	
Db	28169	ATATTACACCGTCAACCCCTAAACAATAGTTACAAACAGTTGGTTTATGGCCGCGCCACC	28110	Db	27089	TTAAGCTGAATAAAGCGATTTCGTTTGTATAAAGCCACGAGCATATCTCCGAGAATATC	27030
QY	2751	GTTTCCGCCCGCCGCTCGGTGGCTCCATGTTCTCACCGCGGGGTATCTGACCGAGC	2810	QY	3821	TATCAAAATCACCAATATTTCTTAATAACGGTCTCAACATTTGACCATGCGGTCTCTGAGTAAA	3880
Db	28109	GTTTGTGTAACACGGGATCAATTGCTTCCATATTTTCCACAGCGGCTTAATTTAAACAGAT	28050	Db	27029	TGGCAAGTAATAGAAAGTATTTATGATGACTTAACCATTTGACAGCAATGTGTGGGTAA	26970
QY	2811	TGTACCGTGAAGGGAAGGACCTGTCATCCGGACACCTCGCTGTTTCGGGCTGGAATCCGGC	2870	QY	3881	ATCTTCTGGTGGTGTACTGATGGTCACTATCAGCTTGTATGTGGCCGGTCACTGATA	3940
Db	28049	TATATCGGAAGCGAAAGATTTTCATCTTGACAAATTTCTCAATATCACCTGAATAAAGGAC	27990	Db	26969	CTGTTTATGTTCAATATATATGAGCACTATAATATTTAGCGTCAGCATGCGCTGTGA	26910
QY	2871	GTCCGACCTGGCGGCGCTGGCCCTTAGCCAGAAATATATGACGAGAGCTCTCCACCC	2930	QY	3941	TTGTCAACGAAACCATCAGTGACCGGCTTCAGCGCGGAAACCGGCTGTGTCAACGAC	4000
Db	27989	GCCCGGACATGCTTCCACTGGCACTGACACAGAAATATATGAGTAAGAAATTTCCACAT	27930	Db	26909	TTGTGTCAATCAGATACAGCAATATTTCCACTAAACAAACCCAGTCAITTTACATG	26850
QY	2931	TGAGCCTGTCCAATGAGCTACTGTATCGCGGTATCGGGCAGCGGAGGGCTTGACGAGC	2990	QY	4001	CTGTTTCAACACCCCAACCGCTGAAACGGCCAGCTGTTTCTGCAGATGATACCCCTCCGAC	4060
Db	27929	TATCCTTATCTAATGAATTTACTGCTGCATAAATTCAGACGTTAGAGAAAACCTGACTATA	27870	Db	26849	CTGTTTCAATACACCGCTATTAAATGGCCCAAGAGTTTCTGCTGATAATACCAAACTGGAT	26790
QY	2991	ACAGCGTCAAGGAGCTGCTCGCCGGGTATCGCCTGACCGCCCTGACCCCTATCACTGGG	3050	QY	4061	TTACGCTGTGAAGCAACCGGAGATGCTTTCGCTCTCAGCGTACTGAAACGGCATTTAAC	4120
Db	27869	ACGGTGTATGAATAATGTTGCTCCACTTACCGCAACACCGGCAATGACACCTATCATCTGC	27810	Db	26789	TTAACCCCGGTGATCAAAAAAACCAITTTTATTTGGGAATAATGAAACGTCCTTCAGA	26730
QY	3051	CGTACAGGCGGCGCCGCAAGCCATTTCTGGTGACGACCGGAGCTGATGGGTTTCAGCC	3110	QY	4121	ATCAGCGCTCGGGGCTTTTCCACGCTCTGGCAGTTGGCCAGCGGTGACAGCAGCGCTGGG	4180
Db	27809	CGTATGAGTCAGCCCGCTCAGGCAATTTTATTCAGATATAAAACCTTCACCGCATTTAGCC	27750	Db	26729	GTGAATGATCTGAATCTGTATACATTATGGAACCTGGCTAATGCGGAAACAAATCCAGAA	26670
QY	3111	GTAATCCGGATGCGCGCAGCTTATGACCCCTGCCCTCCATGCTGGCCATTGAAGCCGATA	3170	QY	4181	TTTAGTCTCTGTGTGACAAATATCCCGCACTCTACCGAGTGAAACTCTGGCTGACATC	4240
Db	27749	GTAAATACAGCGTAGCGGAATTAATGACCCACATCGCTACTGGCTATTAAGACTGATA	27690	Db	26669	TTTATGTGTTCCATCGAGAACCTGTCTCTGCTTTTATCGGTTCTGCTGTGCGACACAT	26610
QY	3171	TTTCCACCGAGCTGTATCAGATACCTGGCCGAAGAAATACGACAGACAGTTACGAAGCAC	3230	QY	4241	CAGGACCTTATCGCTGGTGAGCTGCAATGTGCTCGCTCCGCTCCCTTTTCAGCGGGTG	4300
Db	27689	TATCGCTGAATTTGTATCAATCTTGTGAAGAAATTTACCGCGGAAATTTCAACAGAAC	27630	Db	26609	CATCATCTGACAGTGAATGAATATCCATGTTGTTGTCGGTTTCTCCCTATGTGAACAGC	26550
QY	3231	TCGGAGTAGAATTTTGGTGATATGCCCTCCCTCCCTCAGTGTATCTTATGATGACTTG	3290	QY	4301	GCCGCGGCTCGCTCTCGGATAATGAGCTGACGCA-----GTTTCTGTACCAGACC	4351
Db	27629	TGATGAAGAAAAATTTCCGTACAGATGATGATCTGATTTTAAAGATTATGCTTCTTTGG	27570	Db	26549	AAAAATTGCCCTTTTCTGTATACAGCAATTAACGCAATTAATCAGCTTCTGTTCCAATGC	26490
QY	3291	CAACATTTTATGATCTTGATACGATGAGCTAACTTCGTTATTGTCTAATTAAGGCTGGACT	3350	QY	4352	ACCACCTGGCTCAGGAGAGGCTGGAGCTGAGGTCAGGATGTTTCTGTGATGCTGAGCAGC	4411
Db	27569	CTCGCTACTACGATTTGCTTATGATGAACCTCAGTTTATTTGTCAATCTCTCCTCGGTA	27510	Db	26489	ACCCAGTGGCTGACACACAGAAAAATGGTCTGTGTCAGTGTGTTTCTGATGACCAACGAT	26430
QY	3351	TTTCAAAATCAAAACAATGAATATCAATTAATAGTCAAATTAAGTGTGTAATCTCTGAATG	3410	QY	4412	CAGTACGCTACCTCTGACCCCGACATTTGAGAACCTGCTCGCTTCCCTGGCGCAACGGA	4471
Db	27509	AGAAAAATCAAAATCAACAGTATAAGAAATGAGCAACTGATAACATTTGGTCAATGACGGGA	27450	Db	26429	AATTACAGCACTGTCTTACGCCGATATGAAAACTTATCAGACACTAAGTAATGGA	26370
QY	3411	AAAGCACTGGTTTAAATCACTATACATCATTTTAAAGACGCTTAGCGGAGACTCACAGC	3470	QY	4472	CTGTGGGCGGTGAGCTGTTCCCGGAAAGCTTCCCGGCGATGGCGCTCCCTTTATPGCC	4531
Db	27449	ATGATACGGCAACGGCAAGATTGAATTAAGCGAACCCGCAAGATTTCTACGATTCACAT	27390	Db	26369	TTATCAACACTTTTCACTCGGTGATGACGAACCTGATCCGTGACGTCGCCCGCTGATTGCT	26310
QY	3471	AGATTAAACCTGAGCTTATACCTTATGGGATGGAACATATCTTTATTAATTTTCAGCGTGG	3530	QY	4532	GCGGCATGCACTGAGCCCAACGGATACGGGGAAGGCGATGCTGACTTGGCGGACCCAG	4591
Db	27389	TAAACTATGAGAGCTAATTTCCAATCAAGAAATGAATGAATAATTAATTTTCAGTGA	27330	Db	26309	GCCAGCATTTCAAATGGATTTCAGCAAAAACAGCAGAAAACTATTTTGTGTTGATTAATCAG	26250
QY	3531	TGTCAAGATATCAGAGGATAGTTTCAACTAGGGCTGTTAGGTTCTTAACAGTAGCAATC	3590	QY	4592	TTGAAGCCAGAGGGCTGACGCTGACGGAATTTATTTTGTGTTGATGAATCGCGCCCA	4651
Db	27329	AAAAAACAGAACCTGACCACTTGGATTTTCTGCTCCAGAAATGGAGATGAAGAAATATAT	27270	Db	26249	ATAAACCAAGAGACTGACATTCGATGATTTTCATGATTTTTCGGCTAACCGTATCGC	26190
QY	3591	TTTACTCTGGGATTTACGCTTCMAAAGGGTTCGCTATAGCATTTCTGTTTGAATAG	3650	QY	4652	AATGACGACGAGCGGGCCAGATGGCAGGGTTCTGCCAAGCCCTGTGGCAATGGCACTG	4711
Db	27269	ACCAAGATAAAATTTTCGTCCTCCATTCCTAATACCCATACAGTATTTCCCAATTAATGA	27210	Db	26189	TCAGAGAAATGAACCCAGCAACATGGTGGCTTTTGTGTCAGTACTGGGGCACTTTCTCTG	26130
QY	3651	ATGAAGGAAAGTTAAATGATGGGATCAATAGAGATTGAGTAGGAAA-----GGG	3700	QY	4712	ATCATCCGAGCAGCCGCTCAGCAGCGCGAGCTGACGCTGCTGGTCAGCCAGCGGGA	4771
Db	27209	CGACAGAGCAAAATCACCACGGTATACACTCCGCTTATGCGAGTTTAAACCAATCCGTC	27150	Db	26129	ATTGTGCGCAATTTTGGACTCAGCGAAAAACGAACTGACCTGTGTGTGACAAAAACGGAG	26070
QY	3701	GGGGGATATTACTCAACAGTAATCTTCACTCTGATGGAATATGATCTCGTGGATTTTCATT	3760	QY	4772	CGTCTCCGACAGGATGGCACCATCTGCCCATGACCTGCCCGCGCTTCGCGACATTTAGC	4831
Db	27149	GGATGCTATCAATGCCAATGCACACTTTTAAATGATGAGGTTCCCGGTGATATATCTCCTG	27090	Db	26069	AAATTCCAATCAGAAACACACAGCACTGCAACATGATCTCCCACTTTGCAAGCGCTGACC	26010
				QY	4832	CGTTTTTATGCTCGTTTAAACCGCAGCGGCAAGCCATGCGCGGGAGGTCCTGACCGCACATT	4891

Db	26009	CGCTTCATCTGTCATCATCGCTGTGTGAAGCTACGCGACAGAACTCTTAACAGCATTTGG	25950
Qy	4892	GAGACCGGAGAACTGTGCTCAGCCCTGCTGGCCGGCCCTGTGCACAG--AATGACGAGG	4949
Db	25949	AACCTTAGACGGTGTGACTGCGGAACTAATTTGGCGGTGGCGGTAAATTTTGTGCTCAGG	25890
Qy	4950	ATGTGACCGGCGCTTTGGCGCAGGTCAGGTCAGGGGGCCGCTGAACAGGACAAACAGCGTGTTC	5009
Db	25889	TTGTGACACAAGCATTTGCAACAGACCGGTTTG-----GGAGTGAATACCTTTAC	25841
Qy	5010	CTCTCTGGGAAGAGTGGACACAGGCTGACAGTGGCTGGACATGAGTGACCCCTGTTC	5069
Db	25840	CAACTGAGAACTTAGATGTCACTCTGCAATGGCTGGATGTGCTGTCTACATTTGGGTA	25781
Qy	5070	TTAGCCCATCCGCTCTGGCTAGCTGATTTGCCCTGAAGTACATCAATGTGTCGATGACA	5129
Db	25780	TTACCCCGATGGTGTGTCGACTCATATAAATTAATAATATGTCGGTGAACCGGAACCC	25721
Qy	5130	GTGACCCGTTGTACAGCCAGTCAGGTGTATCCGCTCTGCTGCAGGCGGGCTGAAAA	5189
Db	25720	CGATGCCAACATTTGATGATTTGGCAAGCCCGACTCTTTGTTGCAGGCGGACTGAC	25661
Qy	5190	GCAGCCAGAGCTCGGCGCTGCACGATTAATCTGGAGAGGGGACAGCAGCGCCCTTTGTG	5249
Db	25660	GTCAACAATCCGACAGCTTCAGGCAATGCTGGATGAAGCCAGCAGCAGCGCCGAGTG	25601
Qy	5250	CGTATTATCTGCGTATCTGCGCAGCAATGATATCCGGCGCGATGACTCTTCGGGT	5309
Db	25600	CTTACTACATCAAAAATGGTGCACCTCAACAGATTTAAGCCCGGATGAGTTGTACAGCT	25541
Qy	5310	ATCTGCTGCTGGATAATCAGGTGTGACCCAAAGGTAAAAACACCCGATTTGCCGAGGCCA	5369
Db	25540	ATCTGCTGATGATACCAAGTTTCTGCCCAAGTGGAACCAACCCGTTGGCAGAGCCA	25481
Qy	5370	TCGCCGGCATA CGGCTGTATATCAACCGGGCCCTTAACGGAAATAGAACTCAGCGCCATGG	5429
Db	25480	TTGCCAGCATTCAGTTATATGTCAACCGGGCGTTGAATATGTTGAAGGAAAAAGTATCA	25421
Qy	5430	CAGAGGTGAGGGGGCGTCACTGTTTCTGACCTGGGATGAGTTCAACAAAGTTACAGCA	5489
Db	25420	AGCCAGTGAACACCCGTCAGTTCTTTCGCACTGGGGAACCTACAAATCGCAGGTATAGCA	25361
Qy	5490	CTTGGGCGGCGTCTCAGAGCTGTTTACTATCCGAAAACTACTCTGCAGCCCGACCGTCC	5549
Db	25360	CTTGGGCGGCGTATCTGACTGGCTTATTCGGBAACTATATCGACCCACAGATTC	25301
Qy	5550	GTATCGGCGACACCGGATGATGACACCTCTGTGAGTCTGTGACCGAGCAGATATCA	5609
Db	25300	GTATTGCTCAGACAGGTATGATGAACAAACCTGTTACAGCAACTTTCCAAAGTCAGTTAA	25241
Qy	5610	ACCGCATACCGTGGAGGATGCTTTTAAACCTATCTGACCAAGTTTGGACGATTTGCCA	5669
Db	25240	ATATCGATACCGTTGAAGATAGCTTTTAAATAATATCTGACCGCATTTGAAGATGTGCTA	25181
Qy	5670	ATCTGAACACTGTGAGGATATCAGATTAACGACGATGACGAGGGGACTACATGGT	5729
Db	25180	ACTTGCAGGTGATTAGCGGATATCATGACAGTATTAATGTCAATGAGGGGCTCACTATT	25121
Qy	5730	ATGTGGTCCGAGATCAGAGATCAGACTAATCTGGTACTCGGCGAGCGCCAAACACAGCA	5789
Db	25120	TAATTGGTTATAGCCAGACAGAACCCAGATATATTATTGGCGCAATGTGATCACCAAA	25061
Qy	5790	AAATCCNAGACTCAATGATCCCGCGAATCCCTGGACCGATGGACAAAATTAACCTGCG	5849
Db	25060	AGTGCCAGACCGTCAATTTGCTGCTGGCTGCTGGGAGAAATGAAAAAATGAAATAC	25001
Qy	5850	GAATGAATCCGTTGTCAGATCTGTGTGCTGGTGTGTTTCAACAGTTCGCTTTATGTGCG	5909
Db	25000	CCATCAATGTATGGCAGGAAAAATACAGACTGTATTATTAACAGTCTGCTTTGTTTAC	24941
Qy	5910	TCGTGGTTCGAAGAGAAATCAGTCTGCTGATACGGAGGCGAGAGACGACCAACCGCAGC	5969
Db	24940	TTGTGCTGGAAACAAAAGAGCTGAAAAAATGAAGTGAAGTGGCAAGATAGATATCACTG	24881
Qy	5970	AGAGCTACAGCTGAACTGTCTTCGGCGCTACGACGCTACATGAGTTTCCCGGTGT	6029
Db	24880	AT---TATATATTAAACTGTACATATTCGTTATGATGGCAGCTGAGGCTACCGTTTA	24824
Qy	6030	CGTTCGACATTACCGGCAACATGCGATTTCCGG-----AAACGAGGCGCATGCAATGTG	6082
Db	24823	ATTTTAATGTGACTGATAAAATAGAAAAACCTGATCAATAAAAAAGCAGCATTTGGTATGT	24764
Qy	6083	ACCTGTAATCCCTGACTGAGCAGCTCTATTGGCGCTTTTATCTCGCTCACCACGAAGCC-	6141
Db	24763	ATTGTTCTTCTGATTAATGAAAAAGACGCTCATTTATGTTTATTTTCCATGAAAAAAGACA	24704
Qy	6142	-----GGACTTTGATTAACGCTCAGCTGATTTCTGTGGATAATGATATGACGC	6188
Db	24703	ATTATTTCTTTAATAGTCTTCTGCAAGAGAGGATGACCATTAACCTTGATATGACAT	24644
Qy	6189	TAAATGTCATCTCAGATA-----TAGGGATTTTAAAGAGCGTCAGTCACGAAATTTA	6239
Db	24643	TATCCATTCTCAGAAAAATGATTTAGACGCCATTCTTAAGAGCACAATTATCAGAACTTG	24584
Qy	6240	ATACGAGCAGCTG---AGAAATTTAATAATGTTTTTTCAGACCCCTTCGCTAATTTATT	6296
Db	24583	ATACCAGGACAGAAATCAAAAGTCAACAATTTGCTACAGATTTATTTGGCCGAAATATA	24524
Qy	6297	TTGTGAGTCAACGAGTGTAAATTTGA--TGATGTTATCCACAGCGATTTCTCACTCCTTA	6353
Db	24523	AGGATCTATACCAAAAAAATAAATTAGCCAGTTTTTACCGGAAATATTTTTTGATCTCT	24464
Qy	6354	ATTCTAAAACTCAAGTACTGTTTTTAAAGAGATTTCTCTCTTTTGGACCCAGAGC	6413
Db	24463	CGTATATATCACCAGGAAATGGTCATATTAAATTAAACGTTCAATCTTCAATGGAATTA	24404
Qy	6414	TTCAATATTACAGCAATGTTTCGTGTTTGTAGTA-----CTG	6452
Db	24403	ATTTTTCAAAAGGCAATATATATAATGATGAGGTTAAATACTGTTATCGATGGTAGAAG	24344
Qy	6453	CTGGCATCCCACTCAATCTACCATAGAAAAATTCGTTTCAGGCGAGGATAGAAATTTGAGG	6512
Db	24343	ATGAAACGGTTATTTTATTTGATTATGATAGATCATGAAATGCTTGGAAAGAGAGAG	24284
Qy	6513	AAATTAAT-----TTTTATGAGCCGAGGCGCCGCGGAGTTTTCAGG	6555
Db	24283	AGTTTTTTCATTTATGAACTTTTGGATTTTATTTATTTTCCATCGATCTTAAAAATGCGCAAT	24224
Qy	6556	ATTGTGGGAGTGGATGTTTCTAATTTCAAAAGTATACAGGTC--GGAAAAAGAGCAGTTG	6614
Db	24223	ATTTTAGAGTGTTAATGTCATCTAAGAAACCAAGGAAAAAATTCCTAGAAAAATCAGAAATG	24164
Qy	6615	GTGTCACTGTAAAACTCTATTCGTCACCTGGCGTTAGTGT-----CTGTTGAGTTATT	6669
Db	24163	GAGTTGGTATAAATTATGATTTATGAATCAGATGATGCTGAAATCAAACTTGATACCTAACA	24104
Qy	6670	TATTGATTCAATAAATACTTCAGCGAAATTTTGTGAGATA---AAATGATAACCGC	6726
Db	24103	TAGTATTAGATTGGAAGATAACACAGGAGTAGGCATATAATGTAATCATTTTACTA	24044
Qy	6727	TTTAATTAGGGCAGTACATCAAAAGTAAATTAACGTGTGCTGTTTGGCTCTCAAGATTT	6786
Db	24043	ATGATGTTTCAATCAATTAATCAATGGAATAATTCGGGCACCTGTTCTTCGCGAGGATC	23984
Qy	6787	TTGAGGTGTAAGTCCCTCATGCGGCAC--TTTCAGATATATGAATTAATTAATCGATGATC	6844
Db	23983	CATGGGTGATTATTGTTTCAACAGCCACAGATAAATAAATCTGTTCTATCTATGATCGA	23924
Qy	6845	ATACTGACATCCGCGCTAAATGGGACTGAAATTTAAATCTCGGCTTCCTCGCTGAATGGTAT	6904
Db	23923	ACAGATCAAGATAAAAAACATTAGTTTTTTTATTTAAAAAATGGCTCTGATAT--TCTAGTGG	23865
Qy	6905	AATGATAAGCTGAGTCTGCATCCGGGAATAATCTTTTCAACACCAAAATCGCTGAGTTTT	6964
Db	23864	AGTTAAATGCTGAAGACCATGTGGCATCTAAACCTTCAACAGAAATCTGACCCCTATGTTAT	23805

QY 6965 ACCGTTAAATACCAAGTATTA--TTGTTGAAGATGAGTTTGACGTGACGTTTACGTTTACCG 7022
 Db 23804 ATGATTTTAACTCAAGTAAAGTTGATTTGAAGGCTATGATATCTCTGTTGAGCGAGT 23745
 QY 7023 CTGTCGATCAGAAATACGTCGTGCGCCGCGGAGCGGCATATTAACCGTCATTT--- 7078
 Db 23744 TTATTATTAAAGCAACCCGACGCGGTTTAAACGATATTTTATTGAATCGCAATTTTATA 23685
 QY 7079 -----CGAAACATTAATAATGACATCTCGTTTATGCAATTAAGTAAATAATGCGTGGCG 7133
 Db 23684 TAAACATTAATAATGCAAGATACAGTAAAGTTATATCATCTGATTAATAATGCCATCAGCA 23625
 QY 7134 CGCAGTATATTCGTTTCACTCGGGGTAACGATGTGCGCTTATTCGCTCAACACCTCT 7193
 Db 23624 CACAATATATGACATTTGGCCCTTACA-----GAACCGGTTAAATACTTTAT 23577
 QY 7194 TTGCCCCGACCTGTCGACCGGCGAATACCGGATTCACACCATTTCTTCCATGGAGA 7253
 Db 23576 TTTCCAGAAATTTAGCTGAAAGAGCAATATTGGTATTGATTAATGTTTAAAGTATGGAAA 23517
 QY 7254 CCCAGAGGCTTACCGAAACCGCCCTGGAAGAGGGAGTGTATGTTTATGAGCTTCTC-- 7311
 Db 23516 CGCAAAATTTACAGAGCCGCAATTAGGTGAAGGTTTATGACATTTAAAGTTGCCCC 23457
 QY 7312 ----- 7311
 Db 23456 CCTACAATAAAGAGGAGCATGTTGATGAACGTTTGAATCCATATTTGGGAATATTG 23397
 QY 7312 ----- 7311
 Db 23396 ATGGCAATTCGCCAGACAACTTATTACGAAGGATGTTATCTGATATTGAACACACAG 23337
 QY 7312 ----- 7311
 Db 23336 TAACGCTCTTTGTTCCCTATGCTAAAGGATATTACATACGTGAAGGTGTCAGATTAGGG 23277
 QY 7312 ----- 7311
 Db 23276 TTGGGTACAAAAAATTTATCTATGACAAATCTCTGGGAATCTGCTTTCTTTTATTGATG 23217
 QY 7312 ----- 7311
 Db 23216 AGAGGAAATCAATTTATATTCACTAAATGATCCGATCATGATTCCGGNATGACACAAC 23157
 QY 7312 ----- 7311
 Db 23156 AGGGATAGTAAAAAATATCAAAAAATATAAAAGGGGTATTCAAGTCGTGTCTATGAAAA 23097
 QY 7312 -----CGAGCCCAATGCCCTCTATTCTTCTGGAGCTGTCT 7346
 Db 23096 TAACACTGAACCCATGATTTCAACCGCGCCCAATGCAATCTATTTCTGGGATTTGTTCT 23037
 QY 7347 ATTAC-ACGCGGATGATGTTTCCAGCGTTGTTGAGGAAACAGCACTTTCCCGAAGCC 7405
 Db 23036 ATTACAGCCCATGATGTTTCCAGCGTTTATGCAAGAGCAGATTTTACCGG-ATCG 22978
 QY 7406 ACCGCTGGCTGAGTATGTTGGAACCCGCGCGGACGCTGTGTAACGGGTGCTGCGAG 7465
 Db 22977 ACAGCTGGCTGCGCTATATCT-GAACCACCGGATATTCCGTTTACGGTTCAGGGTGAATGCG 22919
 QY 7466 AATTACACCTGGAATGTCGCTCGCTGGAGAGGACACCGGCTGGAACGACTCGCGGCTG 7525
 Db 22918 GATTATTACTGGAACGTCGCGCCATTTGAGGAGATAGCTCTTGGATGCCATCCGCTG 22859
 QY 7526 GACTCCATTTACCCGATGCAATAGCCGATGACGCCCATGCAATTAACAAGTTCGCCACC 7585
 Db 22858 GATTGCGTGCATCCGAGCGCGTTTCCCGAGCATGATCCGATGCACTATAAAGTGGCTACC 22799
 QY 7586 TTTATGTCGATCTGACCTGCTCATTTGCGCGGTCATGCGGCTACCGGCTGCTCGAG 7645
 Db 22798 TTTATGAATGCTGGATTTGTTGATTACCCGCGGAGATAGGCGCTATCCGAGCTTGAA 22739

QY 7646 CGGACACCCCTTAACGAGGCCCGGATGTTGTTACGTCAGGCGCTGAACCTTCTCGGCGAC 7705
 Db 22738 CGTGATACCTTTAAACGAAGCTAAAAATGTTGTTATGATACAGGCGCTCACTTTATTGGGTAT 22679
 QY 7706 GAGCCCTATATTTCTTTGACCGCGACTGTTGCGGCTTGACCTCTGGGTGAACGACGCGACG 7765
 Db 22678 GAGCCTTATTTTTCATTTGGATAACGATTTGGTTCAGAGCCAGGCTGGAAGAGCTGCCAGC 22619
 QY 7766 GAGGTGACGCGACGCGATTTACAGAGGCCCTGTGCGCGTGTGCGCGGTTGGTGCCTGCT 7825
 Db 22618 CAAACAATGCGCATCATTTATCAACATAAAATGCTCAAACTGCGTCAGCGCGCTGCATTA 22559
 QY 7826 CCCGAGACAGGAGCGGAGAA--TTCCCTGACGCGACTGTTCTCCGCGAGCAGAGAGGT 7884
 Db 22558 CCCAGAAACGTAACGCAAAATTTGTTAACCGCATTTGTTCTCTCTCTAAATTAATAAAA 22499
 QY 7885 GCTCAAAAGGCTACTGCGCAAACTTTGGCACACGCGCTCCATAACCTGCGCCCAACCTCTC 7944
 Db 22498 ACTGCAAGTTTACTGGCAGACATTGACGCAACGCTCTATAACTTACGCCATAACCTGAC 22439
 QY 7945 CATGACGCGCAGCGCTTTCTGTCGCTGACGCGCGCTCCGAAACGCTCGCCCT 8004
 Db 22438 AATCAGCGTCAGCCACTGCTATATCTCTATGTCGCGCGGATCGGTCATGTT 22379
 QY 8005 GCAGAGTCCGTCGTCAACAGCGCGCGGCTGTCAGCACTGCGCGCGCGGCTGATGCC 8064
 Db 22378 ACTGAGTCTGCCATCATCTGCTTCAAGGCGCGCGCATTTTACCTCATGAGTATGCC 22319
 QY 8065 GCTTTACAGTTTCCCGTTCATGCTGGAGAAACGCGCGGGATGTTGAGCTGCTGACCGG 8124
 Db 22318 GATGTACCGTTTTCGCGTGTCTGGAATAATGCCAAGTGGGGGTAAAGCAGTTGATACA 22259
 QY 8125 GTTCGCGACACATGCTCGGTATTACCGAGCTCAGGATGCGGAGGCGCTGGCCAACT 8184
 Db 22258 ATTTGCGCAATACCTGCTCAGCATTTACTGAAACGCGGAGTGCAGAAAGCTTGGCTGAAT 22199
 QY 8185 GCTGCAGACCCAGGCGAGTGAACCTGATACGCGAGGCGCTTCGCCAGCAGGATAACGCTCT 8244
 Db 22198 ACTGCAACTCAAGCAGTGTAGTCCCTGCAAGTATTAAATGCAAGGATAAGGTCAT 22139
 QY 8245 CGAGAAATTCGATGCGGATTTGCGCGCTTGAGAGAGAGCCGCGCGGCGCAGATGCG 8304
 Db 22138 GCGTGAATTTGATGCTGATAAATTTGCGCTTTCAAGAAACCGCTCATGTTGTCAGCTGCG 22079
 QY 8305 TTTTGAAGTTTCAAAAGTTTGTAGAGCGGAGCTCAACACCGCGGCAAAACAGCGCAT 8364
 Db 22078 TTTTGACAGTTTCAATAACGCTGTACGAGATGTTAAACGCTGTTGAAACAGCGAT 22019
 QY 8365 GGACTTTGACCTCAGTTGCTGCTGTCGTCATCAACCGCGCGCTCTTTTGGCGCA 8424
 Db 22018 GGATCTTTTACCTCTCTTCACTGCTTGAACACCGCGCAACAGCTTATGCGCGC 21959
 QY 8425 GCGCGCGCGGATGCTGCGCAATTTTACGGGCTGCGCGCTGCGCGGCTCCCGCTATGCG 8484
 Db 21958 GCGCGCGGAGATCTGCTCCCAATTTTACCGGTTTGTCTGTTGAGGTTTCCGTTTGG 21899
 QY 8485 GGCACATTTTAAAGCCACCGCATCGGATTCAGGTGCTCTCCGATGCCACCGCATATC 8544
 Db 21898 GCGCTTTTCAATGCGAGTCCGATTTGGTATCGAAATTTCTGCTCAGCAACAGTATTGC 21839
 QY 8545 AGCGGCAAAATCAGCAGTCCGAGTGTACCGCGTCCCGGAGGAGTGGGAATCCA 8604
 Db 21838 CGCAGCAAAATCAGCAATCAGAAATATACCGTCCCGTCCGCAAGTGGGAATTTCA 21779
 QY 8605 GCGTGTAGTGGCGAGTCTGACGTGGCGCAGATTTGATGCCAGCTGCGCGCGCATGCGAGT 8664
 Db 21778 GCGCAATATGCGAGCTGAGATAAAACAAATTTGATGCTCAATTAGCCAGCTGGCTGT 21719
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 Db 21718 AGTCTGTAAGCGCGAGTATTACAAAAAACTATCTGGAATCTCAGCAGGCAAACTCA 21659
 QY 8725 GCGCGAGTTGGCATTTCTCTCAGAGTAAGTTCAACAATACGGCTCTCTGACAGCTGGCTGCG 8784

Db 21658 GGGCAGCTAGCCTTTCTGCAAGTAATTCAGTAATGCAGCGCTATACAACTGGCTCCG 21599
 Qy 8785 GGGCAGCTAGCCTTTCTGCAAGTAATTCAGTAATGCAGCGCTATACAACTGGCTCCG 8844
 Db 21598 TGGAACTGCTGCGCTATTTATATATCAGTTTATGATTTGGCGCTCTCACTCTGTTTAA 21539
 Qy 8845 GGGCAACAGCGCTGGCAGTGGGA--TAAATCGAGACTAGTTCGTTTATCAGCGCGG 8901
 Db 21538 GGCAGCAACTTATCAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 21479
 Qy 8902 GGCCTGATGGGCAAAATCCGCTGCTGCGCGGGAACCTGATGATGATGATGATGATGAT 8961
 Db 21478 TGCTTGCACTGGCACTTATGCGGTATTAGCGGTGAAACCTGATGATGATGATGATGAT 21419
 Qy 8962 GCAGTGGAGCAGCGCTGCTGCGCGGATGAGCGGCAATAGAGTACGCGGACGCT 9021
 Db 21418 ACAGATGGAAGAAAGCTATTGGAAAAAGATGAACGGGCACTGGAGGTCAACGAACCGT 21359
 Qy 9022 CTGCTGCTGCGAGTCTATACAGCCTCGCGGAGATGCGGCACTCTCTGCGCGACAA 9081
 Db 21358 TTCTCTGCTGAGTGTATGCTGCTGACAGAAAT--AGTTTCAATTTTAAAGATAA 21302
 Qy 9082 GGTGCTGGAATCGTCTAGTAACTGCGGCGGATGCGGCGGATGCGGCGGATGCGGCGG 9141
 Db 21301 AGTGACTGAGTTAGTCAATGAGTGAAGCAGTGCAGGCAACAGCTTAACGGTTTGA 21242
 Qy 9142 GATGATCAACAGCACTGAGGCGCCCTGGAACCTGCTGCTGCTGCTGCTGCTGCTGCT 9201
 Db 21241 CGTGAAGGACACAACTGCAAGCGCCTCAAAATTCGATCTGAATATGCTACCGA 21182
 Qy 9202 TTACCGGCTCTCCCTGCGCAGTATGAGCGCATCAACAAATAGCGTCAAGCTCCGCG 9261
 Db 21181 TTATCTGACGTTTAGTAAATCACCCGATCAACAAATCAGTGTGACGTTACCTGC 21122
 Qy 9262 GCTGCTGCGCCCTTATCAGGACGCTCGTGGGTTCTCAGCTAGCGGGAAGTATGCTCAT 9321
 Db 21121 CCTTTAGGCTTATCAGGATGCTCGGCAATCTGAGTTATGCGGCGAGTACAATGAT 21062
 Qy 9322 GCGCGGGTTCAGCGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9381
 Db 21061 GCCACGTGGCTGCAAGCGATGCTGATCTCACATGGCATGAATGACAGTGTCAATTC 21002
 Qy 9382 ACTGATTTCAATGACCGGCTTACCTGCGGTTTGAAGGACTTCCAGTTGATGACACAG 9441
 Db 21001 GATGATTTCAATGATCTAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20942
 Qy 9442 GACCTGACACTGAGCTTCCCGGATGCTGACGCAACAGCGGATGCTGCTGCTGCTGCT 9501
 Db 20941 CACATTAACCTCAGTTTCCCGGATGCTGACGCAACAGCGGATGCTGCTGCTGCTGCT 20882
 Qy 9502 GAGGACATCATCTGATATCCGTTTACACATATCAGCTGAT 9545
 Db 20881 GAGGATATCATTTTGCATATCCGTTTACACATATCAGCTGAT 20838

RESULT 8

ABS52584
 ID ABS52584 standard; DNA; 4431 BP.

XX AC ABS52584;

XX DT 30-DEC-2002 (first entry)

XX DE P. luminescens (W-14) tcdB gene.

XX Gene; ds; toxin A; toxin B; TcdA; protoxin; TcdB; Tcc2; transgenic;
 KW monocot cell; dicot cell; oral toxin; insect; pest; TcBa.

XX OS Photorhabdus luminescens.

XX Key Location/Qualifiers
 FT CDS 1..4431

FT FT /*tag= a
 XX /product= "TcdB"
 PN US2002078478-A1.
 XX 20-JUN-2002.
 PD 26-MAR-2001; 2001US-00817514.
 XX 24-MAR-2000; 2000US-0191806P.
 PR (FFRE/) FFRENCH-CONSTANT R H.
 PA (BOWE/) BOWEN D.
 PA (ROCH/) ROCHELEAU T A.
 PA (WATE/) WATERFIELD N R.
 XX Ffrench-Constant RH, Bowen D, Rocheleau TA, Waterfield NR;
 PI MPI; 2002-655379/70.
 XX P-PSDB; ABG32652.
 DR Novel nucleic acid sequences which encode genes, tcdB and tcc2 from
 PT Photorhabdus luminescens W-14, useful in heterologous expression of
 PT orally active insect toxins.
 XX Claim 2; Page 15-20; 40pp; English.
 XX The invention discloses an isolated nucleic acid that encodes TcdB or
 CC Tcc2 from Photorhabdus luminescens W-14. Also disclosed is a transgenic
 CC monocot or dicot cell and a transgenic plant (including the seeds) both
 CC with genomes comprising tcdB and tcc2 nucleic acids. The nucleic acids
 CC are useful for producing Toxin A or B of P. luminescens W-14 in a
 CC heterologous host and for encoding TcdB or Tcc2 for producing an orally
 CC active insect toxin in a host, where the host also expresses TcdA or TcBa
 CC from P. luminescens W-14. Heterologous expression of Toxin A does not
 CC afford the level of oral toxicity to insects as that of the native toxin,
 CC but the coexpression increases this toxicity. The transgenic plants
 CC expressing effective amounts of the toxins protect themselves from insect
 CC pests. When the insects feeds on the transgenic plant it also ingests the
 CC toxins and this deters the insect from further biting into the plant and
 CC may even harm or kill the insect. The sequence presented is the P.
 CC luminescens (W-14) tcdB gene
 XX
 SQ Sequence 4431 BP; 1151 A; 1167 C; 1094 G; 1019 T; 0 U; 0 Other;
 Query Match 5.9%; Score 1108.8; DB 6; Length 4431;
 Best Local Similarity 56.0%; Pred. No. 6e-253;
 Matches 2493; Conservative 0; Mismatches 1732; Indels 225; Gaps 12;
 Qy 9598 ATCGAAATCATCAAGCATGCGCATCTACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 9657
 Db 1 ATCGAAATTCACAAACATTCAGTGTACCGAGCTGTCTATTACCAAGCGGCGGCGCT 60
 Qy 9658 GTCACCGGCTCAAGGCTGATATCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 9717
 Db 61 ATTACCGGTATGGTGAAGCATTAACACAGCGCGGCGGCGGCGGCGGCGGCTATCC 120
 Qy 9718 ATTCCCTTCGCGTTAGCCCGGTTAGCGGGTTACGCCCCCACTGGGGGCGACTTAATATCAC 9777
 Db 121 CTGCCATTACCATTTCCGCGGCGGCTGGTTAGCAGCCCTCGCTCACTCTGATTTACAA 180
 Qy 9778 AGCGGCTCGGGGAACGCGCCCTTTGGCATTTGGCTTGGGACTGCGCGGCTCATGGCAATTCGT 9837
 Db 181 AGTGGAAACCGGTAAACAGCCCAATTTGGTCTCGGTTGGGACTGCGCGGCTCATGGCAATTCGT 240
 Qy 9838 CGTCGTACGCGCAACGAGCACCTACTACGATGATGATGATGATGATGATGATGATGATGAT 9897
 Db 241 CGTCGACCAAGTACCGGCGGTACCGAATACGTAAGAAACCGATCTTTCTGGGGCGGAA 300
 Qy 9898 GGTGAGTGTCTGCTGCGGCGGCTCAGCGGCTGCTGGGCAACCAAGAACCGAGCGCCACC 9957
 Db 301 GGTGAAGTGTGCTGCTGAGCATTAAATGAGGAGGTCAGCTGATATCCCGCAGTGAATCC 360

Db 2512 GCTTTCGGCGGTTTACGCCACGTTTACTCTCTGGAAAGAGGCGAAGATGTTTCCACTG 2571

Qy 12175 ACTCG---GACGACAGCAACATCTCTGGTTCAGCGAGCCCTGAAAGGCATCCTCGTG 12231

Db 2572 ACACCGGAAGATGACCATATCTATCTGTTTAAACCGGGCGCTAAAGGTTCAGCACTG 2631

Qy 12232 CGCAGTGATATACGGTTCGGATGCGACGACGCGCGATATCCCTTACAGCGTCACT 12291

Db 2632 CGTAGTGAATCTACGGGCTGGATGGCAGCGCACAGCAACAGATCCCTATACAGTGACT 2691

Qy 12292 GAGTCTCGCCGCGAGGTACGGTATGTAAGCGAATG---GAGACTACCGGTGGTGG 12348

Db 2692 GAATCCCGTCCACAGGTGCGCAATTAAGATGCGCGCACCGGTTTCCCGGTGCTCTGG 2751

Qy 12349 CCGATGGCGGGAAGCGGTACGTCACTGTTTATGAACGGTACCAATGATCTCTCAATGC 12408

Db 2752 GCCTCAGTCTGGGAAGCGGTATATCACTACGAAAGTATATCACTGATCCCACTGC 2811

Qy 12409 CAACAGAGGGGTACTCTCAGTGATGATACGTTTCCCATCTGCGTCAAGTCACTGTC 12468

Db 2812 AATCAGGATATCAGTTGTCCAGTGACCTATTTCCGGCAACCACTGAAACAGGTTTCCGTA 2871

Qy 12469 AATTATCCAGACGCCCTCGTCCGCGGCAATCCATATCCGGCTCTTACCGCGCAGC 12528

Db 2872 CAATATCCCGCCCAACAAACCAACCAATCCGTATCCCGATACCTACCGGATACG 2931

Qy 12529 CTGTTGCCCAACAGTTATGACGAGCAGCAGATATATAGCCTGGGGTTGCAACAGAGC 12588

Db 2932 CTGTTGCCAGCAGTTATGACGATCAACACAGCTATTGGATTAACTGCGGACATCC 2991

Qy 12589 AGTCCACATACCTTTGTTCACTGCTGAGGGGCAATGTTGTTGGGGTTGGCGAGCG 12648

Db 2992 AGTTGGCACCATCTTAIT-----GGTAATGAGCTAAGAGTGTGGGATTACCGGATGC 3045

Qy 12649 TCGCGGACAGTATTAATCACTCTCGGACAACTGTCGGAGAGGGGTCTACGCTG 12708

Db 3046 ACAGCAGTATGCTTTTACTTACGATGCAACAGGTACCTGTCGATGCTTAAATCTG 3105

Qy 12709 GAACACCTGTTGGCGCCGAAAGCCTGCTCTCGATAGTCAAGTTCGGTACGCTGGCGGT 12768

Db 3106 GAACCTCTGCTGTAATAGCTGATTCGCGATGATAACTCGGATACCTCAAT 3165

Qy 12769 CAGCAGCAAGTCTGTTATCTGATTCACAGAGTTCGCCACGCTCGCTGCTCGGCCACTC 12828

Db 3166 CAGCAACGAACGTTCTATACCGACGGGAAACCAACACCGCTGAAACACACGACAGCA 3225

Qy 12829 CCCCCAAGTAGCTTTTATCGAAACCGCGTCTGATGAGGTATGCTAGTTCACTG 12888

Db 3226 CAAGCGTTAATCGCTTTTACCGAAACCGCGGTATTAACGGAATCTCTGTTATCCGCGTTT 3285

Qy 12889 GCTGCCTACATTGTGGATGA-----ACATCTCGAGCAAGCGGTTACCGGCAA 12936

Db 3286 GATGGCGGTATACGCCAGAGTAATACCGGATATCTGACAGGCCGGATACCAACAA 3345

Qy 12937 TCGGGATACCTTTTCCCTCGAGGAGGGAAGCAGAACAGGCATTTGTGGACCCAGTGTGAG 12996

Db 3346 GAGCCTTATCTGTTTCCACGACCGCGGAAACAA-----AGTTTGGGTAGCGCGTCAA 3399

Qy 12997 GGATATGTTACCTATGCGCGGACAGCANTTTCTGGTACCGTATCTCTTTCCGAGCAGT 13056

Db 3400 GGCTATACCGATTACCGGAGCGGAAGCAAAATTTTGGGCTCTGTCGCAACAGTAAACAGC 3459

Qy 13057 ATGTTGACCGGCCAGTTACCGTGAACGCGTGAACGCTACGCTACGCTACGCTACGCTG 13116

Db 3460 CTGTTAACCGGGAATGAGTTAAATGGGATACTCACTATTGTGTCATCCCAAC 3519

Qy 13117 CAGGATCCGAGGATTTGACCAACGCGGACTATGACTGGCGCTTCTCTGAGCGCCGCTC 13176

Db 3520 CAAGATGCTCGCGGCTCACCGTCTCAGCCAAATATGACTGGCGTTTCTCACACCAACG 3579

Qy 13177 CCGGTGACGACCCCAATGATATCTGCACTCGGTCTCTCTGATGCTCTGGGCGGGGT 13236

Db 3580 CAACTGATGACATCAACGATATGTGCTATCTCATACCTTGGATGCTCTGGGACGCGCT 3639

Qy 13237 ACCACCTCGGATTTCTGGGACGAGATGGTATTTGCCACCGGTTTACAGT----- 13287

Db 3640 GTCAAGCAAGTCTTCTGGGGATCGAAAGCGGTGCGCAACAGGTTTACTCTTCAATCAAG 3699

Qy 13288 GATGCCACGTTGTCGGTTCGGACGCGCAGACGCGCTCTGGCGTTGACGCGCCCTTA 13347

Db 3700 GAAAAACCAATCTCTCCACCAACGATATCGATACCGCTATTAATCTAAACGGAACCACTC 3759

Qy 13348 CCAAGTACGACAGTCTGGTGTATGTCACGACAGTTGG----- 13386

Db 3760 CCTGTGCAAGTGTCTGGTCTATGACCGGACAGTTGATGCACTATTCAAGTCAAGAA 3819

Qy 13387 ----- 13386

Db 3820 ACCTTCAACACATTAACGACGAGAGCAGCGCTGCGTATTCACGTATTATCAAG 3879

Qy 13387 -----GGAGATGACGACAAATGAGAAAA----- 13408

Db 3880 GAAGATTTGGCGTATTTGGCGCACTGACTCGCGCGCTTGGCTACAAAGTCAAAAGATCAGT 3939

Qy 13409 -----TGCCCCCGCAGTGGTCTGCTG 13431

Db 3940 ACACCATAGTTAACTGTTAAACACAGCATTTGTTTACCTCCCATTAACCTTACCGCTG 3999

Qy 13432 GCTACCGATCGCTATGACAGTATACCGGACAGCGTCCGCCAACAGGTGACATTTCAGT 13491

Db 4000 ACCACAGCGTTATGACCGGACTCTGACGACGAATTCGCCAACAGTTCGCAATTTAGT 4059

Qy 13492 GACGGTTTGGCGTGAATCGGCAACCCGCGAGCGGCGGCAACGCTGCGCAA 13551

Db 4060 GATGGTTTGGCGTCTGCTACAAAGCTCTGTACGACATGAGGCGAGCGGCGCTGCGCAA 4119

Qy 13552 CGAGGACGCGACCGCAACTGTTGTCAGCGGCGTGTGCGGTCATCTGTAGCAAGC 13611

Db 4120 CGTAACCAAGACGGTTCTCTGTTGACAAAAGTGA-----GAATACC 4161

Qy 13612 AATTTCCGCTGGCGGCTCACCGGAGCGGAGTATGACAAATAAGGTCTGCTGTTCCG 13671

Db 4162 AAACCGGTTGGCGGCTCACGGACGCCAAGATATGATTAAGGGCAACGATACGC 4221

Qy 13672 GTTTATCAGCGGTTTCTGGAAGTGGCAATATCTCAGTGTGACAGTGGCGCCGCGAG 13731

Db 4222 ACTTATCAGCGCTTCTTCTCAACGACTGCGGATATGTCACTGATGACGCGCCAGAAA 4281

Qy 13732 GACCTGTATGCGCAGCAGCATTCTTTAGGATCCGACGCGAAGTGGCAGGTTATTACG 13791

Db 4282 GAAGCCTATGCGGATACTCATATTTATGATCCAAATTTGGGCGAGAAATCCGGTTATTACT 4341

Qy 13792 GCAAAAGGTGAACGCGGACAGGTTGTTATACCCCGTGGTTTGTGTCAGTGAAGACGAG 13851

Db 4342 GCAAAAGGCTGGCTGGCCAAAGCCAAATTTCCCGTGGTTTACCGTGTAGTGAGATGAG 4401

Qy 13852 AATGATACCG 13861

Db 4402 AATGATACCG 4411

RESULT 9

ADN61378

ID ID

ADN61378 standard; DNA; 4434 BP.

XX

AC ADN61378;

XX

DT 01-JUL-2004 (first entry)

XX

DE Photorhabdus strain W14 tcdB1 toxin complex DNA.

XX

XX Cry; toxic; lepidopteran pest; toxin complex; insecticide; strain W14;

XX

XX ds; tcdB1.

XX

XX Photorhabdus sp.

XX

PN WO2004002223-A2.
 XX 08-JAN-2004.
 XX 27-JUN-2003; 2003WO-US020082.
 XX 28-JUN-2002; 2002US-0392633P.
 XX 21-JAN-2003; 2003US-0441647P.
 XX (DOWC) DOW AGROSCIENCES .LLC.
 XX Bintrim SB, Bevan SA, Zhu B, Merlo DJ;
 XX WPI; 2004-082821/08.
 XX Screening a culture of *Paenibacillus* isolate for Cry protein or toxin
 PT complex protein, useful for controlling lepidopterans, comprises
 PT obtaining DNA or protein from the culture and assaying the presence of
 PT the gene or protein.
 XX Example 12; SEQ ID NO 42; 220pp; English.
 XX The invention relates to a novel method for screening a culture of a
 CC *Paenibacillus* isolate for a gene encoding a protein selected from a Cry
 CC protein that is toxic to a lepidopteran pest and a toxin complex protein.
 CC The method comprises obtaining DNA from the culture and assaying the DNA
 CC for the presence of the gene or obtaining a protein produced by the
 CC culture and assaying the presence of a protein that indicates the
 CC presence of the gene in the isolate. The method of the invention has
 CC insecticide applications and may be useful for screening *Paenibacillus*
 CC sp. for toxin complex (TC)-like genes and proteins which may themselves
 CC be used to enhance or potentiate the activity of a stand-alone
 CC *Xenorhabdus* toxin protein. The method may also be useful for screening
 CC *Paenibacillus* sp. and others for insecticidal thiaminase genes and
 CC proteins for controlling insects, particularly lepidopterans. The current
 CC sequence is that of the *Photorhabdus* strain W14 tcdB1 toxin complex DNA
 CC of the invention.
 XX
 SQ Sequence 4434 BP; 1152 A; 1167 C; 1095 G; 1020 T; 0 U; 0 Other;
 Query Match 5.9%; Score 1108.8; DB 12; Length 4434;
 Best Local Similarity 56.0%; Pred. No. 6e-253;
 Matches 2493; Conservative
 9598 ATGCAAAATCATCAAGACATGGCCATTACTGCCCCCAGCTTGGCTTCGGGGGGGGTGG 9657
 4 ATGCAAAATTCACAAATTCAGTGTACCGAGCTGTCAATACCCAAAGGGGGGGCGCT 63
 9658 GTCAACCGGCTCAAGGGTGATATCGCGGGGAGGCGCGATGGTGGCGGACCCCTGAGT 9717
 64 ATTACCGGTATGGTGAAGCATTAACACAGCGGGCGCGATGGTATGGCGGCTTATCC 123
 9718 ATTCCCTTCGGGTAGCCCGGTTCGGGGTTACGCCCCCAGCTTGGGGCAGCTTAATTATCA 9777
 124 CTGCCATTACCAATTTCCGCGGGCGGTGTACGACCCCTCGCTCACTCTGAATTACAAC 183
 9778 AGCCGCTCGGGGAGACCGCCCTTTGGCATTTGGTGGGTATCGGCGGTGCTGCTCCAG 9837
 184 AGTGGAAACCGGTAAACAGCCATTTGGTCTCGGTGGGAGCTGGCGGCTCATGGCAATTCGT 243
 9838 CGTGTACCGGCAACGGAGCACCTACTACGATGATCTGATGAATTCACCGGTCCGGAC 9897
 244 CGTTCGACCAAGTACCGGCGTACCGAATTACGATGAACCGATATCTTTCTGGGGCCGAA 303
 9898 GGTGAGGTGCTGTGCGGCACTCAAGGTGCTGGCAACCCCAAGACACGCGAGGCCACC 9957
 304 GGTGAAGTGTGCTGTAGCATTAATGAGGCAAGTCAAGCTGATATCCGAGTGAATCC 363
 9958 TCACTACTGGGTAATACCCAGCGGAAGCTTCAAGTTTCAGTTTACGTTTACGCTACGATG 10017
 364 TCATTGAGGGCATCAATTTGGGTGCGACCTTCACCGTTACCTGTTATCGCTCCCGCCTA 423
 10018 GAGGGTAGTCTCAGCGCGCTTGAGCGTTGGCTGCCCGGACGAGACAGAAACGGAATTT 10077

Db 424 GAAAGCCATTTTAAACCGGTTGGAATACGGCAAAACCCAAACAAACCGGCGCAACCGGATTC 483
 QY 10078 TGGGTGTTATATACCCCTGACGGAAGGTGGTCTGTGGGCGGAAATCGCGAGGCTCG 10137
 Db 484 TGGCTGATATACAGCCCGGACGAGGTCCATTTACTGGGCAAAATCTCTCAGGACGT 543
 QY 10138 ATCAGCAACCCACAGCCCAACAGAGCGGGGTTTGGCTGATGGAGTCTCGGTATCA 10197
 Db 544 ATCAGCAATCCAATCAATGTTAACCAACAGCGCAATGGCTGTTGGAACCTCGATATCA 603
 QY 10198 CTTACCGCGCAACAGATGTTATACCAATACCGTGGGAGAGATGATGACGGTGTGACGAG 10257
 Db 604 TCCCAACAGCAACAGATTTATATCAATATCGCGTGAAGATGAAGCAGGTTGTGAACC 663
 QY 10258 GCGAGCGGACGCGGACCCGAGCGGCGGCCCAACGTTATTCGGTGGCGGTCTGGTAT 10317
 Db 664 GACGAGCTAGCAGCCCAACCCAGCGCAACCGTTACGCGCTACCTGCAACAGTACATTAC 723
 QY 10318 GGTAAACCGTACGCGGCTCGGACGCTACCGGCGCT---GGTGTGACACCATCAATGAT 10374
 Db 724 GGAACCTGACCGCCAGCGACGTTTCTTCACTAAACGGAGATGACCACTTAAATCT 783
 QY 10375 AGCTGGCTGTTTATCTGCTGTTGATTATGATGAGCGTAGCTCGGTGCTGTCTGAAGCG 10434
 Db 784 GGTGATGTTCTGTTAGTATTTGACTACGCTGAGCGCAAAACAGACTTATCTGAATG 843
 QY 10435 CCGGCTGCAAAACACGAGGAGTGGGAGTGGTGTGTCGTCAGGATGTTTTCGGGG 10494
 Db 844 CGCTGTTTAAAGCCACAGGCA-----ATTGGCTTGGCGAAAGACCGGTTTCCCGT 897
 QY 10495 TATGAGTTGGTTTAAACCTGCGGACTCGCGGCTGTCGCGTCAAGTTTGTATGTTCCAT 10554
 Db 898 TATGAGTACGGTTTGAATTTGCTACTCGCCCTTATCGCCCAAAATCTGATGTTTAC 957
 QY 10555 TACCTAGGTGTTCTCGCGGGAGTTCGGGAGCGAATGATGCGCCAGCATTTGATTTCTCG 10614
 Db 958 CGCTACAAACCTCTCTGTCAGGCAAGGGGATGATGAACCTGCGCTAGTGTGCGCT 1017
 QY 10615 CTGTGCTGGAATACAGGGAAGTCTTCACTAGTCTGTCGAGAACGTGACACAGGTG 10674
 Db 1018 CTGATCTGGAATATGACGAAACCGGATGGTTCAGTACGCTGCTGTCGCGGGTA 1077
 QY 10675 GCTTATGCTCGGAGCGGAGCTTTGCTGCTGCGGCACTGCGCATTTGGGGTGGCAAC 10734
 Db 1078 GGCCATGAGCAAAACACGCTTACCGGCTGCCACCACTGGAATGCGCTTATGAGCT 1137
 QY 10735 TTTACCCCGCCGACATTTGTCGCATGGCAGACGCGTGAAGATATGGGCAAGTTGAGTTG 10794
 Db 1138 TTTGAGCCAGCAAAACCGCACTCTGGCAATCAATGGATGTACTGGCAAAATTTCAACAC 1197
 QY 10795 CTTCAACCCCTATCAGCTTGTAGACCTTAAACGGGGAAGGTGGTGGGTATCTGTATCAG 10854
 Db 1198 ATTCAGCGCTGGCAACTGCTTACCTGAAAGGAGAGGCGTCCCGGCAATCTCTATCAG 1257
 QY 10855 GACAGCGTCTGCTGTTGATCGGTGAACCGGTACCGCACTGCGGGAGTATCCGATGCT 10914
 Db 1258 GATAGAAATGGCTGGTGGTATCGATCTGCCAACGTGAGCGCGGGAAGATGAATGG 1317
 QY 10915 GTGACCTGGGGGGCGGCTCGCGCCCTTCCGCAAAATCTTTCATTAACAGCGGCATC 10974
 Db 1318 GTCACTGGGGGAAATGCAACTCTCTTCCCATCACACAGCTGTGCAAGATAACGCTCA 1377
 QY 10975 CTGGCGGATCTTAATGGGGATGCTGGCTGGAGTGGTGGTACCGCCCGGCTGTGGG 11034
 Db 1378 CTGATGATTAATTAACCGGTGACCGGCAACTGGATCTGGTGAATTTACCGGGCGGGCTAA 1437
 QY 11035 GGGATGATGATGCGACCCCGCGCGCACTGCTGTTGCAATTTTCAACCCCTGTGTCAGGCT 11094
 Db 1438 GGTATCAAGCAACACCCGATGAGTGGAGTGGAGCGGTTTACGCCATTTACATGCCCTG 1497
 QY 11095 CCGGTAGATATGCGCATCCAAAGCAGTGTCTCGCGATATCTTGGGGCTGGTGTAAACG 11154

Db	1498	CCGATAGAAATATCTCACTCCGCTCAACTTGGCCGATTTAATGGGAGCCGGCTGTC	1557
Qy	11155	GACATGCTGCTTATCGGGCCGCGCAGTGTTCGCTCTATTCGCGCAAAAACGATGGTTGG	11214
Db	1558	GATTTAGTCTAATTTGTTGCCAAAGTGTGGCTTATATGTCAATAACCGTGATGGTTTT	1617
Qy	11215	AATAAAGGGAGACCGGTGACGAAACGGAAAGACTCACTTCGCGGTCCCGGGGTTGAC	11274
Db	1618	ACCGAAGGGGGGATGTGGTCAATCCGGTGATATCACCTTCGCTACCGGGCGCGAT	1677
Qy	11275	CCAGTACCCTCGTGGCGTTCAGTGATATGGCTGGAGTGACAGCAGCATTTGACGGAG	11334
Db	1678	GCCCGTAAGTTAGTGGCATTTAGTGACGTACTGGGTTTCAGGCCAAGCACAATCTGGTTGAA	1737
Qy	11335	GTGCGTCTAATGAGTACGTTACTGGCCAAACCTGGGGCAGCGTCTGTTTCGGTCAGCCG	11394
Db	1738	GTTAGTCCAACTCANGTCACTGCTGCGCAATCTGGGCAATCTGGGCAATGGCCGTTTGGTCAGCCA	1797
Qy	11395	GTGAATATTCGCGTTTTAGCCAGTCACTAGTGACTACGTTTAAACCTGACCCAGATATTGCTG	11454
Db	1798	ATCGTATTCGCGGATTCAGCCAATCTGCGCCAGTTTAACTCTGATCGATTCTATCTG	1857
Qy	11455	GCCGATACGACCGTTCGGGTACCAACGACCTGATTTATGGATGAGTGACCGGTGATGTC	11514
Db	1858	GCCGATTTGATGGGAGCGCCCTGCGCAATCTGGGCAATCTGGGCAATGGCCGTTTGGTCAGCCA	1917
Qy	11515	ATTATTTTCAACAGAGTGTGTAATTTTCGCGAGCGCATACGCTGCTCTTTCGCGAAA	11574
Db	1918	ATTTCAGCAATGAAGTGGCAACGTTTTCGAAACCAATTCACACTCTCTTTCCTGAC	1977
Qy	11575	GGTGTGCGCTATGATCCGACCTGCGAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGTG	11634
Db	1978	GGCTGCGTTTGTATGATACCTGCGCACTGCAAGTAGCCGATGTACAAAGGTTTAGCGGTT	2037
Qy	11635	CCTAGCTGTACTGACGGTCCCGCTATGTCGGCTCATCTGCGGTGTCGCAATTTATCG	11694
Db	2038	GTGAGCTGTATCTTAAGCGTACCGCATATGGCGCCACATCATTTGGCGCTGCGATCGACC	2097
Qy	11695	GCAGACAAACCTGTGTTGTAATGGCATGAACAAATATGGGGCCCGCGATGCACTG	11754
Db	2098	AACGGAAACCGTGTACTCTAGTGAACGAAACAAATATGGGGCCAAATCAACCTTG	2157
Qy	11755	CACATCGCAGTTGGTGAGTTCTGGCTGGATGAGAAACCGAGGCACTGGCGGCGAGGC	11814
Db	2158	CATTACCGTAGCTGTGCCAGTTCTGGCTGGATGAAAGCTGCGGCATTTGGCTACCGGA	2217
Qy	11815	AGTTCCCTGCTGCTACCTGCCATTTACATTTGATACCTGTGGCGTTGCGTGGTGACG	11874
Db	2218	CAAAACCGGTCTGTACCTGCGCTTCCCGGTCCATACCCCTTTGGCAACAGAAACCGAG	2277
Qy	11875	GATGAGATCACCGTAAACCGTCTGGTCAGCGAGCTGCTTTATCGCCACGGCGTCTGGAC	11934
Db	2278	GATGAAATACGGGCAATAGTTAGTGACACAGTTACGTTATGCTCAGCGCGTTGGGAT	2337
Qy	11935	GGGACAGAAACCGAGTTTCGGGGGTTTGGTTTGTGAGATCAGGGATACCGATACCTTG	11994
Db	2338	GGACGTGAACCGGAAATTTGCTGGCTTTGGTTATGTTGAGCAGACAGACGCCATCACTC	2397
Qy	11995	GCAAGCCAGGTACGGGCAACGAACTAGTATGCTTCTGTGACCGGAACTCGGTATGCC	12054
Db	2398	GC---TCAGGGCAATGCGCGGAAACGTACACACCGGCACTCACAAAAGCTGTGTATGCC	2454
Qy	12055	ACGGGGTACCGGAGTAGACGAGCTCTCGCGGAGAGCTATTGGGCAAAACGATGCGCC	12114
Db	2455	ACCGGATTAACCTGGGTAGTATAGCGTTATCCCGGGGTTATGGCTGGCGATAGAGCAA	2514
Qy	12115	GCTTTTCCGATTTCCGACCCGTTTCACTGTGCTGGTTTTCAGGAGGATGACAGACATAT	12174
Db	2515	GCTTTGCGCGTTTACGCCACGTTTACTCTCTGGAAAGAGGCAAGATGTTCCACTG	2574
Qy	12175	ACTCCG---GACAGACAGCAAGACATTTCTGTTGGAGAGCCCTGAAAGCATCTCTGCTG	12231
Db	2575	ACACCGGAAGATGACCAATATCTATATCTGTTTAAACCGGGCGCTTAAAGGTCAGCCACTG	2634
Qy	12232	CGCAGTGAGTTATACGGTCCGATGGCAGCAGCCAGCCGATATCCCTTACAGCGTCACT	12291
Db	2635	CGTAGTGAATCTACCGGCTGGATGGCAGCGCACAGMACAGATCCCTTATACAGTACT	2694
Qy	12292	GAGTCTGCGCCGCGAGGTACGGCTAGTTTGAAGCGAATG---GAGACTACCGGTTGGTGG	12348
Db	2695	GAATCCCGTCCACAGGTGGCCAAATTACAAAGATGGGCCACCGTTTCCCGGTGCTCTGG	2754
Qy	12349	CCGATGGGCGGAAAGCCGTACGTCAAGTTTATGAACGGTACCAATGATCTCAATGTC	12408
Db	2755	GCCTCAGTCGTGGAAAGCCGTAGTTATCACTACGAAAGCTATTACAGTATCCCACTGTC	2814
Qy	12409	CAACAGCAGCGGTACTCTCCTCAGTGTGATCGTTTCCACCTGCGTCAAGTCAGTGTC	12468
Db	2815	AATCAGGATATCAGTTGTCAGTGACCTTATTCGGGCAACCACTGAAACAGGTTTCCGTA	2874
Qy	12469	AATTATCCAGCAGCCCTCCGTCGCGGGAACAATCCATATCCGCGTCTTTACCGGCGACG	12528
Db	2875	CAATATCCCGCGCAACAAACCAACCAATCCGTTATCCCGATACCTTACCGGATACG	2934
Qy	12529	CTGTTCCGCAACAGTTTATGACGAGCAGCAGATATTACCGCTGGGTTGCAACAGAC	12588
Db	2935	CTGTTTCCGACAGTTTATGACGATCAACACAGCTATTGCGATTAACTCTGCCACATCC	2994
Qy	12589	AGTGCACTCACCTGTTTCTGAGGGGCATTTGTTGTTGGGTTTGGCGGAGCGC	12648
Db	2995	AGTTGGCACCATCTTATTT-----GGTAATGAGCTAAGAGTGTGGGATTTACCGGATGGC	3048
Qy	12649	TCGCGGACAGATATTCAGCTACTCTGCGGACAACAGTTCGCGGAAGGGGCTTGACGCTG	12708
Db	3049	ACACGAGTGTGCTTTTACTTACGATGCCAAACAGGTACTCTGCGATGCTTAAATCTG	3108
Qy	12709	GAACACTGTTGGCGCCGMAAGCCTGCTCGATAGTCAGGTGCGTTCGCTGGCGGGT	12768
Db	3109	GAACACCTGTGTCTGAAATATAGCTGATTCGCGGATGAATAACCTCGCGAATACCTCAAT	3168
Qy	12769	CAGCAGCACTGTGTATCTGGATTCAAGAGCTTGCACCGCTGCTCGCTGCTCGCCACTC	12828
Db	3169	CAGCAACGAACTGTTCTATACCGACGGGAAACCAACACCGCTGAAACACCGACAGA	3228
Qy	12829	CCCCCAAGGTAGCTTTTATCGAAACCGCGCTGCTGGATGAGGGTATGGTCAGTTCACTG	12888
Db	3229	CAAGCGTTAATGCTTTTACCGAAACCGCGTATTAAACGGAATCTCTGTTATCCGCGTTT	3288
Qy	12889	GCTGCTCTACATTTGTGATGA-----ACATCTCGAGCAAGCCGTTTACCGGCAA	12936
Db	3289	GATGGCGGTATTACGCCAGACGAATTAACCGGGAATTAACGAGGCGGATACCAACAA	3348
Qy	12937	TCGGGATACCTTTTCTCCTCGAGCAGGAAAGCAGGCAATTTGGACCCAGTGTGAC	12996
Db	3349	GAGCCTTATCTGTTTCCACGACCGCGGAAACAA-----AGTTTGGGTAGCGGTCAA	3402
Qy	12997	GGATATGTTACCTTATCGCGCGCAGACATTTCTGGCTACCGCTATCTTTCCGGGACGT	13056
Db	3403	GGCTATACCGATTACGGGACGGAAGCACAATTTTGGCGCTCTGTCGACAACTGTAACAGC	3462
Qy	13057	ATGTTGACCGGCCAGTTTACCGTGACCGCTGACCGCTACGACTGCGTATCAGCAGTGG	13116
Db	3463	CTGTTAACCGGGAAATGACGTTTAAATGGGATCTCACTATTGTGTCTATCACCACCAACC	3522
Qy	13117	CAGGATGCGCGAGGATTTGTCACACAGCCGATATGACTGGCGCTTCTTGACGCGCGCTC	13176
Db	3523	CAAGATGCTGCCGCCCTCACCGTCTCAGCCCAATTTATGACTGGGCTTTTCTCACCAACAG	3582
Qy	13177	CGGGTACGAGACCCCAATGATATCTGCACTCGCTCACTCTGATGCTCTGGGCCGGGTG	13236
Db	3583	CAACTGACTGACATCAACGATAATGTGCTCTCATCACTTGGATGCTCTGGGACGCGCT	3642
Qy	13237	ACCACCTCGGATTTCTGGGGCAGGAGAAATGTTATTTGCCACCGGTTACAGT-----	13287
Db	3643	GTCAACGAAACGTTTCTGGGGGATCGAAAGCGGTGGCAACAGGTTACTCTTCTCATCAGAA	3702

QY 13288 GATGCCACGTTGTCGTTCCGACCGCGCAGCAGCGCTCTCGGCTTGACGGCGCCCTA 13347
|||
Db 3703 GAAAAACCATTCCTCCACCAACGATATCGATACCGCTATTAATCTAACCGGACCATC 3762
|||
QY 13348 CAGGTAGCACAGTGTCTGGTGTATGTACGGACAGTTGG- 13386
|||
Db 3763 CCTGTCCACAGTGTCTGGTGTATGTACCGGACAGTTGGATGCCACTATTTCAGTCAAGNA 3822
|||
QY 13387 ----- 13386
|||
Db 3823 ACCTTCAACACATTAACGAGGAGGAGCAGCGCTCGTGTATTCACGTATTATACG 3882
|||
QY 13387 -----GGAGATGACGACATGAGAAA- 13408
|||
Db 3883 GAAGATTGGCGTATTTCGCGCACTGACTCGCCCGCTTGGCTCAAAAGTCAAAAGATCATG 3942
|||
QY 13409 -----TGCCCGCCGACGCTGTGCTGCTG 13431
|||
Db 3943 ACACATTAGTTAACTGTTAACCAACAGCATTTGTTTACTCCCATTAACCTTACGCTG 4002
|||
QY 13432 GCTACCGATCGCTATGACAGTATACCGACAGAGTCCGCGCAACAGTGACATTCAGT 13491
|||
Db 4003 ACCACAGACGTTATGACCGCACTCTGAGCAGCAAAATTCGCCAACAGTCTGCATTAGT 4062
|||
QY 13492 GACGTTTGGCGTGTGCAATCGCAACCCGCGAGCGGAGGCAACGCTGGCAA 13551
|||
Db 4063 GATGGTTTGGCGCTGTCTACAGCCTGTGTACGACATGAGCAGCGCAAGCCTGGCAA 4122
|||
QY 13552 CQAGGACGCGACGCGCAAACTGGTGACGCGCAGTACGCGATTCGCGGTCACTGTAGCAACG 13611
|||
Db 4123 CGTAACCAAGACGGTTCTCTGGTGACAAAAGTGA- 4164
|||
QY 13612 AATTCCGCTGGCGGTACCGGAGGCGGAGTATGACAAATAAAGTCTGCGTCTCG 13671
|||
Db 4165 AAAACGCGTTGGCGGTACGCGACGACCGAATATGATAATAAAGGCAACGATACG 4224
|||
QY 13672 GTTTATCAGCGTATTTCTGGACAGTTGGCAATATGTAGTATGACAGTGCCTGCCAG 13731
|||
Db 4225 ACTTATCAGCCCTATTTCTCAACGACTGGCGATATGTAGTATGACAGCGCGCAAAA 4284
|||
QY 13732 GACCTGTATCGCACACGCACTTTTACGATCCGACGCGACGGGAATGGCAGGTTATACG 13791
|||
Db 4285 GAAGCCTATCGGATCTCATATTTATGATCCAAATGGGCGAGAAATCCGGGTATTACT 4344
|||
QY 13792 GCAAAAGTCAACGGGACAGGTGCTGTATACCCCGTGTGTGCTGCTGATGAGACGAG 13851
|||
Db 4345 GCAAAAGGTGGCTGGCCCAAGCCAATATTTCCCGTGGTTTACCCTGATGAGGATGAG 4404
|||
QY 13852 AATGATACCG 13861
|||
Db 4405 AATGATACCG 4414
|||

RESULT 10
ACF69437
ID ACF69437 standard; DNA; 4431 BP.
XX
AC ACF69437;
XX
XX 20-NOV-2003 (first entry)
XX
XX Photorhabdus luminescens nucleotide sequence #7904.
DE
XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough; gene; ds.
XX
OS Photorhabdus luminescens.
XX
XX W0200294867-A2.
XX
XX 28-NOV-2002.

XX 07-FEB-2002; 2002WO-1B003040.
XX PF
XX 07-FEB-2001; 2001FR-00001659.
XX PR
XX (INSP) INST PASTEUR.
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
XX PI Buchrieser C;
XX WPI; 2003-148459/14.
XX
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
XX Claim 2; SEQ ID NO 7904; 1205pp; French.
XX
XX The invention relates to the isolation of genes and their encoded
XX proteins from Photorhabdus luminescens. The isolated sequences are
XX sources of probes and primers for detecting the genome of P. luminescens
XX and related species; to study polymorphisms; for gene analysis and for
XX detection/amplification of the genes. Antibodies (Ab) raised against the
XX polypeptides encoded by the genes are used for detection/identification
XX of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
XX carry a gene-containing vector are used to select compounds that
XX modulate, regulate, induce or inhibit expression of the genes in plants,
XX animals or microorganisms other than P. luminescens and are able to alter
XX response or sensitivity to toxins and antibiotics produced by P.
XX luminescens. Cells transformed to express the genes are useful for
XX recombinant production of the proteins, particularly toxins and
XX antibacterials useful as insecticides, bactericides and fungicides. The
XX genes, proteins, vectors containing the genes and Ab are also useful
XX therapeutically (to treat microbial infection by bacteria or fungi that
XX are sensitive to P. luminescens-encoded toxins or antibiotics) and as
XX biopesticides. Other uses of the genes and the proteins are as virulence
XX factors and for identifying targets of human diseases for which P.
XX luminescens is a model (particularly plague and whooping cough). This
XX sequence represents one of the isolated P. luminescens genes
XX
SQ Sequence 4431 BP; 1161 A; 1136 C; 1085 G; 1049 T; 0 U; 0 Other;
Query Match 5.7%; Score 1074; DB 10; Length 4431;
Best Local Similarity 55.4%; Pred. No. 1.2e-244;
Matches 2465; Conservative 0; Mismatches 1760; Indels 225; Gaps 11;
QY 9598 ATGCAAAATCATCAAGACATGCGCCATTACTGCCCCACGCTTCCGCGGCGGTGCG 9657
|||
Db 1 ATGCAGAAATTCACAGACATTCAGTGTGCCGAGCTGTCTATTACCAAGGCGCGGGCA 60
|||
QY 9658 GTCAACCGGCTCAAGGGTGATATCGCGCGCGGCGCGAGTGTGCGGCGACCTTGAGT 9717
|||
Db 61 ATTACCGGTATGGTGAAGCATTAACCAACTGGCGCGATGGTATGCGCGCTTATCC 120
|||
QY 9718 ATTCCCTTCCGGTATAGCCCCCGGTTCGGGTTACGCCCCACCTGGGGCACTTAATTATCAC 9777
|||
Db 121 CTGCCATTACCATTTCTGCCGGGGTGGTTACTCCCATCGCTCACCTTGAATTACAGC 180
|||
QY 9778 AGCCGGTCCGGGACGGCCCTTGGCATTGGCTGGGGTATCGGGGCTGCTGTGTCAG 9837
|||
Db 181 AGTGGAGCCGTAACAGCCCCGTTGGTCTCGGTGGGACTGCAACCTTATGCAATTCGT 240
|||
QY 9838 CGTGTACCGCAACCGGACCTACCTACGATGATCTATGATGAATTCACCGGTCCGGAC 9897
|||
Db 241 CGCCGACACAGTACTGGCGTACCGAATTACGATGAACCGATCTTTCTGGGGCCAGAA 300
|||
QY 9898 GGTGAGGTGCTGTGCGCGCACTACGCGTGTGGCACCCCAAGACGACGGAGGCCACC 9957
|||
Db 301 GGTGAAGTGTGTGTCATAGCATTAATGAGAACGGTCAAGCTGATATCCGAGTGAATCC 360
|||
QY 9958 TCACTACTGGGATAAACCAGCGGAAGCTTCAACGTTTCAAGTTTACCGTTTACCGTATCG 10017
|||
Db 361 TCATTGACGGGATCAATTTGGGGGAATCTTCACCGTTTACCGGTTATCGTTCCCGTTG 420
|||

Qy	10018	GAGG	TAGTCT	CAGCG	CGCTTG	AGCG	TTGG	CTGG	CGCG	CGAG	GAC	AGAA	CCGA	ATTT	10077	
Db	421	GAAAG	CCCATTT	TAGCT	TGGT	TGGA	TAT	TGG	CAAC	CCAAA	CAAC	AGGT	TAC	CAACG	ATTC	480
Qy	10078	TGGT	GTATAT	ACCCT	CAGC	GAG	TGG	CTCT	TGCT	TGGG	CCGAAA	TGCC	CAGCG	CTGC	10137	
Db	481	TGCT	GATAT	A	CAGC	CCCG	AGC	GAC	GTCC	ATTT	TACT	TGGG	AAAA	AAAT	TCTC	540
Qy	10138	ATCAG	CAACCC	CAC	AGCC	CAAC	CAC	AGAC	CGCG	GGTT	TGG	CTG	ATGG	AGTCT	TCG	10197
Db	541	ATCAG	CAATCC	ACT	CAAT	TGTT	TAGC	CAAA	CAG	CGCA	ATGG	TGTT	TGGA	AGCT	TCG	600
Qy	10198	CTTAC	CGGCAAC	CAG	ATGTT	TAC	CAAT	ACG	TGCG	GGAAG	ATG	ATG	ACG	GTG	TGA	10257
Db	601	TCCCA	CGGCGAA	CAG	ATTT	TAT	TAT	CAAT	ATC	GAG	CCGA	AGAT	TGA	AA	CAAA	660
Qy	10258	GCGG	CGCG	CAC	CGC	GAC	CGC	GAG	CGCG	CGCC	CAAC	AGTT	ATC	CGT	GGCG	10317
Db	661	GAC	AGTT	CAC	AGCC	AT	CGG	AA	CGC	ACCG	TCT	CAA	CGCT	ACCT	GCA	720
Qy	10318	GGTA	ACCGT	CAG	CGG	CTCG	AG	CTCA	CGG	CGCT	---	GGT	GTG	CA	CA	10374
Db	721	GGTA	ACCT	GAC	CGC	AGC	GAA	GT	TTT	TCC	AC	CGCT	CAAC	CGG	ATG	780
Qy	10375	AGCT	GCGT	CT	TTAT	CT	TGTT	TGAT	TAT	GTG	TGAG	CGT	AGCT	AGT	CTCT	10434
Db	781	GGCT	TGTT	GTCT	GT	TGAT	TAT	TGAT	TAC	GGT	TGA	ACG	CA	AA	CAG	840
Qy	10435	CCGG	CTGG	CAAA	CAC	ACG	AGT	TGGG	AGT	GGCT	GTGT	CGT	CAG	AGT	GT	10494
Db	841	CCG	CGCT	TTA	AGC	CTCA	-----	AGT	CTCT	TGGCT	TTG	CGC	CA	AG	ACCG	894
Qy	10495	TATG	AGTT	TGGTT	TTT	TAAC	CTG	CGG	ACT	TCG	CGC	CTGT	GC	CGT	CA	10554
Db	895	TATGA	ATAC	GGT	TTT	TGAA	TG	TGG	CA	CCCG	CGCT	TAT	G	CGG	TCAA	954
Qy	10555	TAC	TAGT	GT	TC	TGCG	GGG	AGT								

QY	11095	CCC	G	T	A	G	A	T	A	T	G	C	G	A	T	C	A	A	A	G	C	A	G	T	G	T	C	G	C	G	A	T	A	T	C	T	G	G	G	G	T	G	G	T	T	A	A	C	G		11154
DB	1495	CCG	A	T	A	G	A	T	A	T	T	C	T	C	C	C	G	T	G	T	C	A	A	T	T	G	C	G	A	T	T	A	T	T	A	T	G	G	G	G	C	C	G	G	T	G	C		1554		
QY	11155	G	A	C	A	T	G	T	G	C	T	T	A	T	C	G	G	G	C	G	C	A	G	T	T	G	C	T	C	T	A	T	T	C	G	G	C	A	A	A	A	A	C	G	A	T	G		11214		
DB	1555	G	A	T	T	A	G	T	A	C	T	A	T	T	G	G	C	C	C	C	A	A	A	G	T	A	C	G	T	T	G	T	A	T	G	C	T	A	A	T	A	A	C	C	G	T		1614			
QY	11215	A	A	T	A	A	G	G	G	G	A	C	C	G	T	G	C	A	A	A	C	G	A	A	A	A	C	T	C	T	G	C	C	G	T	A	T	C	C	G	G	G	T	T	G	A		11274			
DB	1615	A	C	C	A	A	G	G	G	G	A	T	G	T	G	T	C	A	A	T	C	C	G	T	A	T	C	A	C	T	C	T	G	C	T	G	C	T	A	T	C	C	G	T		1674					
QY	11275	C	A	C	G	T	A	C	C	T	C	G	T	T	C	A	G	T	A	T	T	G	G	C	A	G	C	A	G	T	G	G	A	T	T	G	G	A	C	A	G	A	T	T	G	A		11334			
DB	1675	G	C	C	C	T	A	A	G	T	T	A	G	T	G	C	A	T	T	A	G	T	A	C	G	T	C	G	T	C	G	T	C	G	T	C	G	G	C	A	A	G	C	A	C	T		1734			
QY	11335	G	T	G	C	T	G	T	A	T	G	G	A	T	A	C	T	T	A	C	T	T	A	C	T	T	G	G	C	A	A	C	T	T	G	G	C	A	A	C	T	T	G	C	G		11394				
DB	1735	G	T	T	A	G	T	G	C	A	T	C	A	C	T	G	C	T	G	C	C	A	A	T	C	T	G	G	C	A	A	T	C	T	G	G	C	A	A	T	C	T	T	G	T		1794				
QY	11395	G	T	G	A	T	A	T	T	C	C	G	G	T	T	A	G	C	C	A	G	T	A	C	T	T	A	A	C	C	T	T	A	A	C	C	T	G	A	C	A	G	A	T	T		11454				
DB	1795	A	T	T	A	C	A	T	T	G	C	C	G	G	A	T	C	G	C	A	A	T	C	T	G	C	C	A	A	T	T	A	T	T	A	T	T	A	T	T	A	T	T		1854						
QY	11455	G	C	C	A	T	A	C	G	C	G	T	T	C	C	G	T	A	C	C	A	G	C	T	G	A	T	T	T	A	T	T	T	A	T	T	T	A	T	T	T	A	T	T		11514					
DB	1855	G	C	C	A	T	C	T	G	G	A	T	G	T	G	T	C	C	G	A	T	T	G	A	T	T	G	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		1914					
QY	11515	A	T	T	A	T	T	C	A	C	A	G	T	G	T	A	T	T	T	C	G	G	A	C	C	G	A	T	A	C	T	T	T	T	T	T	T	T	T	T	T	T	T		11574						
DB	1915	A	T	T	T	C	A	A	G	A	T	G	A	A	T	G	T	T	G	C	A	A	C	C	A	A	T	T	A	T	T	T	T	T	T	T	T	T	T	T	T	T		1974							
QY	11575	G																																																	

Db 2572 ACACCGGAAAAATGATGATTAATCTGTACTGTTCAACCGGGCACTAAAGGTCACTACTG 2631
QY 12232 CGCAGTGAGTTATACGGTGCCTGAGGAGAGCCAGGCGGATATCCCTTACAGCGTCACT 12291
Db 2632 CGTAGTGAGCTTACGGGCTGGATGATCAGCGAAACAGCAAAATATCCCTTATACAGTGACT 2691
QY 12292 GAGTCTCGCCCGCAGGTAGGCG---TAGTTGAAGCGAATGGAGACTACCCGGTGGTGG 12348
Db 2692 GAATCTCGTCCCAAGTGGCCAAATTACAAGATGGCACTACCCGTTCCCGCGTGGCTTGG 2751
QY 12349 CCGATGGGCGGAAAGCCGTACGTCACTGTTTATGAACGGTACCACAAATGATCCTCAATGC 12408
Db 2752 GCCTCGGTCTGGAAACCGTAGTATCACTATGAACGATATATCGGTGATCCTCAGTGC 2811
QY 12409 CAACAGAGCGGTACTCCTCAGTGATGAATACGGTTTCCACTGCGTCAGGTCACTGTC 12468
Db 2812 AATCAGGATATTACGCTGTCACGCAACCAATTCGGGCAACCTCTGAACAGAGTTTCAATG 2871
QY 12469 AATTATCCAGCGCCCTCGTCCGCGGACAATCCATATCCGGCGTCCCTTACCGCGAGC 12528
Db 2872 CAATATCCCGCGCGCAATCAACCAACAACCAATCCGTATCCCGATACACTACCGGATACG 2931
QY 12529 CTGTTGCCCAACAGTTATGACAGCAGCAGCAGATATTACGCCCTGGGGTTGCAACAGAGC 12588
Db 2932 CTATTTGCCAGCAGTTATGACGATCAACAACAATATTGGATTAACTGCCAGCAATCC 2991
QY 12589 AGTGCAATCACTGTTTCACTGTCTGAGGGGCAATTGTTGTTGGGTTGGCGAGGCG 12648
Db 2992 AGTTGGCACCATCT-----AACCGGTAATGAACTCAGAGTGTGGGATTACCGGATGGT 3045
QY 12649 TCCGCGGAGATGATTACGTTACTCTGCGGACAACGTCGCCGAAGGGGTCTGACGCTG 12708
Db 3046 ACACGAGTATGCTTCACTACGATGCCAACAACAGGTGCTTGTATGTTTAAATCTG 3105
QY 12709 GAACACCTGTTGGCGCCGAAAGCCCTGGTCTCGGATAGTCAGGTCCGTACGCTGGCGGT 12768
Db 3106 GAAGCCCTATGCTGAAATAGTCTGATTGCCGATGACAAACACCGCAATACCTTAAT 3165
QY 12769 CAGCAGCAGTCTGGTATCTGGATTCAAGAGGTTGGCAACCGTCCGCTCGCCGCACTC 12828
Db 3166 CAGCAAGAAGCTTCTATACCGATGGGAAACCAAGCGCATTGGAAATACCGACACGA 3225
QY 12829 CCCCCAAGTACGTTTTATCGAAACGGCGTCTCGATGAGGATGTCAGTTCACTG 12888
Db 3226 CAAGCTTTAATCGCCTTTACCGAAACGGCGATTAAACAGATCTCTGTTATCCGCATTT 3285
QY 12889 GCTGCCCTACATTGTGGATGAACA-----TCTCGAGCAAGCCGGTTACCGGCAA 12936
Db 3286 GATGGCGGTATACGCCACGATGAATTAACCGGCATTTCTGACACAACGAGGATATCAACA 3345
QY 12937 TCCGGATACCTTTTCCCTCGAGCGAGGAGCAAGCAAGCATGTGGACCCAGTGTCTAG 12996
Db 3346 GAGCCTTATCTGTTTCCACGCAACCGCGGAAACAA-----AGTCTGGGTAGCACGTCAA 3399
QY 12997 GGATATGTTACCTATCCCGCGCAGAGCAATTTCTGGCTACCGTATCCTTTCCGGACAGT 13056
Db 3400 GGCTATACCGATTACCGAATCAGGACATGAGGCACAATTTTGGCGTCTCTCGCAACAAGTAACCC 3459
QY 13057 ATGTTGACCGGCCAGTTACCGGTGACCGGTGACCGTACGACTCGCTCATCAACGCAAGTGG 13116
Db 3460 CTGTTAAACCGGAAACGAGCTGCAATGGGATACCCACTACTGTCTCATCACTCAAAACC 3519
QY 13117 CAGGATGCCGCGAGGATATGTCAACAAGCCGATATGACTGGCGTCTCTGACGCCGCTG 13176
Db 3520 CAAGACCGGCTGTTTGAATGCTTTAGGCAATTAATGACTGGGCTTTCTCAACCTGTG 3579
QY 13177 CGGGTCACGACCCCAATGATATCTGAGTCGTCAGTCTGATCTGAGTCTTGGCGCGGTG 13236
Db 3580 CAACTGACTGATATTAATGATTAATGTCATCTCATTAACCTTGGATGCATTAGACGCCCT 3639
QY 13237 ACCACCTCGCATTTCTGGGGCAACGAGAAATGGTATTGGCCACCGGTTTACAGT----- 13287

Db 3640 GTCACACACAGTTTCTGGGAATCGAAATGCTGTGAAACAGGTTTACTCTCCACCGGAA 3699
QY 13288 GATGCCAGTGTTCGTTCCGTTCCGAGCGGCGCAGCGCTCTCTGCGTTGACGGCGCCCTTA 13347
Db 3700 GAAAGCCGCTTCTCTCCACCAATCGATATCAATACTGTCATTTGCTCTAAACCGGACCACTC 3759
QY 13348 CCAGTAGCAGCAGTGTCTGGTGATGTCACGGACAGTTGGGGAGATGACGACAAATGAGAAA 13407
Db 3760 CTTGTGCGCAGTGTCTGCTATGCAACCGGACAGTTGATGCCACTATTTCAGTCAGGAA 3819
QY 13408 A----- 13408
Db 3820 ACCTTCAACACATTAACGCGAGGAGAGCAGACACTCGCTGATTTACGGATTATCAACG 3879
QY 13409 ----- 13408
Db 3880 GAAGATTGGCGTATTGTTGCACTGGCTCGCCCGTGGTTGCAAAAGTCAACAGGCTAGT 3939
QY 13409 -----TGCCCCCGCACGTCGTTGCTG 13431
Db 3940 AGCCCATTTGGTTAATCTGTTAACTAACAGCATCGGTTTACTCTCCCTAACTTACGCTG 3999
QY 13432 GCTACCGATCGTATGACAGTGTATACCGACAGAGGTCCGCCAACAGGTGACATTCAGT 13491
Db 4000 ACCCGGATCGTATGACCGGATTTCTGGCAGGCAAAATTCATCAGCAAGTTCGCAATTCAGT 4059
QY 13492 GACGGTTTGGCGGTGAGTTGCAATCGGCNAACCCGCGAGCGGCGAGGCAACGCTGGCAA 13551
Db 4060 GATGGTTTGGCGGTTGTTGTCAGCATCTGTACGGCATGAGGCGAGGCGGAAGCTTTGGCAA 4119
QY 13552 CCAGGACGCGACGCGCAAACTGTTGACGCGCAGTACGCGATTGCCGTGCTACTGTAGCAACG 13611
Db 4120 CTTAACCAAGATGGTTCTCTGGTGACAAAATGGA-----AGATACC 4161
QY 13612 AATTTCCGCTGGCGGTGTCACCGGAGGCGGAGTAGTATGACAAATAAAGGTCTGCTGTTCGG 13671
Db 4162 AAAACGCGCTGGCGGTTCACGCGGACGCACTGAATATGACAAATAAGGACAGACGATACGA 4221
QY 13672 GTTTATCAGCCGATTTTCTGGACAGTTGGCAATATGTCAGTGATGACAGTCCGCCGAC 13731
Db 4222 ACTTATCAGCCCTATTTCTCAACGACTGGCGATATGTGAGTGATGACAGCCGCGAATA 4281
QY 13732 GACCTGTATCGGACAGCAGCTTTTACGATCCGACGCGCAATGGCAGGTATTATACG 13791
Db 4282 GGGGCTATGCCGATACGCAATTTATGATCCGATTTGGCGGGAATATCCGAGTTATTACC 4341
QY 13792 GCAAAAGGTGAACGCGCAGAGTGTGTATATCCCGTGGTTTGTGGTCAAGAACGAG 13851
Db 4342 GCAAAAGGTGGCTGCGACAGAGCCAATATTTCCCGTGGTTTACTGTGAGTGAGGATGAA 4401
QY 13852 AATGATACCG 13861
Db 4402 AATGATACCG 4411

RESULT 11

ACF69428

ID ACF69428 standard; DNA; 4428 BP.

XX ACF69428;

AC ACF69428;

XX 20-NOV-2003 (first entry)

DT 20-NOV-2003 (first entry)

XX Photorhabdus luminescens nucleotide sequence #7895.

DE Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;

KW detection; food; gene expression; plant; animal; microorganism; toxin;

KW antibiotic; biopesticide; virulence factor; disease model; plague;

KW whooping cough; gene; ds.

XX Photorhabdus luminescens.

OS Photorhabdus luminescens.

XX WO200294867-A2.

PN WO200294867-A2.

Db 1417 GGATATCATAGTCAACGTCAGATGGCAGTTGGACAGCTTTTACCCCACTCAATGCTCTG 1476
Qy 11095 CCGGTAGATATCGGATCCAAAGCAGTGTCTCGCCGATATCTTGGGGCTGGTTAACG 11154
Db 1477 CCGGTGGAATATCTCATCGTGGCAACTCGCCGATTTAATGGGAGCCGGCTCTCT 1536
Qy 11155 GACATGGTCTTATCGGCGCGCAGTGTTCGCTCTATTTCCGGCAAAACAGATGTTGG 11214
Db 1537 GATTAGTCTGATCGCCCTTAATAGTGTGCGTTTATATGCCAATATCTGACGCGCTTC 1596
Qy 11215 AATAAAGGGAGACCGTCAGCAAAACGAAAGACTCACTCTGCGGTCCCGGGGTTGAC 11274
Db 1597 GCCAAGGAAGAGATGTGGTCAATCCGGTGATGTACGCTGCCAGTACCGGGTCCGAT 1656
Qy 11275 CACGTACCCTCGTGGCTTCAGTGATATGGCTGGCAGTGGACAGCAGATTTTGACGGAG 11334
Db 1657 CCGCGTAAGCTGGTGGCTTTAGTGATGTATTGGGTTCGGTTCAGGCACATCTGGTTGAA 1716
Qy 11335 GTGCGTCTAATGGAGTACGTTACTGSCCAAACTGGGCACGGTCTGTTTCGGTCAAGCG 11394
Db 1717 GTAGCGCAACTAAGTCACTCTGCTGCTTAATCTGGGCGATGGAGCTTTTGGTCAACCC 1776
Qy 11395 GTGAATATTCGCGTTTATAGCCAGTCACTGACTACGTTTAAACCTGACCAAGATTTGCTG 11454
Db 1777 ATTACCCTCGCGGATTCAGCCAGCCAGAGGCTATATTTAAACCGGCTCAAGTTTATCTG 1836
Qy 11455 GCGGATACCGAGGTTCCGGTACACGGACCTGATTTATGCGATGAGTACCGGTTAGTTC 11514
Db 1837 GCGGATCTGGATGGCAGCGGCCAACGGATCTGATTTATGTTTACACCAACCGTCTGGAC 1896
Qy 11515 ATTATTTCAACAGAGTGTATTTATTTTCGCGAGCCGATACGCTGCTTTGCCGAAA 11574
Db 1897 ATCTTCTGAATAAAGTGGCAACGGTTTTTGGCGACCGATGACATGCGCTTCCAGAA 1956
Qy 11575 GTGTGCGTATGATCGACCTGCACTCTGCAAGTGGCGGATATCCAGGGCTGGGGTG 11634
Db 1957 GGCTTGGTTTTGACCATACCTGTCAAGTTACAAGTGGCCGATATACAAGGGTTAGGTGC 2016
Qy 11635 CTTAGCCTGTACTAGGTTCCCGATGTGCGGCTCATCATCTGGGTGGCATTTATCG 11694
Db 2017 GCGAGCTGATCTAGAGTGGCCACATATGACCCCGCATCTGCGGCTTGTGATCTAAC 2076
Qy 11695 GCAGACAAACCTGTGTTGTAATGGCATGAACAAATATGGGGCCCGGATGCACCTG 11754
Db 2077 AGCGCAAAACCTGGTTACTCAGCGAATGAACAAATATGGGAGCCACACACCTTG 2136
Qy 11755 CACTATCGAGTTCGGTTCAGTTCGGCTGGATGAAAGCCGAGGCACTGGCGGAGGC 11814
Db 2137 CGTTACCGAGTTCCTCCAGTTCGGCTGGATGAAAGCCGCGCACTGGTTGCCGA 2196
Qy 11815 AGTTCCCTGCTGCTACCTGCCATTTACATTCGATACCGTGTGGGTTCCGTGTGGCAG 11874
Db 2197 CAACACCGGTTTGTATCTCCCTTCCCGGTACACACCTATGGCAAAACGAAACAGCG 2256
Qy 11875 GATGATACACCGTAACCGTCTGCTGTCAGCGCTCTTTATCGCCACGCGCTCTGGAC 11934
Db 2257 GATGAATCAGCGCAACAAATTAGTCAACACTGCTTATGCTCTGCGCGCTGGAT 2316
Qy 11935 GGCAGGAAACGAGTTTCGGGGTTTGGTTTTGTTGAGATCAGGGATACCGATACCTTG 11994
Db 2317 GGGCGTGAACGGGAAATTCGCGATTTGGTTATGTTTGGACAGACAGACCATCACTG 2376
Qy 11995 GCNAGCAGGTTACGGGACGGNACTGAGTATGCTTCTGTGACCGGAACTGGTATGCC 12054
Db 2377 GC---CCAAAGGCAACCGTCAAGACGCCACCCCGCATGACCAAAACTGGTATGCC 2433
Qy 12055 ACCGGGTACCGGCACTAGACAGCGTCTGCGCGAGACGTTATGGCAAAACGATCCGCC 12114
Db 2434 ACCGGCTACCGGTAATAGATAACATATCAACAGAGTATTTGGCTGGTATATCAG 2493
Qy 12115 GCTTTTGGGATTTTCGGACCCGTTTCACTGTGCGTTTCAGGAGGATGAGCAGACATAT 12174
Db 2494 GCTTTTGGCGGTTTTTCAACACGCTTTACGACTTGGCAAGATGGCAAGATATTTCTGTTA 2553

Qy 12175 ACTCGGACGACAGCAAGACA---TTCTGGTTGCAGCGAGCCCTGAAAGGCATCCTGCTG 12231
Db 2554 ACACCGGAATGATGAACAGCAGTATTGGCTAAAACCGGGCACTGAAAGGTCAACTGCTA 2613
Qy 12232 CCGAGTGTAGTTATACGGTCCGATGGCAGCAGCGAGGCGGATATCCCTTACAGCGTCACT 12291
Db 2614 CGTAGTGAGTGTACGGATTGGACACAGTACAAATAAACAGTTCCTTATCTACTGTCAT 2673
Qy 12292 GAGTCTCGCCCGCAGGTACGGC---TAGTTGAAGCGAATGAGAGACTACCCGCTGCTGG 12348
Db 2674 GAAATTCGTCACAGCTAGTCTGATTAACAGAGGAGATAACCAATACCCGCTACTTTGG 2733
Qy 12349 CCGATGGCGCGGAAAGCCGTACGTGATTTATGAACGATACCAATGATCCTCAATGC 12408
Db 2734 TCATCTGTAGTTGAAAGCCGAGCTATCATTTACGAGCGTATCCGAGCGACCCCAATGC 2793
Qy 12409 CAACAGCAGCGGTACTCTCTCAGTATGATGAATACGGTTTCCCACTGCGTCAGGTCAGTGC 12468
Db 2794 AGCCAGATATTTACGCTATCCAGTGATCTATTTGGCCAAACCGCTAAACAGGTTTCGTA 2853
Qy 12469 AATTATCCAGCAGCCCTCCGTCGGGGAATAATCCATATCCGGCGTCTTTACCGGCGAG 12528
Db 2854 CAGTATCCAGCGCGAAAGCAACAGCAATCAGTCCGTATCTCTGATACGCTGCTGATGAA 2913
Qy 12529 CTGTTGCGCAACAGTTATGACGAGCAGCAGAGATATTACGCTGGGTTGCAACAGAGC 12588
Db 2914 TTGTAGGCCAACAGCTATGATGAACAGCAACCCCAATTAACGCTCACCTATCAACAATCC 2973
Qy 12589 AGTGACATACACTTGTGTTTCACTGCTGAGGGGCAATGGTTTGGGGTTGGCGAGGCG 12648
Db 2974 AGTTGGCATCATCTGACTGACATACCGT-----TCGGTGTAGGATTTACCGGATAGT 3027
Qy 12649 TCGGGGACGATGTATTCAGTACTCTCGGGAACAAGTCCGGAAGGGGTCTGACGCTG 12708
Db 3028 ACCCGCAGTGATATCTCACTTATGAAGCTAAATAATGACTGCTGCTGTTTAAATCTG 3087
Qy 12709 GAACACTGTTGGCGCCGAAAGCCTGCTCGGATAGTCCAGTCCGTACGTCGCTGGCGGT 12768
Db 3088 GAACACTGATGATTAAGATAGCCTGATTCGGATATATAAACCGGCGTAATATCTCGGC 3147
Qy 12769 CAGCAGCAAGTCTGCTATCTGATTTCAAGAAGCTTGCACCGCTGCTCTCGCCACATC 12828
Db 3148 CAGAAAAAACCATTTATACCAATGGAAAAATGACGCGCATTCGCAACGCCAACGCGA 3207
Qy 12829 CCCCCAAGGTAGCTTTTATCGAAACGCGCTGCTGGATGAGGGTATGCTAGTCTACCTG 12888
Db 3208 CAAGCGCTAGTTGCTCTTTACCGAGACACGCTATTTAGTCAATCCACACTATCAGCGTTT 3267
Qy 12889 GCTGCTACATTTGTTGATGAACA-----TCTCGAGCAAGCCGCTTACCGCAAA 12936
Db 3268 GATGGAGATCCCATCTGCTCAATTGTCAACGAGCTGGAAACAGCGGATACCAACAA 3327
Qy 12937 TCCGGATACCTTTTCCCTCGAGGAGGAAAGCAGAAACAGGCAATTTGGACCCAGTGTGAG 12996
Db 3328 ACAATATCTATTTCTTCGCAACCGGAGAAG-----ATAAATCTGGGTAGTCTCAT 3381
Qy 12997 GATATGTTACCTATGTCGGCGCGCAGACATTTCTGGCTACCGCTATCTCTTGGGACAGT 13056
Db 3382 GGTATATACCGGATACGGTACAGCCGACAGTTCTGGCGCCGCAAAAACAGAGCAACCC 3441
Qy 13057 ATGTTGACCGCCGATTTACCGTACGCGTACGCTGAGCGGTATGCTGCTATACGCAAGTGG 13116
Db 3442 CAACTCAGGGCAAAATTAACACTCTTGGGATGCAACTATGCTGCTTGCATCACAAACC 3501
Qy 13117 CAGGATGCGCGAGGATTTGTACCAACAGCCGACTATGACTGCGCTTCTCTGACGCCGCTG 13176
Db 3502 CGAGATGCTGCTGGCTGCAACACCTCAGCAAAATATGACTGCGGTTTTCTGACCCCTGTG 3561
Qy 13177 CCGGTGACGGACCCCAATGATTAATCTGAGTCCGCTCACTCTGATGCTCTGGGCGGGTG 13236
Db 3562 CAACTCAGAGATATCAATGACCAATCAGCACCTTTATCATGCTGATGCTGCGCGCGGCA 3621

QY 13237 ACACCCCTGCGATTCTCGGGGACCGGAGATGGTATTGCGCACCGGTTACAGT----- 13287
Db 3622 ATCACACTGGCGTTTGGGGAACCTGAAAAACGCAAGATGACCGGTTACTCTTACCCGAA 3681
QY 13288 GATGCCACGTTGTCGGTTCGGAGCGGCGCAGCAGCGCTCTGGCGTTGACGGGCGCCCTA 13347
Db 3682 AAGACACCGTTTCTCCACCGCTCGGATGTGAACTCCCGCTATTGAGTTAAAAAACCGCTC 3741
QY 13348 CCAGTAGCAGAGTGTCTGGTGTATGTCTACGGACAGATTGGGGAGATGACGACAAATGAGAAA 13407
Db 3742 CCTGTAGCAGAGTGTCAAGTTTACGCCACCAAGAGCTGGATGCCAGTATTAAAGTCAGAAA 3801

RESULT 12
ADN61379
ID ADN61379 standard; DNA; 4425 BP.
XX
AC ADN61379;
XX
DT 01-JUL-2004. (first entry)
XX
DE Photorhabdus strain W14 tcdB2 toxin complex DNA.
XX
KW Cry; toxic; lepidopteran pest; toxin complex; insecticide; strain W14;
KW ds; tcdB2.
XX
OS Photorhabdus sp.
XX
PN W02004002223-A2.
XX
PD 08-JAN-2004;
XX
XX 27-JUN-2003; 2003WO-US020082.
XX
XX 28-JUN-2002; 2002US-0392633P.
PR 21-JAN-2003; 2003US-0441647P.
XX
XX (DOWC) DOW AGROSCIENCES LLC.
XX
XX Bintrim SB, Bevan SA, Zhu B, Merlo DJ;
XX WPT; 2004-082821/08.
XX
PT Screening a culture of *Paenibacillus* isolate for Cry protein or toxin
PT complex protein, useful for controlling lepidopterans, comprises
PT obtaining DNA or protein from the culture and assaying the presence of
PT the gene or protein.
XX
XX Example 12; SEQ ID NO 43; 220pp; English.
XX
XX The invention relates to a novel method for screening a culture of a
XX *Paenibacillus* isolate for a gene encoding a protein selected from a Cry
XX protein that is toxic to a lepidopteran pest and a toxin complex protein.
XX The method comprises obtaining DNA from the culture and assaying the DNA
XX for the presence of the gene or obtaining a protein produced by the
XX culture and assaying the presence of a protein that indicates the
XX presence of the gene in the isolate. The method of the invention has
XX insecticide applications and may be useful for screening *Paenibacillus*
XX sp. for toxin complex (TC)-like genes and proteins which may themselves
XX be used to enhance or potentiate the activity of a stand-alone
XX xenorhabdus toxin protein. The method may also be useful for screening
XX *Paenibacillus* sp. and others for insecticidal thiaminase genes and
XX proteins for controlling insects, particularly lepidopterans. The current
XX sequence is that of the *Photorhabdus* strain W14 tcdB2 toxin complex DNA
XX of the invention.
SQ Sequence 4425 BP; 1207 A; 1157 C; 1050 G; 1011 T; 0 U; 0 Other;

Query Match 5.5%; Score 1046.4; DB 12; Length 4425;
Best Local Similarity 56.4%; Pred. No. 4.6e-238;
Matches 2166; Conservative 0; Mismatches 1606; Indels 66; Gaps 9;

QY 9598 ATGCAAAATCATCAAGACATGGCCATTACTGCCCCACAGTTGCTTCCGGGGGGGGTGGC 9657

Db 1 ATGCAAAATTCACAAGATTTTAGTATTACGAAACTGTCACTGCCCCAAAGGGGGGGCGCT 60
QY 9658 GTCACCGGGCTCAAGGGTGATATCGGGCGGAGGGCCGATGGTGGCGGACCCCTCAGT 9717
Db 61 ATCAGCGGAATGGTGAAGCAITTAACCCCACTGGACCGGATGGTATGGCGCGGCTATCT 120
QY 9718 ATTCCCTTGGCGGTAGCCCCGGTTCGCGGGTTACGCCCCCACTGGGGGACATTAATATCAC 9777
Db 121 CTACCATTTGCTATTCTCGCGGGCGGGTTATGCTCCCGCATTCATCTCTGAATTACAAC 180
QY 9778 AGCGGTTCGGGGAACCGGCCCTTTTGGCATTTGGGTGGGGTATCGCGGTGCTGTCTCCAG 9837
Db 181 AGCGGGCGCGGTAAACAGTCCATTTGGTCTGGGTGGGATGCAACCGTTATGACTATCCGC 240
QY 9838 CGTGTACCGGCAACGAGGACCTTACTAGATGATATGATGAATTCACCGGTCCGGAC 9897
Db 241 CGCCGACCCATTTTGGCGTCCCCCATTTATGAGCAACCGATACCTTTTGGGGGCCAGAA 300
QY 9898 GGTGAGGTGCTGTGCGGCACTCAGCGGTGCTGGCACCCCAAGACACGCGAGGCCACC 9957
Db 301 GCGGAAGTGTGGTG-----GTAGCGGATCAACTCTCGGACGATCC 342
QY 9958 TCACTACTGGGGATAAACCCAGCGGAAGCTTCAACGTTTCAGTTTACCGTTTCACTGACG 10017
Db 343 ACATTACAGGGTATCAATTTAGCGGCCACCTTTACCGTTTACCGGTACCGGTTCCTCGTCTG 402
QY 10018 GAGGGTAGTCTCAGCGCCCTTGGAGCTTGGCTGCCCGCCGACGAGACAGAAACGGAATTT 10077
Db 403 GAAAGCCATTTTCAGCCGATTTGGAAATTTTGGCAACCCCAAAACAAACAGGTAAACAGATTTT 462
QY 10078 TGGGTGTATATACCCCTGACGACAGGTGGCTCTGCTGGGCGCAAAATGCGAGGCTCGC 10137
Db 463 TGGTTGATATATAGCCAGATGGGAGGTGATCTACTTGGTAAATCACCAGCGCGCGG 522
QY 10138 ATCAGCAACCCACAGCCCAACACAGACGCGGTTTGGGTGATGGAGTCTCTCGGTATCA 10197
Db 523 ATCAGCAACCCATCCCAACAGCAACAAACAGCAACAATGGCTGTGGAAAGCTCTGTATCA 582
QY 10198 CTTACCGGCAACAGATGATTTACCAATACCGTGGGAGAGATGATGAGGTTGTGACGAG 10257
Db 583 TCACGTGGCGAAACAAATTTATTAATCAATATCGCGCCGAAAGATGACACAGGTTCGGAAGCA 642
QY 10258 GCGGAGCGGACGCGCACCGCGAGCGCGGCCCAACGTTTATCCGTGGGGGTCTGTAT 10317
Db 643 GATGAATTTACGACCATTTTACAGGCTACAGCGCAACGTTTATTTACATCTGTGTATTAC 702
QY 10318 GGTAAACCGTTCAGCGGCTCGGACGCTACCGGCGCTGGTGTGCGA---CACCATCAATGGAT 10374
Db 703 GGCACCGGTACAGCCAGCGAAACATTTACCGGCTCTGGATGGCAGCGCCCATCACAGCA 762
QY 10375 AGCTGCGTGTATCTCTGTTGATTTATGTTAGGTAGCGTAGCTCGGTGCTGTCTGAAGCG 10434
Db 763 GACTGGTGTCTCTCTCTGTTTATTTGATTTACGGGGAACGCAAGTAAACACCTCAAAACGCCA 822
QY 10435 CCGGCTCGGCAACACACGAGAGTGGGAGTGGCTGTGTCGTCAGAGATTTGTTTTTCGGG 10494
Db 823 CCAGCATTTTCTGACTAAGTAG-----CTGCTTTTCCGTCAGGACCGTTTTTCCCGT 876
QY 10495 TATGAGTTTGGTTTTTAACCTGCGGACTCGCGGCTGTGCGCGTTCAGGTTTGTGTTCCAT 10554
Db 877 TATGAATATGGCTTTTCAGATTCGTACCCCGCTTATCGCGTCAGGTATTGATGTACCAT 936
QY 10555 TACTAGTGTCTTGGGGGGAGTTTCGGGAGCGAATGATGCGGCAGCATTTGATTTCTCGC 10614
Db 937 CACCTCAAGCACTGGATAGTAAGATAACAGAAACACACGACCAACGCTGGTTTTCACGC 996
QY 10615 CTGTTCTGACTACAGGGAAGTCTTCACTCAGTCTGCTCGAGAACGTCGACCGAGTGTG 10674
Db 997 CTGATCTCAATTTACAGCAAGAACGCGATAGCAGCACGCTAGTATTTCGTTCCGCGAGTG 1056
QY 10675 GCTTATGAGTCGACGCGGAGCTCTGTGCTTCCCGCACTGGCATTTGGGGTGGCAAAACC 10734

Qy 12892 GCCTACATTTGGTGAAGA-----TCTCAGGAGAGCCGGTTTACCGGCAATCC 12939
 Db 3268 GGAAGCATCCGTCGATGATAATATCAACGACGCTGGAGCAAGCTGATATCAGCAACA 3327
 Qy 12940 GGTATACCTTTTCCCTCAGGAGGAGGAGCAAGCAGGCAATGTGGACCCAGTGTACAGGA 12999
 Db 3328 AATTATCTATTTCCTCAGCTGGAAG-----ATAAGTTTGGGTAGCCCATCAGCGC 3381
 Qy 13000 TATGTTACCTATGCGCGGAGAGCAATTTCTGGCTACCGCTATCCTTTCCGGGACAGTATG 13059
 Db 3382 TATACCGATTATGTACAGCGGCACAGTTCTGGCGCCGCAAAACAGACACACCCAA 3441
 Qy 13060 TTGACCGGCCAGTTTACCGTACCGGAGCGGTGACGCTGCTGTCATCAGCAGTGGCAG 13119
 Db 3442 CTCACCGGTAAATCACCCTCATCTGGGATGCAAACTATTGCGTTGTGTACAAACCCGG 3501
 Qy 13120 GATGCCCGGAGTTGTACACAGCGGACTATGACTGGCGCTTCTGACGCGCCGTCGG 13179
 Db 3502 GATGCTGTGACTGACAACCTCAGCCAAATATGACTGGCGTTTCTGACCCCGGTGCAA 3561
 Qy 13180 GTGACGGACCCCAATGATAATCTGCAGTCCGTCATCTGGATGCTCTGGCGCGGGTGACC 13239
 Db 3562 CTCACCGATATGATGACATCAGCACTTATCAGCTGATGATGATGGCGGACCAATC 3621
 Qy 13240 ACCCTGCGATTTCTGGGCGAGGAGATGTGTTATGCCACCGGTTA-----CAGTGT 13290
 Db 3622 ACATTGGCTTTTGGGGAACGTGAAACGCGAAGATGACAGGTTATTCTCACCAGGAAAA 3681
 Qy 13291 GCACGTTGTCGTTCCGGAGCGGCGAGCAGCGCTCTGGGTTGACGGCGCCCTACCA 13350
 Db 3682 GCATCATTTTCTCCACCATCCGATGTTAATGCCGCTATTGAGTTAAAAAACCCTCCCT 3741
 Qy 13351 GTACACAGTGTCTGGGTATGTACAGGACAGTTGGGAGATGACGACAATGAGAAAA 13408
 Db 3742 GTACACAGTGTGAGTCTACGACCAAGAGCTGGATGCCAGTATTAAAGTCAGAAAA 3799

RESULT 13

ADP18621
 ID ADP18621 standard; DNA; 4425 BP.

XX AC ADP18621;

XX DT 12-AUG-2004 (first entry)

XX DE Photorhabdus luminescens W-14 tcdB2 encoding DNA SEQ ID NO:9.

XX KW tcd; Photorhabdus luminescens W-14; transgenic plant; Toxin A;
 orally active insect toxin; insect toxin; tcdB2; gene; ds.

XX OS Photorhabdus luminescens.

XX FH Key Location/Qualifiers

XX FT CDS 1..4425

XX FT /*tag= a

XX FT /product= "tcdB2"

XX PN WO2004044217-A2.

XX PD 27-MAY-2004.

XX PF 12-NOV-2003; 2003WO-IB005553.

XX PR 12-NOV-2002; 2002US-0425672P.

XX PA (UYBA-) UNIV BATH.

XX PI Ffrench-Constant RH, Waterfield NR;

XX XX WPI; 2004-411735/38.

XX DR P-PSDB; ADP18622.

XX PT New isolated Photorhabdus luminescens nucleic acids, useful for

PT expressing orally active insect toxin or for generating transgenic plants
 with enhanced resistance to insects.

XX Claim 2; SEQ ID NO 9; 118pp; English.

XX The present invention describes DNA sequences from the tcd genomic region
 of Photorhabdus luminescens W-14. Also described: (1) a transgenic
 monocol or dicot cell having a genome comprising a nucleic acid sequence
 CC that encodes SEQ ID NO:4, 6, 8, 10, 12, 14, or 16; (2) a transgenic plant
 CC with a genome comprising a nucleic acid sequence that encodes SEQ ID
 CC NO:4, 6, 8, 10, 12, 14, or 16; (3) a seed of the transgenic plant; (4) a
 CC progeny of seed; (5) a method of producing toxin A of Photorhabdus
 CC luminescens W-14 in a heterologous host; and (6) a method of producing an
 CC orally active insect toxin. The nucleotide sequences are useful for
 CC heterologous expression of orally active insect toxin. They can also be
 CC used for generating transgenic plants with enhanced resistance to
 CC insects. The present sequence encodes Photorhabdus luminescens W-14
 CC tcdB2, which is used in the exemplification of the present invention.

XX SQ Sequence 4425 BP; 1207 A; 1157 C; 1050 G; 1011 T; 0 U; 0 Other;

Query Match 5.5%; Score 1046.4; DB 12; Length 4425;
 Best Local Similarity 56.4%; Pred. No. 4.6e-238;
 Matches 2166; Conservative 0; Mismatches 1606; Indels 66; Gaps 9;

Qy 9598 ATGCAAAATCATCAAGACATGCGCATTTACTGCCCCCAGCTTTCCTCCGGGGCGGTGCG 9657

Db 1 ATGCAAAATTCACAAGATTTAGTATTACGGAATGTCTACTGCCCAAGGGGGGGCGCT 60

Qy 9658 GTACCGGGCTCAAGGTGATATCGCGGGCGGAGCGCGGATGTGGCGGACCTGAGT 9717

Db 61 ATCAGCGGAATGGGTGAAGCATTAACCCCACTGGACCGGATGATATGGCGCGCTATCT 120

Qy 9718 ATTCCTTCGCGGTAGCCCGGTGAGCCCGCTTACGCCCCCACTGGGACCTTATATATCAC 9777

Db 121 CTACCATTTGCTATTTCTGCGGGCGGTATGTCTCCCGCATTTCACTCTGAATTAACAC 180

Qy 9778 AGCCGGTTCGGGGAACCGCCCTTTGGCATTTGGCTGGGGTATCGCGGCTGTCTGCTCCAG 9837

Db 181 AGCGGCGCGGTAAACAGTCCATTTGGTCTGGGTGGATGCAACGTTATGACTATCCG 240

Qy 9838 CGTCTACGCGCAACGAGACACTTACTACGATGATATGATGAATTCACGGTTCGGAC 9897

Db 241 CGCCGCAACCATTTTGGCGTCCCCCATTTATGAGAAACCCGATACCTTTTGGGGCCAGAA 300

Qy 9898 GGTGAGGTCTGTGTCGGGCACTCACGGTCTGTGGCAACCCCAAGACACGCGAGCCACC 9957

Db 301 GCGGAAGTGTCTGTG-----GTAGCGGATCAACCTCGGAGCAATCC 342

Qy 9958 TCACCTACTGGGATAAACCCAGCGGAAGCTTCAACGTTTACCGTTTACGTTACGTACG 10017

Db 343 ACATTACAGGATATCAATTAGGCGGCACCTTTACGTTACCGGTACCGTTCCCGTCTG 402

Qy 10018 GAGGGTAGTCTCAGCCGCTTGTAGCGTGTGCTGCCCGCCGACGAGACAGAAACGGAATTT 10077

Db 403 GAAAGCCATTTACGCCGATTTGGAATATTGGCAACCCCAAAACACAGGTAACAGATTTT 462

Qy 10078 TGGGTGTTATACCCCTGACGACAGTGGCTCTGCTGGCGCCGAATGCGCAGGCTCGC 10137

Db 463 TGGTTGATATATAGCCAGATGGGCGAGTGTCTACTTGGGTAAATCACCAGCGCGCG 522

Qy 10138 ATCAGCAACCCCAAGCGCCCAACACAGCGCGGTGTTGGCTGTGATGAGTCTCTCGGTATCA 10197

Db 523 ATCAGCAACCCCAAGCGCCCAACACAGCAACAACAGCAATGGTGTCTGGAGGCTCTGTATCA 582

Qy 10198 CTTACCGCGCAACAGATGTATTACCAATACCGTCGGGAAGATGATGACGGTGTGACGAG 10257

Db 583 TCAGTGGCGAACAATTTATTATCAATATCGCGCGCAAGATGACACAGGTGCGAAGCA 642

Qy 10258 GCGGAGCGGACCGGACCCCGGCGGCGCCCAAGCTTATCCGGTGGCGGTCTGCTAT 10317

Db 643 GATGAAATTCAGCCACCATTTTACAGGCTACAGCGCAACGTTATTATACACATCGTGTATTAC 702

Db	2854	TACCGGGCCGACAGCGACGAACTCAATCTGTATCTCTGATACATATTGCCCTGATAAGTTG	2913
Qy	12532	TTGCCCAACAGTTTATGACGAGCAGCAGACAGATATTACGCTCTGGGTTTGCAACACAGCAGT	12591
Db	2914	TTAGCCAAACAGCTATGATGACCAACAACGCCAATTTACGGCTACCTATCAACAATCCAGT	2973
Qy	12592	GCACATCACCTGTTTCACTGCTGAGGGGCAATTGGTTGTGGGTGTGGCGAGGCGTCG	12651
Db	2974	TGGCATCACCTGACCAACAATACCG-----TTCGAGTATTGGGATTTACCGGATAGTACC	3027
Qy	12652	CGGGACGAGTATTTACGCTACTCTCGGACAACGTCGCCGAAGGGGTCTGACGCTCGAA	12711
Db	3028	CGCAGTGATATCTTTACTTATGGCGCTGAAAATGTGCCCTGTGSGTGGTTTAAATCTCGAA	3087
Qy	12712	CACCTGTGGCGCCCGAAAGCCTTGSTCTCGGATAGTCAGSTCGGTACGCTGGCGGGTCTCAG	12771
Db	3088	CTTCTGAGTGATAAAATAATAGCTGATCGCGGACGATAAACACGTGATACCTCGGTCTCAG	3147
Qy	12772	CAGCAAGTCTGGTATCTGATTCAACAGAGTTGCCACCGTGGTGTCTCGGCCACTCCCC	12831
Db	3148	CAAAAAACCGCTTATACCGATGGACAAAAATACAACGCCGTTTGCAAAACACCAACACGGCAA	3207
Qy	12832	CCCAAGGTAGCTTTTATCGAAACGCCGCTGCTGGATGATGGGTATGGTCAGTTTCACTGGCT	12891
Db	3208	GCCCTGATTGGCTTTTACCGAAAACAACGGTATTCAACCAAGTCCACATTATCAGCGTTTAAAC	3267
Qy	12892	GCCTACATTGTGGATGAACA-----TCTCGAGCAAGCCGGTTTACCGGCAATCC	12939
Db	3268	GGAGGATCCGCTCGATTAATATCAACGACGCTGGAGCAAGCTGGATATCAGCAACA	3327
Qy	12940	GGATACCTTTTCCCTCGAGCGAGGGAAGCAGAACAGGCAATTTGTGACCACGAGTGTACGGGA	12999
Db	3328	AATATCTATTCCCTCGCAC TGGAGAAG-----ATAAAGTTTGGGTAGCCATCATCGGC	3381
Qy	13000	TATGTTTACCTATGCCCGGCGCAGACATTTCTGGTACCGCTATCTCTTGGGACAGTATG	13059
Db	3382	TATACCGATTTATGGTACAGCGCAAGTTCTGGCGCCGCGCAAAAACAGAGCAACACCCAA	3441
Qy	13060	TTCAACCGGCCAGTTTACCGTGACGGGTGACGGTACGACTCGCTCATCACGCGAGTGGCAG	13119
Db	3442	CTCACCGGTAAATCAACCTCATCTGGGATGCAAACTATTGGTTGTGGTATCAAAACCCGG	3501
Qy	13120	GATGCCCGAGGATTTGTACCACAGCCGCACTATGACTGGCGGTTCTGACGCCCGTCCGG	13179
Db	3502	GATGCTGCTGGACTGACAACTTACGCAAAATATGACTGGCGTTTCTGACCCCGGTGCAA	3561
Qy	13180	GTGACGGACCCCAATGATTAATCTGCAGTCCGCTACTCTGZATGCTCTGGGCGGGGTGACC	13239
Db	3562	CTCACCGATATCAATGACAAATCAGCACCTTATCACACTGGATGCAATTTGGGCGCGCAATC	3621
Qy	13240	ACCTCGGATTTCTGGGGCACGAGAAATGGTATTGCGACCGGTTA-----CAGTGAT	13290
Db	3622	ACATTGCGCTTTTGGGGAACCTGAAACCGCAAGATGACAGGTTATTCTCTACCGGAAAAA	3681
Qy	13291	GCCAGTTGTTCGTTCCGGACGGCGCAGCAGCGCTCTGGGTTGTGACGGCGCCCTTACCA	13350
Db	3682	GCATCATTTCTCCACCATCCGATGTTAATGCCGCTATTGAGTTAAAAAACCCTCCCT	3741
Qy	13351	GTAGCAAGTGTCTGGTGTATGTCAACGACAGTTGGGAGATGACGAAATGAGAAA	13408
Db	3742	GTAGCACAGTGTCAAGTGTACGCAACAGAAAGCTGGATCCAGTATTAAAGTCAGAAA	3799

RESULT 14
AAV29924

AAV29924
ID AAV29924 standard; DNA: 4458 BP.

XX

AC AAV29924;

XX
DE
07-211C-19

DT 07-AUG-1998 (first entry) XX

DE tcaC gene

tcaC gene from the tca genomic region encoding protein TcaC.

XX

TcaA; *Photorhabdus luminescens* W-14; nematode; symbiotic;
Heterorhabdus; tca; tcb; tcc; insecticidal activity; toxin;
Lepidoptera; Coleoptera; Hymenoptera; Diptera; Dictyophera; Acarina;
Homoptera; Southern; Western corn rootworm; Colorado potato beetle;
mealworm; boll weevil; turf grub; beetle armyworm; black cutworm;
cabbage looper; codling moth; corn earworm; European corn borer;
Tobacco hornworm; budworm; ds.

OS Photorhabdus luminescens.

	Key	Location/Qualifiers
AA		
FH		
FT	CDS	1..4458
FT		/*tag= a
FT		/product= "TcaC"

XX
PN
WO9808932-A1.

05-MAR-1998.
PD
AA

AA
PF 05-MAY-1997; 97WO-US007657.

AA 28-AUG-1996; 96US-00705484.

PR	06-NOV-1996;	96US-VU743699.
PR	06-NOV-1996:	96WO-US018003.

PA (DOWC) DOWELANCO.

PA (WISC) WISCUSIN
XX

PI Ensigh JC, Bowen DU, Pettit J, Ffrench-Constant RH, Rocheleau TA:

FI OFF GL, ROBERTS JL, STRICKLAND JA, GUO L, CICHE TA, SUKHAPINDA K, XX

DR WPI; 1998-1794Z//16.
DR P-PSDB: AAW56546.

Isolated toxins fr

PI control of insect pests.
XX
PS Claim 38; Page 190-196; 321pp; English.

CC The present sequence encodes a protein

CC *Photobacterium luminescens* (Wittig). This is a symbiotic bacterium of the
CC nematodes of the *Heterorhabdus* genus. The bacterium has at least 4
CC distinct genomic regions, tca, tcb, tcc, and tcd. Peptide products are
CC produced from these regions that are associated with insecticidal
CC activity. The native toxins are secreted proteins. The proteins are toxic
CC to insects upon exposure and especially when ingested. The nucleic acid
CC sequence can be used to produce transgenic plants, baculoviruses or
CC microbial hosts for toxin production. They can be used to control insects
CC pests from the Lepidoptera, Coleoptera, Hymenoptera, Diptera,
CC Dictyoptera, Acarina or Homoptera orders, especially the Southern or
CC Western corn rootworm, Colorado potato beetle, mealworm, boll weevil,
CC turf grub, beetle armyworm, black cutworm, cabbage looper, codling moth,
CC corn earworm, European corn borer or tobacco hornworm or budworm
XX
SQ Sequence 4458 BP; 1199 A; 1181 C; 1088 G; 990 T; 0 U; 0 Other;

Query Match 5.1% Score 969.8 DB 2: Length 4458:

Best Local Similarity 33.8%; Pred: No. 8.5e-220;
Matches 2395: Conservative 0: Mismatches 1857: Indels 201:

matchless 2333; conservative 0; mismatchless 1037;

Qy 9598 ATGCAAAATCATCAAGACATGGCCATTACTGCCCCCA CGTTGCGCTTCCGGGGCGGTGCG 9657

[illegible]

Db 61 ATCAATGGCATGGGAGAAGCACTGAATGCTGCGGGCCCTGATGGATGGCTCCCTATCT 120

[illegible]

QY 9778 AGCGGTGCGGGAAACGCGCCCTTTGGCAATGGCTGGGGTATCGCGGTGCTGCTGCCAG 9837
 Db 181 AACAGTCCAGTAAATGGCCCTTTCCGCAATCGGCTGGCAATGGCTGTTATGTCCATTAGC 240
 QY 9838 CGTCTGATCGGCGAAGCGAGCACTTACTAGATGATCTGATGAATTCACCGGTCCGGAC 9897
 Db 241 CGACGCAACCAACATGGCAATTCACCAATACGGTAATGACGACACGTTCTCTATCCCCACAA 300
 QY 9898 GGTGAGGTGCTGTCGCGGCACTCAGCGTCTGCGCACCCCAAGACGACGCGAGGCC--- 9954
 Db 301 GCGAGGTCAATGAATATCGCCCTGAAATGACCAAGGCGAACCTGATATCCGTCAAGACGTT 360
 QY 9955 ACCTCACTACTGGGGATAAACCCAGCGGAAAGCTTCAACGTTCCAGGTTTACCGTTCCACGT 10014
 Db 361 AAAACGCTCAAGGCGTTACTTGGCCAAATTCCTATACCGTGAACCGCTATCAAGCCCGC 420
 QY 10015 ACGGAGGTAGTCTACGCGCCCTTGAGCGTTGGCTGCCCGCGACGAGACAGAAACG--- 10071
 Db 421 CAGATCCTGGATTTTCAGTMAAAATCGAATACTGGCAACCTGCCTCCGTCGAAGAGACGC 480
 QY 10072 GAATTTTGGGTGTATATACCCCTGACGACAGGTGGCTCTGCTGGCCGAAATGCGCAG 10131
 Db 481 GCTTCTGGGTGATATCGACACGCGACGGGCATCTACACATCTTAGGGAAACCCGCGCAG 540
 QY 10132 GCTCGCATCAGCAACCCCAAGCCCAACACAGACGCGGTTGGCTGATGAGTCTCTCG 10191
 Db 541 GCTTGTCTGCAATTCGCAAAATGACCAACAATCGCCAGTGGTGTGGAAGAACT 600
 QY 10192 GTATCACTTACCGCGAACAAGATGTATTAACCAATACCGTGGGAAGATGATGCGTTGT 10251
 Db 601 GTACGCGACCGCGTGAACATGTGAGTATCAATATCGAGCCGGAAGATGAAGCCCATTTGT 660
 QY 10252 GACGAGCGGAGCGACGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTC 10311
 Db 661 GACGACAATGAAGAAACCGCTCATCCCAATGTTTACCGCACAGCGCTATCTGTFACAGGTG 720
 QY 10312 TGTGTATGTAAACCGTCAGGCGGCTCGGACGCTACCGCGCGCTG---TGTGCACACCATCA 10368
 Db 721 AACTACGGCAACATCAACACAGCCAGCGCTGTTGTTACTGATGAATACGCACTCCGCA 780
 QY 10369 ATCGATAGTGGCTGTTTATCTGGTGTGTTGATATATGGTAGCGTAGCTCGGTGCTGT 10428
 Db 781 CCGGAAGAGTGGCTGTTTATCTGGTCTTGTACCAAGTGAAGCGGATACCTCACTTCAT 840
 QY 10429 GAAGCCCGGCTGCGAACAACAGCAAGTGGGAGTGGCTGTGTCAGGATGTTT 10488
 Db 841 ACCGTGCCAACATGGGA---TGAGGTACAGCGCAATGCTGTACCGCGGATATCTTC 897
 QY 10489 TCCGGGTATGAGTGTGTTTAACTTCGCGACTCGCGGCTGTGCGGTCAAGTGTGATG 10548
 Db 898 TCTCGTATGAATATGGTTTGAAGTGGTACTCGCGCTTATGTCAAAGTGTGATG 957
 QY 10549 TTCCATTAAGTGTCTGCGGAGGTTCCGGAGCGGAATGATCGCCAGCAATGAT 10608
 Db 958 TTTTCAACGCAACCGCTCATGGCCGAGAAAGCAGTACCAATGACGCCCGGAACGTT 1017
 QY 10609 TCTCGCTGTGCTGACTACAGGAAAGTCTTCACTAGTCTGCTCGAAGACGTGAC 10668
 Db 1018 GGACGCTTAAATCTGGAATATGAACAAAACGCGCAGGTCACCAAGTGTGATTAATCCGT 1077
 QY 10669 CAGGTGGCTTATGAGTGGAGGAGCGTCTGTGCTTGGCGGCTGCGCATTTGGGGTGG 10728
 Db 1078 CAATTAAGCATGATTCGGAGGAGGCGCAGTCAACCGCACCATTAAGACTAGCTGG 1137
 QY 10729 CAACCTTTTACCCCGCGCAATGTCCGGATGGCAGACGCGTGAAGATATGGCAAGTTG 10788
 Db 1138 CAACGCTTTGATCTGGAGAAATCCCGCATGCGCAACGCTTTGACGCACTAGATAATTT 1197
 QY 10789 AGTTTCTTCAACCCCTAGCTTGTAGACCTTAAACGGGAGGTTGTTGGTATCTCG 10848
 Db 1198 AACTCGAGCAACGTTTATCAACTGGTGTGCTCGCGGAGAGGGTTGCCAGGTATGCTG 1257
 QY 10849 TATCAGACAGCGGTGCTGTTGTTGAGTAAACCGGTACCGCGGAGTATCGCG 10908

Db 1258 TATCAGATCGAGGCGCTTGGTGTATAAAGTCCGCAACGTCAGGAAGACGAGACAGC 1317
 QY 10909 GATGCTGTGACCTGGGGGGCGGCTGGGCGCTGCGGACAAATGCCCGCTTTGATATACAGC 10968
 Db 1318 AATGCCGTCACTTACGACAAAATCGCCCACTACCTACCTACCAATTTGAGGATAAT 1377
 QY 10969 GGCATCTCGCGGATCTTAATGGGATGGTCCGCTGGAGTGGTGGTACCGCCCGCT 11028
 Db 1378 GCTCATTTGATGGATATCAACGAGACGCGCAACTGGATGGGTGTTTACCGCTCCGCT 1437
 QY 11029 GTGGGGGATGTATGATCGCACCCCGCGCGGAGTGGTGTGATTTTCACTTCACTCCCTGTCA 11088
 Db 1438 ATTCCGGATACCATAGTCAGCAACCCGATGGAAGTGAAGCACTTTAGCGCAATCAAT 1497
 QY 11089 GCTTGGCCCGTGAATATGCGCATCAAAAGCAGTGTCTGCGGATATCTTGGGGGTGG 11148
 Db 1498 GCTTGGCCCGTGAATATTTTCAAGCATCCAGTTCGCTGACCTTACCGGGCAGGC 1557
 QY 11149 TTAAACGACATGCTTATCGGCGCGCGAGTGTTCGCTCTATTTCCGCAAAAACGAT 11208
 Db 1558 TTATCTGATTTAGTGTGATCGGCGCGAAAGCGTGGTCTATATGCGCAACGCGAAAC 1617
 QY 11209 GGTGGAATAAAGGGGAGACCGTGCAGCAAAACGGAAGACTCACTCTGCGGTCCCGGG 11268
 Db 1618 GGTGGGTAAAGGAGAGATGTCCCCCAATCCACAGGTATCACCTGCTGTACAGGG 1677
 QY 11269 GTTGACCCAGTACCTCGTGGCTTCAGTATATGGTGGCAGTGGACAGCAGATTTG 11328
 Db 1678 ACCGATGCGCGCAAACTGGTGGCTTTCAGTGTATGCTCGTTCGCTCAACAACATCTG 1737
 QY 11329 ACGGAGTTCGCTGCTAAATGGAGTACGTTACTGCGCAAAACCTGGGCGACGCTGTTCCGT 11388
 Db 1738 GTGGAATCAAGGGTAATCGCGTCACTGTTGGCGAATCTAGGGGATGGCGTTCGCT 1797
 QY 11389 CAGCGGTGAATATTTCCCGGTTTATAGCCAGTCACTGACTACGTTTAAACCTCACCAGATA 11448
 Db 1798 CAACCACTAACTCTGTAGGATTTAGCCAGCCCGAAATAGCTTCAATCCCGAACGGCTG 1857
 QY 11449 TTGTGGCGGATACCGAGCGTTCGGGTACACGACCTGATTTATGCGATGATGACCGG 11508
 Db 1858 TTTTGGCGGATATCGAGCGTTCGGCACACCGACCTTATCTATGCGCAATCCGCTCT 1917
 QY 11509 TTAGTCAATTTTCAACAGAGTGGTAAATTTTCGCGGAGCGGACGCTGCTGCTG 11568
 Db 1918 TTGCTCAATTTCTCAACCAAGTGTATCAAGTTTGTATGGCTTGTGATTTAGCGTTG 1977
 QY 11569 CCGAAGGTGTGCGCTATGATCGCACCTGCACTGCTGCAAGTGGCGGATATCCAGGGGCTG 11628
 Db 1978 CCAGAAGGGGTACAAATTTGACAACTTGGCAACTTCAAGTCCCGATATTCAGGGATTA 2037
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 Db 2038 GGGATAGCAGCTTGTATCTGACTGTGCGACATATCGCGCCACATCACTGGGCTTGTGAC 2097
 QY 11689 TTATCGGAGACAAACCCCTGGTGTGATGCGATGACAAACAAATATGGGGCCCGCAT 11748
 Db 2098 CTGTCACTGACCAACCCCTGGTGTGATGTAATGTAATGAAACAAATACCGGGCGCACATCAC 2157
 QY 11749 GCATGCACTATCGCATTTCCGTTGCGTGGATGGATGAGAAACCGGACCTGGCG 11808
 Db 2158 AGCTACATTTATGATGTTCCGCGCAATCTGTTGGATGAAATAATTACAGCTCACCABA 2217
 QY 11809 GAGGAGTTCCTCCCTGCTGCTACTGTCATTTTAAATTTGATACCTGTGGGCTTGGGTG 11868
 Db 2218 GCAGGCAATCTCCGCTGTTTATCTGCGTTTCCAAATGCAATTTGATGTTATACCGAA 2277
 QY 11869 GTGCGAGTATGATCACCGGTAAACGCTGCTGGTACGAGCTGCTTTATCCACCGCGTC 11928
 Db 2278 ATTGAGGATGAATCAGCGGCAACCGGCTCAACAGTGAAGTCAACTACAGCCACCGGCTC 2337
 QY 11929 TGGGAGCGGACGAGTTCGCGGCTTTCGCGGCTTGTGTTTGTGATCAGGATACCGAT 11988

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Db 2338 TGGGATGGTAAAGAGCGGGAATTTCAGAGGATTTGGCTGCATCAAAACAGACAGATACCACA 2397
Qy 11989 ACCTTGGCAAGCCAGGCTAGCGGACAGAACTGAGTATGCTTCTGTGAGCGGAACTGG 12048
Db 2398 ACGTTTTC---TCAGGACACGCCCCGAAACAGGCGGACCGTGCCTGAGTATTAGCTGG 2454
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Db 2455 TTTGCCACCGGATGGATGAAGTAGACAGCAATTAGCTACGGAATATTGGCAGGCAGAC 2514
Qy 12109 GCCCGCGTTTGGCGATTTCCGACACCGGTTTCACTGTGG-----TTCAGAGAGGAT 12162
Db 2515 ACGCAAGCTTATAGCGGATTTGAACCCGTTATACCGTCTGGGATCACCAACCCAGACA 2574
Qy 12163 GAGCAGACATATACTCCGGACGACAGCAAGACATTTCTGTTGACGAGCGCTTGAAGGC 12222
Db 2575 GACCAAGATTTACCCCAATGACACACAGTAACTTGGCTGACGCGAGCGCTTAAAGGC 2634
Qy 12223 ATCTGTGCGCAGTGAATTATACGGTGGCGATGGCAGACGACGCGCGATATCCCTTAC 12282
Db 2635 CAACCTGTACGCACTGAGCTCTACGGTCTGACGGAACAGATTAAGCAACAGTGCCTTAT 2694
Qy 12283 AGCGTCACTGAGTCTCCCGCGCAGGTAGCGTAGTTGAAGGAATGGAGA---CTACCGG 12339
Db 2695 ACCGTCACTGAGTCCGCGCTATCAGGTACGCTCTATTCGCGTAAATAAGAAACCTGAATTA 2754
Qy 12340 GTGTGTGGCGGATGGCGGGAAGCGGTACGTCACTTTATGAACGTTACCAACATGAT 12399
Db 2755 TCTGCTTGGTGACTGCTATTGAAATTCGAGCTACCACATGATGAACATATCATCACTGAC 2814
Qy 12400 CCTCAATGCCAACAGCAGCGGTACTCTCAGTGATGAATACGGTTTCCCACTGCGTCAG 12459
Db 2815 CCACAGTTACGCCAGAGTATCAAGTTGCAACACAGATATCTTTGCTCAATCACTGCAAGT 2874
Qy 12460 GTCAGTGTCAATTTATCCAGACGCGCTCCGTGGCGGACAAATCATATCCGGGTCTTTA 12519
Db 2875 GTCGATATTGCTGGCGCGCGCGGAAAAACACAGCAGTGAATCCCTACCGCGCTACCCCTG 2934
Qy 12520 CCGGCGAGCTGTTCGCAACAGTTATGACGAGCAGCAGCAGATATTACCGCTGGGGTTG 12579
Db 2935 CCGGAAACGCTATTGACAGCAGCTATGATGATCAACAACTATTACGTCTGGTGAGA 2994
Qy 12580 CAACAGACGAGTGACATCACTTGTTCCTGCTGAGGCGCATTTGGTTTGGGGTTG 12639
Db 2995 CAAAAAATAGCTGGCATCACTGACT-----GATGGGGAACACTGGCGATAGGTTTA 3048
Qy 12640 GCGGAGCGGTGCGGGAGCATGATTTACGTAATCTCGGACACAGCTGCGGGAAGGGGT 12699
Db 3049 CCGAATGCACACCGCGTGATGTTTATATCTTATGACCGGAGCAAAATTCACACCGAAGGG 3108
Qy 12700 CTGACGCTGGACACCTGTTGGCGCCGAAAGCTGCTCGGATAGTCAGTTCGTTACG 12759
Db 3109 ATTTCCCTTGAATCTTGCTGAAAGATGATGGCGCTGTAGCAGATGAANAAGCGCGCTT 3168
Qy 12760 CTGGCGGCTCAGCAGCAAGTCTGGTATCTGGATTCAAGACGTTGCCACCGCTCGTCT 12819
Db 3169 TATCTGGGACAAACAGAGCTTTTACCGCGGCTCAAGGGAAGTCACTCTAGAAAAA 3228
Qy 12820 CCGCACTCCCGCCCAAGGTAGCTTTTATCGAAACGCGCGTGTGGATGAGGGTATGGTC 12879
Db 3229 CCCACGTTAAGCACTGGTCCGCTTCCAAAGAACCGCCATGATGGACGATACCTCATTA 3288
Qy 12880 AGTTCACTGCTGCTACATTTGGATGAACATCTCAGCAGACGCGGTTACCGCAATCC 12939
Db 3289 CAGCGGTATGAAGCGGTGATTTGAAGACGACAGTGAATACCGCGCTGACACAGGCGGT 3348
Qy 12940 GGATACCTTTTCCCTCGAGGACAGGA-----AGCAGAACAGGCATTGTGGACCACTGT 12993
Db 3349 TATCAGCAAGTCGGCGGTTGTTTAAATACCGATCAGAAAGCCCGGTATGGCGGACCG 3408
Qy 12994 CAGGGATATGTTACCTATGCGCGGCGCAGACATTTCTGGCTACCGCTATCCTTTTCGGGAC 13053
Db 3409 CAAGGTTATACCGATTACGTTGACGCGCGCACAGTCTCTGGCGGCTCAGGCTCAGCGTAAAC 3468
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RESULT 15
ACF65385 0
WP Sequence split into 7 fragments LOCUS ACF65385 Accession ACF65385

WP	Fragment Name	Begin	End	
WP	ACF65385_0	1	110000	
WP	ACF65385_1	100001	210000	
WP	ACF65385_2	200001	310000	
WP	ACF65385_3	300001	410000	
WP	ACF65385_4	400001	510000	
WP	ACF65385_5	500001	610000	
WP	ACF65385_6	600001	618776	
ID	ACF65385 standard; DNA; 618776 BP.			
XX	AC			
XX	ACF65385;			
XX	20-NOV-2003 (first entry)			
DT				
XX				
DE	Photorhabdus luminescens nucleotide sequence #38.			
XX				
KW	Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;			
KW	detection; food; gene expression; plant; animal; microorganism; toxin;			
KW	antibiotic; biopesticide; virulence factor; disease model; plague;			
KW	whooping cough; gene; ds.			
XX				
OS	Photorhabdus luminescens.			
XX				
PN	WO200294867-A2.			
XX				
PD	28-NOV-2002.			
XX				
PF	07-FEB-2002; 2002WO-IB003040.			
XX				
PR	07-FEB-2001; 2001FR-00001659.			
XX				
PA	(INSP) INST PASTEUR.			
PA	(CNRS) CNRS CENT NAT RECH SCI.			
XX				
PI	Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;			
PI	Buchrieser C;			
XX				
DR	WPI; 2003-148459/14.			
XX				
PT	Genomic sequence of Photorhabdus luminescens and encoded polypeptides,			
PT	useful e.g. as therapeutic antimicrobials and agricultural pesticides.			
XX				
PS	Claim 1; SEQ ID NO 38; 1205pp; French.			
XX				
CC	The invention relates to the isolation of genes and their encoded			
CC	proteins from Photorhabdus luminescens. The isolated sequences are			
CC	sources of probes and primers for detecting the genome of P. luminescens			
CC	and related species; to study polymorphisms; for gene analysis and for			
CC	detection/amplification of the genes. Antibodies (Ab) raised against the			
CC	polypeptides encoded by the genes are used for detection/identification			
CC	of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that			
CC	carry a gene-containing vector are used to select compounds that			
CC	modulate, regulate, induce or inhibit expression of the genes in plants,			
CC	animals or microorganisms other than P. luminescens and are able to alter			
CC	response or sensitivity to toxins and antibiotics produced by P.			
CC	luminescens. Cells transformed to express the genes are useful for			
CC	recombinant production of the proteins, particularly toxins and			
CC	antibacterials useful as insecticides, bactericides and fungicides. The			
CC	genes, proteins, vectors containing the genes and Ab are also useful			
CC	therapeutically (to treat microbial infection by bacteria or fungi that			
CC	are sensitive to P. luminescens-encoded toxins or antibiotics) and as			
CC	biopesticides. Other uses of the genes and the proteins are as virulence			
CC	factors and for identifying targets of human diseases for which P.			
CC	luminescens is a model (particularly plague and whooping cough). This			
CC	sequence represents one of the isolated P. luminescens genes			
XX				
SQ	Sequence 618776 BP; 181854 A; 139249 C; 125634 G; 172037 T; 0 U; 2 Other;			
	Query Match 5.1%; Score 968.6; DB 10; Length 110000;			
	Best Local Similarity 53.9%; Pred. No. 1e-218;			
	Matches 2405; Conservative 0; Mismatches 1859; Indels 201; Gaps 12;			
QY	9586 AGGAGACTGAGCATGCAAAATCAAGACATGGCCATTACTGCCCCACGTTGCCTCC 9645			

Db	26544	AGGAGTACTTTTATGACAGGATTCACAGAAAGTATCGATTACACCGTGTCACTTCCAAA	26603
QY	9646	GGGGCGGTGCGGTACACGGGTCAAGGGTGTATATCGCGCGCGCAGGGCGGATGTGGG	9705
Db	26604	GGTGGGAGACTATCAATGGCATGGAGAAGCGTAAGTGTCTGCGGCCCTGATGAATG	26663
QY	9706	GGGACCTGAGTATTCCTTGGCGGTAGCCCGGTGCGGGTTACGCCCCCACTGGGGCA	9765
Db	26664	GCCACTCTATCTGCGGTGCGCCCTTCGACTGGCAGAGGACTGCGCTGGATTATCG	26723
QY	9766	CTTAATTATCACAGCGGTGCGGGAACGCCCTTTTGGCATTTGGCTTGGGCTATCGGCGT	9825
Db	26724	CTGCTTACAGCAGTAGTCAGGTACCGGCCCTTTTCGGTATCGGTGCAATGTGCGCT	26783
QY	9826	GCTGCTGTCCAGCTGTACGCGCAACGAGACACCTACCTACGATGATACTGATGAATTC	9885
Db	26784	ATGACTTATTTAGCGGACGCCCAACATGSCATTTCCACAATACGGTAATGACGACGTTT	26843
QY	9886	ACGGTCCGGACGGTGTGCTGTGTCGGGCACTCACGGCTGTGGGCAACCAAGAGCA	9945
Db	26844	TTATCTCCACAAGGCGAAGTCAATATTTGCCCTTAATAACCAAGGCGCAACGATATC	26903
QY	9946	CGGCAAGGCC--ACCTCACTACTGGGGATAAAACCCAGGCGGAAGCTTCAACGTTCA	10002
Db	26904	CGTCAAGAGCTTAAGACGCTCAAGCGTGACCTTGGCCCAATCTCTATACCGTGACCCG	26963
QY	10003	TACCGTTACGTPACGGAGGGTGTCTCACGCCCTTTGACGCTTGGCTGCCGCCGACGAG	10062
Db	26964	TATCAAGCCCGCAGATCGTGATTTTACGAGAATCGAATACTGGCAACCGGCTCCGCT	27023
QY	10063	ACAGAA---ACGGAATTTTGGTGTATATACCCCTGACGGACAGGTGCTCTGTGGGC	10119
Db	27024	CAAGAAGGACGCGCTTCTGGCTGTATATCGTCAACCGGACGGCAATGCACTCTTAGGG	27083
QY	10120	CAAAATGCGCAGGCTCGCATCAGCAACCCACAGCCCCAACACAGACGCGCTTTGGCTG	10179
Db	27084	AAACCGCACAGGCTTGTCTGGCAATTCGCAAAATGATCAACAATCGCCAGTGGTTG	27143
QY	10180	ATGGAGTCTCGGTATCACTTACCGCGGAACAGATGTATTAACCAATACCGTCGGAAGAT	10239
Db	27144	CTGGAAGAAACCGTGCACCAACACCGGTGAACATGTCAAGTTATCAATACCGAGCCGA	27203
QY	10240	GATGAGGTTGTGACGAGCGGCGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTAT	10299
Db	27204	GAACCCCATTTGTGACGACAATGAAAAAACCCGCTCAACCCCAATGCTACCGCACAGGCT	27263
QY	10300	CCGGTGGCGGTCTGGTATGGTAAACCGTCAAGCGCGCTCGGACGCTACCGGCGCTGTCG	10359
Db	27264	CTGGTACAGGTGAACACTACGTTAAACATCAACCGCAACACGAGCTGTCTGATGATAAC	27323
QY	10360	ACA---CCATCAATGATAGTGGTGTATTCCTGGTGTATTTGATATGTTGAGCGTAGC	10416
Db	27324	ACACCTCCGACACCGGAAGAGTGGCTTTTCACTCTGGTCTTTGACACCGCTGAACGCGAT	27383
QY	10417	TCGGTGTCTGTGAAGCGCGGCTTGGCAACACCAAGGAGTGGGAGTGGCTGTGCTGT	10476
Db	27384	AGCTCACCTTCATACCGTCCGGAATGGGA---TGCAAGGTACAGACAATGGCTGTACGC	27440
QY	10477	CAGGATTTGTTTTCCGGGTATGAGTTTGGTTTTTAACCTCGCGACTCGCGCGCTGTGCCGT	10536
Db	27441	CAGGATATCTTCTCTCGTATGAATACGGTTTGAAGTACGTACTCGCGCTTATGCCAA	27500
QY	10537	CAGGTTTTGATGTTCCATTACCTAGGTGTCTGGCGGGAGTTCGGGAGCGAATGATGG	10596
Db	27501	CAAGTACTGATGTTTTTACCGGTACCGCGCTCATGCGCGGAGAGCGGTACCAAGTACGC	27560
QY	10597	CCAGCATTTGATTTCTCGCTGTGCTGGACTACAGGGAAGTCCCTCACTCACTGTGCTC	10656
Db	27561	CCGGAACCTGGTGGACGCTTAATATCTGGATTACGATAGAAATGCCAGCGGTACCCATTG	27620
QY	10657	GAGAACGTGACACCGAGTGGCTTTATGAGTCGGACGGGAGCTCTTGTGCTTTCGCGCCTG	10716

Db 27621 ATTGCCCGCCGCAATTAGTACAGAACCGGATGCGACGCCCAATCACTCTGCCACCAATTA 27680
 Qy 10717 GCATTGGGGTGGCAAACTTTACCCCGGACATTTGTGGCATGCGCAGACGCGTGACGAT 10776
 Db 27681 GAGTTGGCTTGGCAGCGGTTCAACTAGAGAGATGCAACATGGAACGTTTGTATGCA 27740
 Qy 10777 ATGGCAAGTTGAGTTTCTTCAACCTCATCAGCTTGTAGACCTTAAACGCGAAGGTGTG 10836
 Db 27741 CTAGATAATTTTAACTGCGACGACGTTATCAATTTGGTTGATCTGCGAGGAGAGGGTTG 27800
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 Db 27801 CCGGGTATGCTGTACCAAGATCGCGGTGCTTGGTGTATAAAGCGCGCAACGTCAGGAA 27860
 Qy 10897 GGGGATGATCCGATGCTGTGACCTTGGGGGCGGCTGCGGCCCTGCGGCAAAATGCGCGCT 10956
 Db 27861 GACGGGATAGTATGCGGTCACTTACGACAAATCGCCCACTGCTTACCCTACCT 27920
 Qy 10957 TTGCATTAACAGCGCATCTTGGCGGATCTTAAATGGGATGGTTCGGTGGAGTGGGTCTT 11016
 Db 27921 TTGCAGGATAATGCTCATTTGATGGATATCAACGAGACGCGCAACTGGATTGGGTAATC 27980
 Qy 11017 ACCGCCCGCGGTGGCGGATGTATGATGCGACCCCGCGCGGAGTGGTGGATTC 11076
 Db 27981 ACCGCTCCGGTATTCGCGGATACCATAGCCAGCAACCCGATGGAAATGGAACGCACTT 28040
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 Qy 11197 GCGAAACAGTGTGGATTAAGGGGAGACCGTGCAGCAAAACGGAAGACTCACTCTG 11256
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 Db 28401 CCGGAAACGCGTGTGTTGGCGGATATCGAGGCTTCGGGCAACCTGACATTTATCTATGCG 28460
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 Db 28461 CAATCCGCTCTTTGCTCAATTTATCTCAACCAAGTGTGAATCAATTTGATGCCCGCTG 28520
 Qy 11557 ACGTGTCTTGGCGGAAGGTGCTGCTATGATCGCACTGCAAGTGTGCAAGTGGCGGAT 11616
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 Qy 11617 ATCCAGGGGCTGGGGTGCCTAGCTGTACTGACGCTCCGCTGCTGCGCTCATCAC 11676
 Db 28581 ATTCAGGGGCTAGGGATAGCCAGTCTGATCTCTGACAGTGGCCACATATGGCACCATCAC 28640
 Qy 11677 TGGGTGTGCCATTTATCGGAGACAAACCTGTTGTTGATGCGATGAACAACAATATG 11736
 Db 28641 TGGGTTGCGATTTGCTGCTHAACCAACCTTGGTTGCTTAATGTGATGAACAATACCGG 28700
 Qy 11737 GGGCCCGGCAATGCACTGCACTATCGGAGTTTCGGTGGAGTCTGGCTGGATGAGAAAGCC 11796
 Db 28701 GGTGCACATCACACTCTACATTTATCGTAGCTCCGCGCAATTTCTGTTGGATGAGAAATTA 28760

Qy 11797 GAGGCACTGGCGCAGGACAGTTCCTGCTGCTTACTGCAATTTTACATTTGCATACCTTG 11856
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 Qy 12328 GAGAGCTACCGGTGTGTCGGCGGATGGCGCGGAAAGCCGATCAGTCACTTTTATGAACGG 12387
 Db 29298 GAAACCGAATTTCTGCTGGGTGACTGCCATTTGAAATCGCAGTACCACTATGAACGT 29357
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 Qy 12568 CGCTGGGTGTCACACAGCAGTGCACATCACTTGTGTTTCACTGTCTGAGGGGCACTGG 12627
 Db 29538 CGTCTGGTGGGCAAAATAGTGGCATCACTGACT-----GACGAGGAAACCTGG 29591
 Qy 12628 TTGTTGGGTTGGCGGAGGCTCGGGGAGTATTTACAGTACTCTGCGGACCAAGCTG 12687
 Db 29592 CGATTAGTTTACCAATGCAACCGCGGTGATTTATATCTTATGACCGGACCAAAAT 29651
 Qy 12688 CCGGAAAGGGTCTGAGCGTGAACACCTGTTGGCGCCGAAAGCCGTTCTCGGATAGT 12747
 Db 29652 CCAACGAAAGGGATCTCTTGTGAAGTCTTGTCTGAAAGCCGATGGCTTACTAGCAGATGA 29711
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 Db 29712 AAGCAGCGGTTTATCTGGGCAACACAGCGTTTACACCGCGGTCAATCGGAATC 29771
 Qy 12808 ACGGTGCTGCTCGGCACTCCCGCCAAAGTGTAGTCTTATCGAAACGCGCGTCTGAT 12867
 Db 29772 ACCTAGAAAGCCCGCTTACAGGCGCTGTTAGCGGTTTCAAGAAACCGCCATGATGAC 29831

Qy	12868	GA-----GGGTATGTCAGTTCTACTGGCTGCCTCAATTTGTGATGAACAATCTCGAGCAAG	12923
Db	29832	GATACCTCAATTCACAGCGTATGAAGGGGTGATTTGAAGAACACGGGTGTGAATACCACTG	29891
Qy	12923	CCGGTTACCGGCAATCCGGATACCTTTTCCCTCGAGG-CAGGGAAGCAGAACAGGCATTG	12981
Db	29892	ACACAGCCCGGTTATCAGCAAGTCCGCGGGTTATTTAATACCGGATCAAGAACGCCAGTA	29951
Qy	12982	TGGACCCAGTGTCCAGGATATGTTACTATGCGCGCGAGACATTTCTTGGCTACCGGTA	13041
Db	29952	TGGGTGGCAGCGCAAGGCTATACCGATTACCGTGATGCCACCCAGTTCTTGGGGCCTCAG	30011
Qy	13042	TCCTTTCCGGA CAGTATGTTGACACGGCCCGAGTTACCGTGACGCGTGACGCGTACAGACTGC	13101
Db	30012	ACTCAGCGTAATCTGTTACTTAA CAGGGAATAACCACTCTGACCTGGATACCAATCATTCG	30071
Qy	13102	GTCAACCGCAGTGGCAGGATCCCGCAGGATTGTCAACACAGCCGATATGACTGGCGC	13161
Db	30072	GTAAATATTCAGACTCAGGATGCGCTGGATTAA CGACGAAGCCGTTTACGATTATCGT	30131
Qy	13162	TTCTCTGACGCCCTCCGGGTGACGGACCCCAATGATATCTGCAGTCCGTCACCTCTGGAT	13221
Db	30132	TTCTTTAGCCGGTCAACTGACAGATATTATGATTAATCAACATTTGTGCACTGGAC	30191
Qy	13222	GCTCTGGCGGGTGACACCCCTGCGATTCTGGGCA CGGAAATGTTATTTGCCACCGGT	13281
Db	30192	CGCGTAGTTCGCGTACCA CAGCCGCTTCTGGGTACGGAGCGAGGCAAGCCACAGGC	30251
Qy	13282	TACAGTGATGCCACGTTGTTCCGTTCCGAGCGGCGCAGCAGCCGCTCTCGCGTTGACCGCG	13341
Db	30252	TATTCATAATCAGCCCTTTACACACCGGATTCCGTAGATAAAGCGCTAGCGTTAACAGGA	30311
Qy	13342	CCCTTACCAGTAGCAGAGTGTCTGGTGTATGTCA CGGACAGTTTGGGA-----	13389
Db	30312	GTACTCCCGTTGCCCAATGTTTGTACTATGCCGTTGTAGCTGATGCCGTTGTATCT	30371
Qy	13390	-----	13389
Db	30372	TTGCTCAGCTTCTCAGTCAC CAGAAGAGG CAGAAGCGCTATGGCGCAACTGCGTCC	30431
Qy	13390	-----GATGACACAAATGAGAAAATG-----	13410
Db	30432	GCTCATATGTTTACCGAAGATGGGAAAGTGTGCGGCTAGCGGGAAACGGGGAATAGGC	30491
Qy	13411	-----CCCCCG	13416
Db	30492	CACGACAACTCAGGATTCATCTATCTCGCTATTGGCAGATATTCGCCGTTTACTTCCA	30551
Qy	13417	CACGTGGTCGTGCTGCTACCGATCGCTATGACAGTGATACGGGACAGCAGGTCCGCCAA	13476
Db	30552	CATGTACTGGGGATCACCACTGATCGCTACGATAACGATCCGCAACACACAGCAACAG	30611
Qy	13477	CAGGTACATTCAGTGACCGTTTTTGGCGTGAGTTGCAATCGGCAACCCGCGAGCGCGAG	13536
Db	30612	ACCGTGAGTTTTAGTGACCGTTTTTGGCCGGTTACTCCAGAGTTTCAGTCCGTCACGAGCCC	30671
Qy	13537	GGCAACCGCTGGCAACCGAGGACGGCAGCGCAACTGTTGTCAGGGCCAGTGACGGATTGCCG	13596
Db	30672	GGTGATGCTTGGCAACGTAAGAGAGACGTTGGGCTGGTTGTGGATGCAAAATGGTGTCTGT	30731
Qy	13597	GTCACTGTAGCAACGAATTTCCGCTGGGCGGTCCACCGGAGCGGCGAGTATGACAAATAAA	13656
Db	30732	GTCAGTGCCGTACACACACCCGATGGGCCGTTTCCGGTTCGACAGATATGACGATAAA	30791
Qy	13657	GGTCTGCTGTTCCGGGTTTATCAGCCGTTATTTTCTGGACAGTTGGCAATATGTCAGTGAT	13716
Db	30792	GGCCAAACCGGTACGTACTTATCAACCCCTATTTTCTGAAATAACTGCGCGCTAGTTAGTAT	30851
Qy	13717	GACAGTCCCGCCAGGACCTGTATCCGACACGCACTTTTACGATCCGACCGGACGGAA	13776
Db	30852	GACAGCGCACGAGATGACCTGTTTGGCCGATACCCACCTTTATGATCCACTGGACCGGAA	30911
Qy	13777	TGSCAGGTTATTACGGCAAAAGGTGAAACGGCGACAGGTGCTGTATACCCCGTGGTTGTG	13836

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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 06:14:03 ; Search time 1470 Seconds
(without alignments)
9156.605 Million cell updates/sec

Title: US-10-070-489A-1

Perfect score: 18937

Sequence: 1 ggatccgaggaaggaatca.....cgtgcccgaggagcatggc 18937

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
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 - 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2368.8	12.5	37948	3	US-09-251-645-11
2	1108.8	5.9	4431	4	US-09-817-514A-3
3	969.8	5.1	4458	4	US-08-851-567B-31
4	903.4	4.8	6055	4	US-08-851-567B-25
5	848.8	4.5	7551	4	US-08-851-567B-46
6	848.8	4.5	7551	4	US-09-637-048C-1
7	848.8	4.5	7551	4	US-09-817-514A-1
8	848.8	4.5	7551	4	US-10-435-835-1
9	815.2	4.3	7577	4	US-09-637-048C-3
10	815.2	4.3	7577	4	US-10-435-835-3
11	815.2	4.3	7621	4	US-09-637-048C-6
12	815.2	4.3	7621	4	US-10-435-835-6
13	781.2	4.1	7512	4	US-09-817-514A-7
14	781.2	4.1	7515	4	US-08-851-567B-11
15	781.2	4.1	7515	4	US-09-637-048C-2
16	781.2	4.1	7515	4	US-10-435-835-2
17	748.6	4.0	7541	4	US-09-637-048C-4
18	748.6	4.0	7541	4	US-10-435-835-4
19	725	3.8	3132	4	US-08-851-567B-60
20	629.4	3.3	2745	4	US-09-817-514A-5
21	608.2	3.2	1740	4	US-08-851-567B-50
22	579.4	3.1	1722	4	US-08-851-567B-54
23	439.2	2.3	5547	4	US-08-851-567B-48
24	388	2.0	5532	4	US-08-851-567B-52
25	277.4	1.5	2557	4	US-08-851-567B-36
26	260	1.4	4832	4	US-08-851-567B-58
27	173.4	0.9	1689	4	US-08-851-567B-29

28	95.2	0.5	1881	4	US-08-851-567B-27	Sequence 27, Appl
29	67.2	0.4	501	4	US-09-543-681A-3481	Sequence 3481, Ap
30	65	0.3	501	4	US-09-543-681A-1125	Sequence 1125, Ap
31	62.2	0.3	658	3	US-08-998-416-595	Sequence 595, App
c 32	57.4	0.3	7218	1	US-08-232-463-14	Sequence 14, Appl
c 33	54.8	0.3	1141	4	US-09-806-708B-22	Sequence 22, Appl
34	54.6	0.3	1141	4	US-09-806-708B-22	Sequence 22, Appl
35	54.4	0.3	6669	4	US-10-204-708-5	Sequence 5, Appli
36	52.2	0.3	5562	4	US-10-204-708-63	Sequence 63, Appl
c 37	52.2	0.3	47981	4	US-09-679-279-1	Sequence 1, Appli
38	51.6	0.3	20674	4	US-09-641-638-651	Sequence 651, App
39	51.6	0.3	20674	4	US-10-170-097-651	Sequence 651, App
c 40	51.2	0.3	447	4	US-09-248-796A-7484	Sequence 7484, Ap
41	50.6	0.3	11049	4	US-10-204-708-24	Sequence 24, Appl
42	50.4	0.3	8961	4	US-10-204-708-80	Sequence 80, Appl
43	50.4	0.3	38584	3	US-09-453-702B-50	Sequence 50, Appl
44	50.2	0.3	5455	4	US-10-204-708-33	Sequence 33, Appl
45	50.2	0.3	10467	4	US-10-204-708-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-251-645-11
; Sequence 11, Application US/09251645
; Patent No. 6281413

; GENERAL INFORMATION:
; APPLICANT: Kramer, Vance C.

; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.

; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.

; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.

; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: CGC1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645

; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11

; LENGTH: 37948
; TYPE: DNA

; ORGANISM: Photorhabdus luminescens
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (15171)..(18035)

; OTHER INFORMATION: orf5
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (23768)..(31336)

; OTHER INFORMATION: hph2
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (31393)..(35838)

; OTHER INFORMATION: orf2
; US-09-251-645-11

Query Match 12.5%; Score 2368.8; DB 3; Length 37948;
Best Local Similarity 54.0%; Pred.No. 0;
Matches 6358; Conservative 0; Mismatches 4747; Indels 671; Gaps 47;

QY	5291	CGCGATGACCTCTTCGGGTCTGCTGGATAATACAGGTGTCAGGTCAGCAAGGTAAACCC	5350
Db	5569	CGTGATGATCTATCAATACCTATTGATCGATAACCAAGTTTCGCGCGACATTAAACT	5628
QY	5351	ACCCGATTGCGAGGCGCATCGCCGATACGGCTGTATATCAACCGGGCCCTTAAACCGA	5410
Db	5629	ACAGAGATCGCTGAAGCTACGCTAGTATCCAACTGTATTAACCGCGCTTGAAAAAT	5688
QY	5411	ATAGACTCAGCGCCATGCGAGGTGAGGGGCGTCAGTTTTTCTACTGACTGGATACG	5470

Db 5689 ATGGAGGAGATACTGTCAAGTGTACACAGCGCTCATTTCTTACCAACTGGGATAAA 5748
QY TTCAACAAAGCTTACAGCACTGGGGGGGGTCTCAGAGCTGGTTTACTATCCGGAAC 5530
Db 5749 TACAAATAAAGCTTACAGCACTGGGGGGGATGGCTTAAACTCTCTTACTATCCAGAGAAT 5808
QY TACCTCGACCGGAGCTCGGTATCGGCGACCGGCATGATGACACCCCTGCTGAGTCT 5590
Db 5809 TACATCGATCCGACGCTACGATTTGGGCAGACAAAATGATGGATACGTTGCTGCAATCC 5868
QY GTGAGCGAGAGTATCAACCGGATACCGTGGAGGATGCCCTTTAAAACTATCTGACC 5650
Db 5869 ATCAGCAAAAGCAATTAATATCGATACCGTAGAAGATGCCCTTTAAATCTTACCTAA 5928
QY ACCTTTGAGCAGATTCGCAATCTGAACACTGTGAGCGGATATCAGATACGCAAGCCAGCATG 5710
Db 5929 TCATTCGAAACAGGTGGCTAATCTGGAATCCTCAGCGCCTACCATGACAACTTAATAAT 5988
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Db 5989 GATCAAGGATTAATCTTATCTTATCGGACGTAGTAAACAGAAAGTGAATCAATATTATTGG 6048
QY CGCAGCGCCAAACACAGCAAAATCCAAAGACTCAATGATGCCCGAATGCCCTGGACCGGA 5830
Db 6049 CGCAGTGTGATCACAATAATCCAGGAAAGTAAATTCGCCGTAAAGCTGGAGTGA 6108
QY TGACAAAAATTAATTCGCGGAATGAATCCGTGGTCTGAGTCTTGTGTGCTCGGTGTTTTTC 5890
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Db 6169 CAACTCTCGCCTGATCTTATCTGCTGCTGGAACAAAAAGGCGACTAAACAGGAAGTGA- 6227
QY AGCAGCAACAAACACGAGCAGAGCTACAGCTGAAACTGTGTTCCGGCGCTACGACGCT 6010
Db 6228 --TAAACCGCCTCGGTTATTATTATGAATGAATTAAGCAGATCCGTTATGACGGC 6285
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QY AACGAGGCGATGATGACCTGTAAATCCCTGACTGAGCAGCTCTATTGCGGTTTTA 6123
Db 6346 AATAAAACCTGGACTTACTGCTCAAGCTTCAAGGAGAGATGAATGCTGGTGATG 6405
QY CTCGCTCACGAGCAAGCCGAGCTTTGATTAACGCTCAGCTGATTTCTGTGGATAATGATAT 6183
Db 6406 TTTTATAAAAAACAAGATCAATTAATCAATACACAAACACAGTACCAATAAAGACTA 6465
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QY AGCAATGTTTCGTGTTTTGTTAGTACTGCTGCACTGCCACTCAATCTACCATAGAA--- 6481
Db 6705 ACTCTCACCAGGTTAAGAAATTAATCATATGAGCTTTGAGCGCGAACAACGCAACATG 6764
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Db 6885 GAACACTACCAATATGAGAAAGGAGCTGCTGCTGTTTTATCGAGAAAGTACTACTAATTT 6944
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Db 7305 TAAATGAAGCAAGTATTGATATCACCTTTATCGATTTGCTGAGAAATTTGACGATAA 7364
QY CCGGAGCGCATATTAAACCGTCAITTCGAAACAATTAATATGACACTTCCGTTATGCAAT 7113
Db 7365 TAGTATGATCTGAATTTAGGCGAAGAACATTTTCAGTATTCGTATTTATCAAAAAAGCGA 7424
QY ACGTAAAAATACGCTGGCGCGCAGTATATTCGTTTCTGCGGGTAAAGTGTG----- 7168
Db 7425 AACTGATATGCCCCGACCTGACCAATATGCAAAACGGGGCGCAATATATGCGATGGGG 7484
QY 7169 -----GCGCTTATTCGCTCAACACACCTCTTTGCGCGCAACTGTCGACGCGCGGAATAC 7224
Db 7485 AAACCTTTGTTATTCGCTTAAATACGCTATTTGCCGTCATTTAGCCGAGCCAAAGC 7544
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Db 7545 GGGGATAGATATATTTTGGATGGACACTCAGAAATATTCAGGAACCTTAAATTAGGAGA 7604
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QY 7396 CCGGAAAGCCACCGCTGGCTGAGTATGTTGGAACCGCGCGGCGGACGCTGTTAAACGG 7455
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QY 7456 GGTGCTGAGAAATTAACCTGGAATGTCGCTCGCTGGAGGAGGACACCGCTGGAACGA 7515
Db 7785 TCAATGCAACATTAACCGCTGGAATGTTGCGCCATTAAGAAGACACTAGTTGGAAACGA 7844
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Db 7845 TGATCCGTTGGATTTCAATTTGATCCTGATACCATAGCTCAACATGATCCAATGACACTACAA 7904

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Dd	7595	AGTCGCCACCTTTATGCGCACCTTAGATCTGTTGATCGAACGGGGATTAACGCTATCG	7564
Qy	7636	GCTGCTCGAGGGGACACCTTTAAAGAGGCGCGGATGTGTAGTCGTCAGGCGCTGAACCT	7695
Dd	7965	CAAATTTGAGCGGGACACCTCGCTGAAGCCAAAATGTGTATATGTCAGGCACTGCATCT	8024
Qy	7696	TCCTGGGCGAGCGCCTATATTTCTTTGACGCGGACTGTCGCGGTGACCTCGGTGA	7755
Dd	8025	ATTGGGTGATAACCTCATCTACACTCAGTTGAGCATGGAATGATCCAGAGCTAGAAGA	8084
Qy	7756	CGCAGCGAGGAGTGAACGAGCGGATTAACAGGAGCGCCTGTCGCGCGTGGCGGTT	7815
Dd	8085	GGCGCAGCTCTTGAAAAACAACAGGCACATGCCAAGAAATAGCAGATTTACGACNAGG	8144
Qy	7816	GGTGCCCGCTCCGAGACACAGGAGCGGGAATTCCTGACGGCACTGTTCTCCGCGAGCA	7875
Dd	8145	ACTTCTTACATCCACAGGGCTAAAGATGAAATCAAAAACAGATCTTTTCTCGCGCAAGT	8204
Qy	7876	GAACGAGGTCTCAAAAGGCTACTGGCAACCTTTGGCACAGGGCTCCATTAACCTGGCCA	7935
Dd	8205	CAACGAAAGTATGCTGAGCTACTGGCAGAACTAGAAACAACGGTGTATTAACCTGGCGCA	8264
Qy	7936	CAACCTCTCCATTTGACCGCGAGCGCTTTCCCTGTCGCTAGCGCCACGCGCTCCGAACC	7995
Dd	8265	TAACTCTATTTGATGTCACCTTTACATTTGCTTATTTTTCGCAACACGAGNATCC	8324
Qy	7996	GTCGCGCTCGAGAGTCGCTGCTCAACAGCGGCGAGGTCGTCGAGCACTGCGCGCGCG	8055
Dd	8325	AAAAAGCCTGCTCAGCGCGCTGTCGCGAGTTCACAAAGTGAAGTAATCTTCATCAGA	8384
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Dd	8385	ATTATATCAGTGTGGCGTTTCCCTCATATGCTGGAATAACCGCTGATGTGCTCAGTCA	8444
Qy	8116	GCTGACCGGTTTGGCAACACACTGCTCGGTATTTACCGAGCGTCAGGATCGGAGGCGCT	8175
Dd	8445	GCTAACCCCAATTCGGCTCCACATTTGCAAAATATTTACGACGTCAGATCGGAGGCATT	8504
Qy	8176	GGCCAAATCTGTGAGACCCAGGCGAGTGAATGATAGCGCAGCGGCTTCGCGAGCAGGA	8235
Dd	8505	AAACACGCTGTTGCAAAATCAGGCGGAGAACTGATATTGACCAATCTCAGCATACAGGA	8564
Qy	8236	TAACTCTCGAGAAATCGATCGGATATTGCGCCCTGGAGAGAGCGCGCGCGCG	8295
Dd	8565	CAAAACCATCCAGAGCTGATGCTGAAATAAACTGTGCTAGAAAAAACCGCGCGGAAC	8624
Qy	8296	GCAGATCGTTTTGAAAGTTTGAAGTGTGTAGAGGCGGAGCTCAACACCGCGGCAAAA	8355
Dd	8625	CCAGTCGCTTTTGATAGCTACAGCAATTTCTACGATGAAGACATCAACGCGGGTGAANA	8684
Qy	8356	ACAGGCAATGAGCTTGTACCTCAGTTCGTCGCTGCTGGCATCAACCGCGCGCTCTT	8415
Dd	8685	ACAGGCAATGGCGTTGCGTTCGCTCGCTGGCATCTCTACAGCCCTTCAAGCATCACA	8744
Qy	8416	TTTGGCGAGCGCGCGCGATATGCTGCCCAATTTTACGGGTCGCGCTCGGGGCTC	8475
Dd	8745	TCCTGGCGGCGCAGCATTTGATCTGGCGCCCAACATCTTCGCTTCGCTGATGTGGCAG	8804
Qy	8476	CCGCTATGGGCGACTATTAAAGCGACCGGCATCGGCATCCAGGTGCTCCCATGCCAC	8535
Dd	8805	CCGTTGGGGGCGATCCGCCAGCCACAGGTAATGTCTAGGATTTCTCCGCCAGTGTAT	8864
Qy	8536	CCGCATATACGGGCAAAAATCAGCCAGTCGGAAGTGTACCGCGCTCGCGGGAGGATG	8595
Dd	8865	GAACACGAAGCGGATAAATCAGCCAACTCTGAAGCCTACCGTCGCGGCTCGTCAGGAATG	8924
Qy	8596	GGAAATCCAGGTCATAGTCGCGATCTGAGTGGCGCAGATTGATGCCAGCTGGCGGC	8655
Dd	8925	GGAAATTCAGCGTAAATACCGCGAGGAGAGCTGAAACAAATCGATGCTCAACTTGGTTC	8984
Qy	8656	CATGGCAGTCCGCGGGAAGGGGCTGAGCTGCAGAAAACTTACTTTAGACCAGCAGAC	8715
Dd	8985	GCTGGCAGTCCGCGTGAAGCCGACGATTTGCGAGAAAAACGAGCTTAAAAACCAACA	9044
Qy	8716	CCAGGCACAGGCGCAGTTGGCATTTCTGCAGAGTAAGTTCAACAATAACGGCTCTGTACAG	8775
Dd	9045	GCAGACTCATGCAACAACGACCTTCTGCAACATAAGTTTCAGTAATCAGCGCTGTACAA	9104
Qy	8776	CTGGCTCGCGGGCAGGTGTCGCGCATTTATTTACAGTTTCTATGACTTGGCAGTATCCCG	8835
Dd	9105	CTGGCTCGGTGTCGATTTGTCGCGCATTTATTTCCAGTTTCTATGATTTAAGGAGTGTG	9164
Qy	8836	CTGCTGATGGCGCAACAGGCTTGGCAGTGGGATAAATTCGAGACTAGTGTG---TTTTAT	8892
Dd	9165	CTGTTTGATGGCGAAATGGCCTTATCGCTGGGAGACTAAGATACCGCATCACGCTTTAT	9224
Qy	8893	CCAGCGGGGCTGTGATGGGGCAAAATGCGGCTCTGTCGCGCGGGGAAACCTGTATGCT	8952
Dd	9225	CAAAACCGCGCTGCGAGGGAACCCATGCGGCTTTGCTCGCGGGTGAACCTTAATGCT	9284
Qy	8953	GATCTGGCGCAGATGAGCAGGCTGCTGACGGGGGATGAGCGGGCAATAGAGGTGAC	9012
Dd	9285	GATCTGGCACAGATGGAAGATGCCCACTGAAACAGGATAAACGCGTACTGGAGGTAGA	9344
Qy	9013	GCGGACGCTGCTGTCGAGGCTTATACAGCCTCGCGGAGGATCGGCATTTCTCTCT	9072
Dd	9345	ACGTACCGTTTCTGCTGGCGAAGTCTATGCCAAATTTACCGCAAGAT---AAATTTATCCT	9401
Qy	9073	GGCGGACAGGTGCTGGAATGCTGATGAAACGTTTCGGGAGTTCGGGTAAGAAAGCAA	9132
Dd	9402	GACTCAGGAAATAGAGAAAGTTGGTGAATAAGTTTCAGGCGGGCGCGCAAGCAATAA	9461
Qy	9133	CGGATTTACAGAT---GCATCAACAGCAA-----CTCGAGGCCACCTGAAACTGGCTGA	9183
Dd	9462	TAACTGGGCTTTAGTACCAATACCAATACCTCTCTAGAAAGCTCAATTCGTTATCTAC	9521
Qy	9184	CCTCGGTATCGGCAACGATTTACCCGCTCTCCCTTGGCAACCATGAGCGCATCAACAAT	9243
Dd	9522	CTTGAACATTTAGCAGCGATTTATCTGATTTCTATTGGTAAAAACCGCTGTTAAACAGAT	9581
Qy	9244	AAGCGTACGCTCCCGCGCTGTCGCGCTTATCAGGAGCTCGGTGCGGTTCTCAGCTA	9303
Dd	9582	CAGCGTTACCTCTGCCAGCAGCTGCTAGGACCTTATCAGGATGTGCAAGCAATTTCTGCTTA	9641
Qy	9304	CGCGCGAA---GATATGTCATGCCCGGGTTCGACGCGCTCGCGCTCTCACAGCAAT	9360
Dd	9642	CAGCGAAAAAGCCTCTGAATTTGGCTGAAAAGTTGCAAAATCATTTAGCGGTTCTCATGGAT	9701
Qy	9361	GAACGACAGCGGCAATTTCAACTGGATTTCAATGACCCCGCTTACTCGCGTTTGAAGG	9420
Dd	9702	GATGACAGCGGTCACTTCCAACTGGATTTCAACGATGGCAATTTCTGCGGTTTGAAGG	9761
Qy	9421	ACTTCCAGTTGATGACAGGAGCCCTTGACACTGACCTGAGCTTCCCGGATGC-----	9468
Dd	9762	AATCAAAATCGATGA---AGGTACGCTGACATTTGAGCTTCCCAATGCAATTTAGTAAAGA	9818
Qy	9469	-----TGACGGCAAAACAACGAGCGATGCTCTCAGTCTGAGCAGCATCAT	9513
Dd	9819	AGACAAAAAAGCAAAAAAGGCAACAACAGCCATGCTGGAGAGTCTGAACGACATCAT	9878
Qy	9514	CCTGCATATCCGTTACACCATTTATCAGCTGATAGGTATCAACATAGCGCA---GGCCCC	9569
Dd	9879	TCGTGATATTCGCTACACCATTCGCCCAATAACGATTTTAATTAAGTCTTAAACAGCGCCC	9938
Qy	9570	CGAACGAGGCTCGGAGGAGCTGAGCATGCAAAATCATCAAGACATGCGCCATTACTGC	9629
Dd	9939	CTAAGCGGGGCTCGCAAGGAGTCTTT-CATGCAAAATTTCAAGATTTTCAAGTATTACAGA	9997
Qy	9630	CCCCAGTTGCTTCCGGGGGCTCGGTCACCGGCTCAACGGGTGATATCGCGGCGC	9689
Dd	9998	ACTATCATTTGCCCAAGGAGGAGCGCTATCAGCGGAATGGGGGAAGCTTTAACCCCCAC	10057
Qy	9690	AGGGCGGATGGTGCAGCGACCTGATGATTTCCCTTTGCCGTTTAGCCCCCGTTCGGGTTA	9749

Db 10058 CGGGCCGGATGGGATGGCGCGCTGCTCTGCGTTGCGCTATCTCTGCGCGCGGGTTA 10117
Qy 9750 CGCCCCCCTAGGGGCACTTAATATACAGCCGGTCGGGGAACGGCCCTTTGGCAATGG 9809
Db 10118 TGTCTCGTCACTCGCTTAAACTACACAGCGCGCGGTAACAGCCCAATTTGGTCTGG 10177
Qy 9810 CTGGGGTATCGGGGCTGCTGTCTCAGCGTCTGACGCGCAACGGAGCACTACCTACGA 9869
Db 10178 CTGGGATTGAAGTTATGACCAATCGCGCGCCGCAATTTTGGGCTTCCCAATTATGA 10237
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Qy 9930 TGGCACCAGAGACGCGACGACCTCACTACTGGGGATAAACCAGGCGGAAGCTT 9989
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Qy 10278 GCAGCGCGGCGCAACGTTATCCGGTGGGGTCTGGTATGTGTAACCGTCAGCGGCTCG 10337
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Qy 10575 GAGTTCGGGAGGAATGATGCGCAGCATTTGATTTCTCGCTGTGCTGAGCTACAGGGA 10634
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DB	16498	CTTTATTG	TGTCAGCGGACA	TCAAAACG	TGTATACGAGCAAAAC	CTGAAC	16557
QY	15954	CGCACGTG	GAGAACTG	CAAAAAGT	GACACCGT	TGCGTGCATGGGGGGC--GGACG	16010
DB	16558	ATAACCG	CGGTGNACTA	CAACATG	GCATTTGGTGAACGGG	CAAGCGGCCCAATGATG	16617
QY	16011	ACAGCAA	AGCTATCGGTAT	GTATGTCGGG	CAGTCAGCGTATTA	CAAAAACCGCACGCGC	16070
DB	16618	ATCGGAAT	TGGTATCGCTAT	AGTAGTGACCGG	AAGGATATTA	AAAAATCAATGAACAGC	16677
QY	16071	AAACTGG	CAACAACGTTT	CAGACACACG	CGGTAGTACTCGCGGGG	CTGAGTTACGTA	16130
DB	16678	AGACCAG	AGCAACTCTCAAA	CACAGAGAAT	AACCTATTGTCGG	AGCTTTGAAC	16737
QY	16131	TCATGCA	AATGGCGTGACG	GA AAAAGCCTGCAG	GTATTACGTTGGCGG	CAGGCTG	16190
DB	16738	TAAACAA	NACAGCAGATCA	CAACCGA	AGATTTGCAAGTAT	CACAGTAGGAGAGCG	16797
QY	16191	GGCGGCA	CAAGTGC	CGGTATTGCACTGG	AGATCGGCAAGCCG	ATGACCTCGATGAGG	16250
DB	16798	GTCCGCA	CACAGGTACGAGT	TATACATTGGGATAG	CGGTCAACCGGA	AGATATCGACAATA	16857
QY	16251	ACTCGT	GCGTTACAGTTACG	ATAACCTGGTGGG	CAGCAGCAGCTG	AGCTGACAGAG	16310
DB	16858	ATCAGCT	ACGTTATAGCTACG	ATAATCTTATCGGTTCC	AGTCAACTTGAAT	TAGACAGCA	16917
QY	16311	AGGGTTAC	CTTATCAGTGAGG	AGAGTTCTACCCGTAT	GGCGGAACGCTGTTCTG	ACGG	16370
DB	16918	AGGAGN	ATATTAGTGAGG	AGAGTACTATCCCTAT	GGCGGACAGCATTATGGG	CNA	16977
QY	16371	CGGAA	GTGAGGTTGAGGCTG	ACTACAAA	CTATCCGATATCAGGCAAGG	AGCGGTGACG	16430
DB	16978	CAAGGA	AGCGGACAGAA	GCAGTTATAAA	ACCATCCGTTATT	TCAGGTAAGAGCGGATG	17037
QY	16431	CGACGGG	CTGGATTATTACG	GTATTCGTTATACCG	CCCATGGSCAGCGG	CGCTGGCTCT	16490
DB	17038	CCACCG	AGCTATATTATTACG	GTATACCGATAT	TATCAGCCTTGGGTG	AGACGATGTTAA	17097
QY	16491	CCA	CGACCCGGCAG	CACCGTGGACGGG	CTGAACTGTCG	CATGTTCCGATGTTGGGGAATAATC	16550
DB	17098	GTGCC	GATCCG	CAGAA	CAGTAGATGGGTG	GAATTTATATCCGATGTTAGGATATATC	17157
QY	16551	CGGTCA	CGCTGTTGA	16566			
DB	17158	CGGTTACT	CTGCTTGA	17173			

RESULT 2

```

US-09-817-514A-3
; Sequence 3, Application US/09817514A
; Patent No. 6639129
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4431
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS

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i. LOCATION: (1)..(4331)		5.9%; Score 1108.8; DB 4; Length 4431;	
US-09-817-514A-3		Best Local Similarity 56.0%; Pred. No. 3.6e-298;	
		Matches 2493; Conservative 0; Mismatches 1732; Indels 225; Gaps 12;	
Qy	9598	ATCGAAATATCATAGACATGCCATTA	ATGCCCCACGGTTCCTTCGGGGCGGTGCG 9657
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Qy	9658	GTCAACGGGCTCAAGGGTGATAT	CGCGGGCAGGCGCGGATGTCGGCGACCTGAGT 9717
Db	61	ATTACCGGATGCGGTGAAGCATTA	ACACGACGCGGCGCGATGATGCGCGCCTTATCC 120
Qy	9718	ATTCCCTTCGGGTAGCCCCGGT	TACGCCCTACGCCCTTGGGGCACTTAATTATCAC 9777
Db	121	CTCCGATTAACCATTTCCGCC	GGGGTGTATACGACCCCTCGCTCACTCTGAAATACAC 180
Qy	9778	AGCCGTCGGGAAAGGCCCTTT	TCGCATTCGCTGGGTATCGCGGTGCTGTCTCAG 9837
Db	181	AGTGGAAACCGGTAAACAGCC	CAATTTGGTCTCGGTTGGGACTCGCGCTCATGGCAATTCGT 240
Qy	9838	CGTCTGACGGCAACGGAGCACT	TACTACGATGATCTGATGAAATTCACCGGTCCGGAC 9897
Db	241	CGTCGACCAAGTACCGGCTAC	CGGAATACGATGAACCGGATCTTTTCTGGGCGCCGAA 300
Qy	9898	GGTGAGGTGCTGGTCGGGCACT	CACGGCTCTGGCACCCCAAGACGACGCGCCACC 9957
Db	301	GGTGAAGTGTGGTGTGATGAT	TAAATGAGGCAAGTCAAGCTGATATCCGCAGTGAATTC 360
Qy	9958	TCACTACTCGGGATAAACCC	AGCGGGAAGCTTCAACGTTTCAGGTTTACCGTTTCACGTACG 10017
Db	361	TCATTGACGGCATCAATTT	GGTGGTGGGACTTACCGTTTACCTGTATCGCTCCGGCTA 420
Qy	10018	GAGGGTAGTCTCAGCGCCTT	GAGCGTTGGTGTGCCCGCGACGAGACAGAAACGGAATTT 10077
Db	421	GAAGGCCACTTTAAACGG	TTGGATTACTGGCAACCCCAACACGCGCGCAACCGATTTTC 480
Qy	10078	TGGGTGTTATATACCCCT	GACGACAGTGGCTCTGCTGGCGCGGAATGCGCAGGCTCGC 10137
Db	481	TGGCTGATATACAGCCCG	CACGGAAGGTTCATTTACTGGGCAAAATTCCTCAGGCACT 540
Qy	10138	ATCAGCAACCCACAGCC	CCCAACAGACGCGGTTTGGCTGATGGAGTCTCCGTATCA 10197
Db	541	ATCAGCAATCCACTCAAT	GTTHAACCAACAGGCAATGGCTGTGGAGGCTCCGATATCA 600
Qy	10198	CTTACCGGCGAACAGATG	PATTAACAATACCGTTCGGGAAGATGATGCGGTGTGACGAG 10257
Db	601	TCCCAACAGCGAACAGAT	TATTAATCAATATCGCGCTGAAGATGAAGCAGGTTGTGAAACC 660
Qy	10258	CGCGACGGCAGCGGCA	CCGCGCGGCGCCCAACGTTATCGGTGGCGGCTCTGGTAT 10317
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Qy	10318	GGTAAACCGTCAGCG	CGCTCGGAGTCTACCGGCT---GGTGTGACACCAATCAATGGAT 10374
Db	721	GGGAACCTGACCG	CACGAGCTTTTCTTACACTAAACGGAGATGACCCACTTAAATCT 780
Qy	10375	AGCTGGCTGTTTAT	CTGGTGTGTTGATTAATGGTGAAGCGTAGCTCGGTGCTGTCTGAAGCG 10434
Db	781	GGCTGAGTGTCTG	TTTGTATTTTACTACGCTGAGCGCAAAACAGCTTATCTGAAATG 840
Qy	10435	CGCGCTGGCAACAC	CACGGAAGTGGGAGTGGCTGTGCTCAGGATGTTGTTTTTCGGG 10494
Db	841	CCGCTGTTTAAAG	CCACAGGCA-----ATTGGCTTTGCCGAAAAGACCGTTTTTCCCGT 894
Qy	10495	TATGAGTGTGTTT	TAACTCGGAGCTCGCGCCTGTGCGCTCAGGTTTTCATGCTCCAT 10554
Db	895	TATGAGTACGGT	TTTGTAAATGCGTACTCGCGCTTATGCGCCCAAAATCTGATGTTTCAC 954
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Db 955 CGTCTAACAACCTATCTGTGTCAGGCAAAAGGGGATGATGAACCTCGCTAGTGTGCGCT 1014
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Db 1015 CTGATAGTGATTTATGACGAAACCGGATGGTACGTACGCTGCTGTCGCGCGGTA 1074
Qy 10675 GCTTATAGTTCGACCGGAGCTCTGTGCTTCCCGCACTGCAATTTGGGTGGCAAC 10734
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Qy 10735 TTTACCCGCGACATTTGTGGCATGGCAGACGCTGACGATATGGCAAGTTGAGTTTG 10794
Db 1135 TTTGAGCAGAAACAAACCGCACTCTGCAATCAATGATGTAATGCAAAATTTCAACAC 1194
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Qy 10855 GACAGCGGTGCTGTGTGTACCGTGAACCGGTACGCGTACGCGGATGATCCGATGCT 10914
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Qy 11275 CACATACCTCTGCGGTTCAATGATATGCTGCGGATGGAACAGCAGATTTGACGAG 11334
Db 1675 GCGCGTAAGTTAGTGCAATTTAGTGACACTGCGGTTCAAGGCAAGCACATCTGGTTGAA 1734
Qy 11335 GTGCGTGCTAATGGAGTACGTTACTGCGCAAACTCGGGCAAGCTGTTTCGGTCAGCG 11394
Db 1735 GTTAGTGCACTCAATGCTACCTGCTGGCGAATCTGGGGATGGCGTTTGTGTAGCCA 1794
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Db 1795 ATCGTATTCGCGGATTCAGCAATCTGCGCGAGTTTAAATCTGATCAGTTTCACTG 1854
Qy 11455 GCGGATACCGAGTTCCGGTACCAAGACCTGATTTATGCGATAGTACCGGTTAGTC 11514
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Qy 11515 ATTTATTTCAACAGAGTGTATTAATTTGCGCGAGCGCATCGCTCTTTGCGGAA 11574
Db 1915 ATTTTCAGCATGAAAGTGCAACGGTTTGGAAAACCAATTCACATCTCTTTCTCTGAC 1974
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Qy 11635 CCTAGCTGTACTGACGGTCCCGCATGTGCGGCTCATCATCTGGGTGTGCCATTTATCG 11694
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Qy 11755 CACTATCGCAGTTCGGTTCAGTCTCGGTGATGAGAAAGCCGAGCCTGCGGCGAGC 11814
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Qy 11815 AGTTCCTGCTGCTACTCCTGCCATTTACATTTGCATACCTCTGCGGTTGGTGGTGAG 11874
Db 2215 CAAACACCGGTCTGTACTCTGCTGCTTCCCGTCCATACCTTTGGCAAAACAGAACCGAG 2274
Qy 11875 GATGAGATCACCGGTAAACCGTCTGCTCAGCAGCTGCTTATTCGCCACCGGCTCTGGGAC 11934
Db 2275 GATGAATCAGCGCAATAAGTTAGTGACCACTGTTATGCTCACGGCGCTTGGGAT 2334
Qy 11935 GGGCAGGAACCGAGTTTCGGGGGTTTGGTTTTTGTGATCAGGATACCGATACCTTG 11994
Db 2335 GGACGTGAACGGGAATTTGCTGCTTGGTTATGTTGACACAGACAGCCATCAACTC 2394
Qy 11995 GCAAGCAGGTTACCGGACGGAACGTAGTATGCTTCTGTGAGCGGAACTGTGATGCC 12054
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Qy 12055 ACCGGGTACCGGCACTAGACGAGCTCTGCCGAGACGTATTTGGCAAAACGATGCCGCC 12114
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Qy 12115 GCTTTTGGCGATTTCCGACCGCTTCACTGTCCGTTTTCAGGAGAGGATGAGCAGACATAT 12174
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Qy 12175 ACTCG---GACGACAGCAAGACATTTCTGTTGTCAGCGAGCCCTGAAAGGATCTGCTG 12231
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Qy 12232 CCGAGTGTGTTTACGGTCCGATGCGAGCAGCGCCGATATCCCTTACAGCGTCACT 12291
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Db 2992 AGTTGGCACCATTCTATT-----GGTATGAGCTTAAGAGTGTGGGATTTACCGATGCG 3045
Qy 12649 TCGCGGACGATGTTATCAGTACTCTGCGGACAAACGTCGCCGAAAGGGGTCTGACGCTG 12708
Db 3046 ACACGAGTGTGCTTTACTTTACGATGCCAAACAGGTACCTGTGATGGCTTAAATCTG 3105
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Db 3106 GAAACCCCTGTGCTGAAAAATAGCCTGATGTCGCGATGATAAACCTCGCGAATACCTCAAT 3165

Db 1858 TTTCTGCGGATATCGAGCGCTCGGCAACCCAGCTTATCTATGCGCAATCCGGCTCT 1917
Qy 11509 TTAGTCAATTAATTTCAACAGAGTGGTAATTAATTTTCGCGAGCGCATACGCTCTCTTG 11568
Db 1918 TTGCTCAATTAATTTCAACAGAGTGGTAATTAATTTTCGCGAGCGCATACGCTCTCTTG 1977
Qy 11569 CCGAAAGTGTGCGCTATGATCGCACTGCGAGTCTGCAAGTGGCGGATATCCAGGGCTG 11628
Db 1978 CCAGAGCGGTACAAATTTGCAACACCTTGCCAACTTCAAGTGGCGGATATTCAGGAGTA 2037
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Qy 13392 -----T 13392
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STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/51,567B
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.93804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 7551 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-851-567B-46

Query Match 4.5%; Score 848.8; DB 4; Length 7551;
Best Local Similarity 48.8%; Pred. No. 2.6e-225;
Matches 3662; Conservative 0; Mismatches 3347; Indels 495; Gaps 31;

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DB 241 GCCAATCTCGCTCCCAATGCTGAACCTGATAGGCTATAACAAATCAATTTAGCGGTAGACC 300
QY 2747 GACGTTTCGCCCGCCCGCTCGGTGGCTCCATGTTCTCAGCGCGGCTATCTGACC 2806
DB 301 AGTCAATATGTGGCGGGTACCGTTTCTTCAATGTTCTCCCGCGCGCTTATTGACT 360
QY 2807 GAGCTGTACCGTGAAGGCAAGGACCTGCATCCCGACACCTCGCTGTTCCCGCTGGACATC 2866
DB 361 GAACCTTATCGTGAAGCAGCAATTTACACGCAAGTCACTCCGTTTATATCTTGGATACC 420
QY 2867 CGGCGTCCCGACCTGGCGGCTGGCCCTTAGCCAGATAATATGGAACGACGAGCTCTCC 2926
DB

421 CGCCGCCAGATCTCAAAATCAATGCGGCTCAGTCAGCAAAAATATGGATATAGAATATATCC 480
2927 ACCCTGAGCCTGTCCCAATGAGC---TACTGTATCGCGGTATCGGGCAGCGGAGGCCTT 2983
481 ACACCTCTCTTTGTCCAATGAGCTGTTATTGGAAGCAATTAATACTGAATCTAACTAGGAA 540
2984 GACGACGACAGCCTCAGGAGCTGCTCGCGGGTATCGCTGACCGGCTTGAACCCCTAT 3043
541 AACTATACTAAAGTGATGGAATGCTCTCCACTTTCGGTCTTCGGGGCAACGCTTAT 600
3044 CACTGGCGGTACGAGGGCGCCCAAGCAATCTCTGGTGAGGACCGGCGCTGATGGGG 3103
601 CATGATGCTTATGAAAATGTGCGTGAAGTTATCCAGCTACAAGATCTGAGACTTGAGCAA 660
3104 TTCAGCGGTAATCCGGATGTGGCGAGCTTATGAGCCCTGCGCTCCATCTGCGGCAATTGAA 3163
661 CTCAATGCAATCACCGCAATTTGCCGGTGTGATGCATCAAGCCTCCCTATTGGGTATTAAAC 720
3164 GCGGATATTTTACCGGAGCTGTATCAGATACCTGCGCAAGAAATTAACGACAGACAGTTAC 3223
721 GCTTCAATCTCGCTCGAGCTATTTAATAATCTGACGGAGGAGATTACCGAAGCTAATGCT 780
3224 GAAGCACTCTGGAGTAAGAAATTTTGTGTATATGCTTCCCTCTCCTCATCTTATCTATGAT 3283
781 GAGGAACTTTTATAAGGAAAAATTTTGTGTAATATCGAAACCGGCTCATTTGGCTATGCCGAA 840
3284 GCACCTTGCACATTTTATGATCTTGTATGAGTACGATGAGCTTAACCTTCTGTTATGTTAAGG 3343
841 TACCTTAAACGTTATTATTATTTAAGCGATGAAGAACTTAGTCAGTTTATTTGTTAAGGCC 900
3344 CTGGACTTTTCAAAATCCAAACAAATGAATACATTAATAGTCAATTAAGTCTGTAACCT 3403
901 AGCAATTTTGGTCAAC-----AGGAATATAGTAATAACCAACTTATTACTCCGGTA 951
3404 CTGAATGAAAGCACTCGTTTAATACTATACATCATATTATTAAGAACGCTAGCGGAGAC 3463
952 GTCAACAGCAGTGTATGCGCGGTTAAGGTATATCGGATCACCGCGCAATATACAAACCAAT 1011
3464 TCACAGCAGATTAAACCTCAGCTTATACCTTATGGGGATGGACATATCTTTATATATTC 3523
1012 GCTTATCAATGGATGTGAGCTATTTCCTTCCGTTGGTGAAGAAATTATCGTTAGATTAT 1071
3524 AGCGTGTGTCAACGATATCAGAGGATAGTTTCAAACTAGGGTCTGTTAGGTTCTAACACGT 3583
1072 AATTCABAAAATTTTATTAATGCTCTTATTTATCCATCAAGTTAATGATAAAGAGAA 1131
3584 AGCAATCTTTACTCTCGGGAATTATCAGCTTCAAAAAGGGGTTGCGTATAGCATTCCTGTT 3643
1132 CTGTGTTTGAACCTGAAGCGCTCTCTCAAGTCAATATAGAATACTCCGCAAAATATCACATTA 1191
3644 GAAATAGATGAAGGAAGTTAAATGATGGAT---CACAAATAGGATTGAGTAGGAAGGG 3700
1192 AATACGCTGATATCAGTCAACCTTTTGAAATTTGGCTCTGACAGAGTACTTCTCTCCGGT 1251
3701 GGGGGAATATTAATCAACAGTAACTTCACTCTGATTTGAATATGATCCTCGATATTCAIT 3760
1252 TCTTGGGATATGCGCGCGCAAAATTTACCGTTGAAGATATTAACCAATACTCTTTCTG 1311
3761 CTTAAATTAATAAAGTTATCCGCTATACAAGGCCACCGGCAATGACACGCGGGAATA 3820
1312 CTAAACCTTAAACGAGCTATTGCTTATCAGTGGCAGAGAAATTTGTACCCACGATTCG 1371
3821 TATCAAAATCACCATAATCTTAATACGGTCTCACCATTTGACCATCGGCTCTGAGTAAA 3880
1372 GAAGGCAATGTGCGCAGTGTAAATCTAACCTGGATATCAACACAGACGTTATTAGGTAAA 1431
3881 ATCTTCTCGTCCGTTTACCTGATGCTCACTATCAGCTTGTATGGCCCGGTCACCTGATA 3940
1432 GTTTTCTGACTAATAATTTATGACGCTTATGCTATTCACTGCTGAAGACTGCCCTGATA 1491
3941 TTGTGCAACGGAACCAATCAGTGACCGAGGCTTACGCGGCAAAACCGGCTGTTTCAACAG 4000
1492 CTATGCAACGCGCTATTTCACAACTTATATGATAATCAACCTTAGTAACTTGTATGTCG 1551
DB

QY	4001	CTGTTCAACACCCACCGCTGACGGCAGCTGTTTTCTGCAGATGATACCCCTCGAC	4060	QY	5033	GCTGAGCAGTGGCTGGACATGAGTGAGACCCCTGTCTCCATTACGCCATCCGGTCTGGCTAGC	5092
Db	1552	CTGTTTAATACGCCATTACTGAAACGACAAATATTTTCTACCGGCATGAGAGATTGAT	1611	Db	2629	ATCCTGCATGGTTAAATGTCGCCACAAATTTGANTGTGCCCCCAGGGCGTTTCCGCT	2688
QY	4061	TTACGGCTCTGAAGCACCGGAGGATGCTTTCGGTCTCAGGGTACTGAAACGCGCATTTAAC	4120	QY	5093	CTGATGCGCCTGAAGTACATCAATGTGTCGGATGACAGTGACCGTTGTACAGCCAGTGG	5152
Db	1612	TTAAATTCAGGTAGCACCGCGCA--TTGGCGAAACCAATACTTAAGCGTGCAITTAAT	1668	Db	2689	TTGGTCGGGCTGGATTATTAATCAATCAATGAAGAGA---CACCGACCTATGCCAGTGG	2745
QY	4121	ATCAGCGCTCGGGGCTTTCACGCTCTGGCACTTGGCCAGCGGTGACAGAGCGCTGGG	4180	QY	5153	CAGGTGGTATCCGGTCTGCTGCAGCGCGGCTGAAAGCAGCAGAGCTCGGGCTGAC	5212
Db	1669	ATTGATGATGCTCGCTCTTCGGCTGCTTAAATTTACCGACCATGATAATAAGATGA	1728	Db	2746	GAACACGGGCAGGCGTATTAACCGCGGTTGAATTCACAAGGCTAATCATTTAC	2805
QY	4181	T---TTAGCTGCTCTGCTGACATATCGCGCACTCTACCGAGTGAATCTCTGGCTGAC	4237	QY	5213	GATTTATCTGGAGAGGGACACAGAGCGCCCTTCTGTGGTATTAATCTCGGTAATCT---	5268
Db	1729	AAAATTAANAATAACCTAAGAAATCTTCCAAATTTATATATTGGAATAATTACTGGCAGAT	1788	Db	2806	GCTTTTCTGGATGATCTCGAGTCCGCAATTAAGCACTACTATATCGTCAAGTCGCC	2865
QY	4238	ATCAGGACCTATCCGCTGGTGAAGTGTCAATGTGCTGCTCCCTCTCCCTTTTCAGCGGG	4297	QY	5269	--GGCACCGAACATGGTATCCGGGCGGATGACCTCTTGGGTATCTGCTGTGATAT	5326
Db	1789	ATTTCATCAATTAACCATTTGATGAACCTGGATTTATTAATTAATGCTGCGGTGAGT	1848	Db	2866	AAGGCAGCGCGGCTATTAAAGCCGTGATGACTTGTATCAATACTTACTGATTGATAT	2925
QY	4298	GTGGCGCGCGCTGCTGCTCGGTATTA---TGAGCTGACGAGTTTCTGTGTAACAG	4348	QY	5327	CAGGTGTCAGCCAGGTAACCAACCCGCTTGGAGGCGCATCGCGGCATACGGCTG	5386
Db	1849	ACTAAATTTATCCGCTATCAGTGATAAGCAATTTGGCTACCTGATCAGAAAATCTCAATACT	1908	Db	2926	CAGGTCTTCGCGCAATAAAACCCCGGATCGCGAAGCAATTCAGATTAATCAACTG	2985
QY	4349	ACCACCACTGGCTCAGGAGCAGGGCTGACCGTCAAGATGTTCTCTGATGCTGACG	4408	QY	5387	TATATCAACCGCGGCTTAAACGGAATAGAACTCAGCGCATCGCAGAGGTGAGGGCGT	5446
Db	1909	ATTACAGCTGGCTTACATACAGAAAGTGAGTGATTTCCAGCTATTTATCATGACCTCC	1968	Db	2986	TAGCTCAACCGGCAATGGAAATCTGGNAGAAATGCCAATTCGGGGTTATCAGCCGC	3045
QY	4409	ACGAGTACGCTACCTGTGACCCCGCAATTTGAGAACCTGCTCGCTTCCCTGCGCAAC	4468	QY	5447	CAGTTTTCTACTGACTGGGATACGTTCAACAAAGTTACAGCACTTGGGCGGGCTCTCA	5506
Db	1969	ACCAGCTATAACAAACGCTAACCGCTGAAATTAAGAAATTTGCTGGATACCGTCTACCAC	2028	Db	3046	CAATTTCTTATCGACTGGGACAAATACAAATAACGCTACAGCACTTGGCGGGTGTCT	3105
QY	4469	GGAAGTGGCGCTGAGCTGTTCCCGGAAACCGCTCCCGGCGATGGCGCTCCTTTAT	4528	QY	5507	GAGCTGTTTACTATCCGGAACCTACCTCGACCGGCGGTCCGTATCGGGCAGACCGGC	5566
Db	2029	GGTTTACAAGGTTTTGATAAAGCAAAAGCAGATTTGCTACATGCTCATGGCGCCCTATAT	2088	Db	3106	CAATTAGTTTTACTACCGGAAACCTATATTGATCCGACCATCGGTATCGGAACAAACAA	3165
QY	4529	GCGCGCCATGAGCTGGACGCGACGATACCGCGAAGCGATGCTGACTTGGCGGAC	4588	QY	5567	ATGATGGACACCCCTGCTGCACTCTGACGCGAGCAGTATCAACCGCATACCGTGGAG	5626
Db	2089	GCGGCCACCTTGCAATATCATCGGAAATGTGCGCCATCTCGTACTCTCTTGGGAGAT	2148	Db	3166	ATGATGGACGCTTACTGCAATCCGTCAGCAGCAAGCCAAATTAACCGCATACCGTCGAA	3225
QY	4589	CAGTTGAAGCCAGAGGGCTGACGCTGACGGAATTTATCTTTTGGT-----	4635	QY	5627	GATGCTTTAAACCTATCTGACAGTTTGAAGAGATTGCCAATCTGAACTGACACTGTCAGC	5686
Db	2149	AAGTTACAGCCCGGACGCGCAATGACAGCAGAAATTTCTGGACTGTTTGAATACT	2208	Db	3226	GATGCTTTTATCTCTGATCTGACGCTTGAACAGTGGCTTAATCTTAAAGTTATTAGC	3285
QY	4636	-----GATGAATGCGGCCCAATGACAGCAGCGGGCCAGATGGCAGGGTCTGC	4687	QY	5687	GGATATCAGATAACCGCAGCATGCGCAGGGGACTACATGTTGTTGGTCTGCAGCATC	5746
Db	2209	AAGTATACGCGCGGTTTCATCGAAGCGGTAGAAACCGAGGAACATATCGTTTCAATGTT	2268	Db	3286	GGATATCAGATAATTAATAACGATCAAGGGCTGACCTATTTTATCGGACTCAGTAA	3345
QY	4688	CAAGCCTGTGGCAACTGGCACTGATCATCCGCGACACCGGCTTCAGCAGCGCGAGCTG	4747	QY	5747	ACAGATCAGACTAATCTGTTACTTGGCGCAGCGCAACACAGCAAAATCCAAGACTCAATG	5806
Db	2269	CAGCTCTGGCAATTTGGAATTTGTTTACATTCACCGGCAATCAAGNAACGGCTTC	2328	Db	3346	ACTGATCCCGGTGAATATTATTGGCGCAGTGTGATCAGATTAATTTCAACGACGTAAA	3405
QY	4748	ACGCTGCTGTGACCCAGCGGACGCTTCCGACAGGATGGACCATCTGCCCC---CAT	4804	QY	5807	ATGCCCGGAATGCTTGGACCGGATGGAACAAAATTAATCTGCGGAATGAATCGGTGCTCA	5866
Db	2329	CGTCTATTTGTGACAAACACAGAGATGTTTGGCGCTGCACTGAGCAGCGCCGCGCAT	2388	Db	3406	TTCCGGCTTAATTCCTGGAGTGAATGGCATATAAATTTGATTTCCAAATTAACCTTATAA	3465
QY	4805	GACCTGCGCGGCTTCGCGACATTAACGTTTTTATGCGGTTCGTTAACCGCAGCGGAGC	4864	QY	5867	GATCTGTGCTCGGTGTTTTTCAACAGTCCGCTTATGCTGCTGCTGGCTCGAAGA---	5922
Db	2389	GATGCCCTTTTCACTGATTTATGCTGACACGTTTTTGGGATTTGGGTGAACGCACTAGGCGAA	2448	Db	3466	AGCACTATCCGTCAGTGATATAAATCCCGCTGTATCTGCTGTGGTTGGAACAAAG	3525
QY	4865	CATGCCGGGAGGTCTGACCGCACTTGACCGGAGAACTGTCTGTCAGCGCTGCTGGCC	4924	QY	5923	-----GAATCAGTCTGCTGATCGGAGGAGAGACGACCAACCAACGACGACAGC	5974
Db	2449	AAAGCGTCTCGGTGCTAGCGGCAATTTGAAGCTAACTCGTTAAGCGGAGAACTGGCT	2508	Db	3526	GAGATCACCACACACAGAGAAATAGTAAAGATGGCTATCAAACTGAAACGGATATCGT	3585
QY	4925	CGGCGCTGTACAGAAATG-----AGCAGGATGACCGCGCTTGGCGCAG	4972	QY	5975	TACACGCTGAACTGCTGTTCCGGCTACGAGGTTACATGAGTTCCCGGTGCTGTTTC	6034
Db	2509	GATGCCATGAATCTTTGATGTAAATTTGCTGTTGCAAGCCAGTATCAAGCACAAATCAT	2568	Db	3586	TATGAATTAATTTGGCGCATATCGCTATGATGGCATTGGAATACGCAATACCTTT	3645
QY	4973	GTAGGGGGCGGTGACAGGACACAGCGTTTACCTCTCGGAGAGGTGGACCG	5032	QY	6035	GACATTACCGGCAACATCGC-----ATTTCCGGAACCGCAGGCGATGATGTGACCTGT	6088
Db	2569	CAACATCTTCCCCCAGTAACTCCAGAAAAATGCGTTCTCTGTTGGACATCTCAATACT	2628	Db	3646	GATGCTAATAAATAATATCCAGCTAAACTTGGAAAAAATAGAGCGCCGAGCTAT	3705
				QY	6089	AATCCC-----CTGACTGACGAGCTCTATTGCGGGTTTTTACTCCGTACCAGAACCGGA	6144

Db 3706 TGTCCCGGTTATCAAGGTGAAGTACGTTGCTGGTGATGTTTATATACCAACAGACACA 3765
Qy 6145 CTTTGATAACCGCTCAGCTGATTTCTGTGGATAATGATATGAGGCT----- 6189
Db 3766 CTAGATAGTTATAAAGCGCTTCAATCGAAGGACTATATATCTTTGCTGATATGGCATCC 3825
Qy 6190 --AAATGTCATCTCAGATATAGGGATTTTAAAGCG-----TCAGTCAGCAATTTAAT 6241
Db 3826 AAAGATATGACCCAGAACAGAGCAATGTTTATCGGGATAATAGCTATCAACAATTTGAT 3885
Qy 6242 ACGAGCACTGAGAAATTTATTAATATGTTTTCAGACCCCTCCGCTAATTAAT- 6295
Db 3886 ACCAATAATGTCAAGAGTGAATAACCGCTATGCAAGGATTATGAGATTCCTTCCTCG 3945
Qy 6296 -TTTGTCAAGTGCACAGGTTTAAATTTGATGTTTAT-----CCACAGC 6337
Db 3946 GTAAGTAGCGTAAGACTATGTTTGGGGAGATTATACCTCAGCATGGTATATAACGGA 4005
Qy 6338 GATTTCTCACTCTTAATTTCTAAACTACAAGTACTGTTTTTAC----- 6381
Db 4006 GATATTCCAACTATCAATTAACAAGCGCATCAAGTGAATTTAAAAATCTATATCTCACCA 4065
Qy 6382 TAATGAAGATTCCTCTCTTTTGAGCCGAGAGCTTCATATTACAGCAAAATGTTTGTGTTT 6441
Db 4066 AAATTAAGAATTTATTCATAATGGATATGAAGGACAGAAAGCGCAATCAATGCAATCTGATG 4125
Qy 6442 TGTTAGTACTGCTGGCATCGCACTCAATCTACCATAGAAAATTCGTTTCAGCAGCGGAT 6501
Db 4126 AATAAATATGCAAACTAGGTGATAAATTTATTTGTTTATCTAGCTTGGGGGTCATPCCA 4185
Qy 6502 AGAATTTGAGAAATTAATTTTATGCAGCGCCAGCGCGCGGATTTTGACGGATTTGT 6561
Db 4186 AATAACTCGTCNAATAGCTCATGTTTACCCGTCATCAATATAGCGGAACACCACT 4245
Qy 6562 GG-----GAGTGGATGTTTCTAATTCAAAGTATAC 6592
Db 4246 GGACTCAATCAAGGGAGACTATTCCACCGTGACACCCTTATCCATCTAAAGTAGAA 4305
Qy 6593 CAGTCGGAAAGAGAGTGTGTCTCATGTGAATCTTATTCGTCACCTGCGGTAGT 6652
Db 4306 GTTTGGATTCCTGGAGCAAAACGTTCTCTAACCAACCAAAATGCCGCATTTGGTGATGAT 4365
Qy 6653 GGTTCCTGTGAGTTATTTATGATTCATCAATAAATACTTCAGCGGAAATTTTGTGATGAT 6712
Db 4366 TATGCTACAGCTCTGATTAACCGGATGATCTTAAGCAATATATCTTTATGA CTGAC 4425
Qy 6713 AAAATGATAACCGCTTTAATTTAGCGGAGTACATCAAAAGTTAAT----- 6757
Db 4426 AGTAAAGGAGCTGTACTGATGTCTCAGGCCAGTAGAGATTAATACTGCAATTTCTCCA 4485
Qy 6758 -----TACGTGCTCTATTGGCTCTCAA 6781
Db 4486 GCAAAAGTTCAGATAATAGTCAAAAGCGGGTGGCAAGGAGCAAACTTTTACCGCAGATAAA 4545
Qy 6782 GATTTTGGAGTGAAGTGCCTCATGCCGCACTTCAGATATATGAATTAATTCGATGAT 6841
Db 4546 GATGCTCCATTCAGCCATCACCTAGCTTTGATGAATGAATTAATCAATTAATGACCTT 4605
Qy 6842 ATCATACTGACATCCGCGTAATAGGACTGAAATTAATCC-----TGG 6886
Db 4606 GAAATAGCGGTTCTGGTCTGAATTTTAAACAACTCAGCCAGTATTGATGTTACTTTT 4665
Qy 6887 CCTTCCGCTGATGATATATGATAGCTGATCTGCAATCCGCGGAATATCTTTTCAAC 6946
Db 4666 ACCGATTTGGGAGGATGGCCGAAACTGGGTATGAAAAGTTTCAGTATTCCTGTTTACC 4725
Qy 6947 ACCAAATCGCTGAGTTTTTACCGTTTAAATACAGTATATGTTGAAGATGAGTTTGACGTG 7006
Db 4726 CTCAGGTAAGTACCGATATGCGCTGACCTCGACCATATGAATGAATGGTGGCGAATAT 4785
Qy 7007 ACGTTTACGTTCAACCGTGTGATCGATCAGATAACGTCGTGCGCGCCCGGAGCGGCATA 7066

Db 4786 ATCAATGGCAATCCTATCGTACCCGCTGAATACTACTATTGTCGCCGAGTTGGTTGCA 4845
Qy 7067 TTAACCGTCAATTCGAAACATTA----- 7088
Db 4846 CGCGCCACCAACCGGAATCGATACAAATCTGAGTATGGAAACTCAGAATATTCAGGAACCG 4905
Qy 7089 ----- 7088
Db 4906 CAGTTAGGCAAGGTTTCTATGCTACGTTCTGCTGATACCTCCCTTAACTTATCAACTCAT 4965
Qy 7089 -ATAATGACACACTTCGCTTATCGCATTTACGTAAATAATACGGTGGCGGAGTATATTCGT 7147
Db 4966 GGTGATGAACGTTGGTTTAAAGCTTTTATATCAAAACATGTTGTTGATAATAATTCACATATT 5025
Qy 7148 TTCACCTGCGGGTAAAGATGTGGCGCTTATTCGCTCAACACCTCTTTGTCGCCCAACTG 7207
Db 5026 ATCTATTAGCCGAGCTAACAGATACAAATATAAACATACATATTATTTCTCTTTGAT 5085
Qy 7208 GTCACCGGGCGAATACCGGGATTGACCCATTCTT----- 7243
Db 5086 GATGTCCCATTTGAATCAAGATTATACGCCCAAGTTTATATGACCTTCAAGAAATCACCA 5145
Qy 7244 ----- 7243
Db 5146 TCAGATGGTACCTGGTGGGCCCTCACTTTGTTAGAGATGATAAGGAATAGTAACAATA 5205
Qy 7244 -----TCCATGAGACCCAGAGGCTTTACCGAACCCGCTCGGAAGAGGGAGTAT 7294
Db 5206 AACCTTAATTCATTTGACCGGCTTACAGCGCTCTATTCTCTGGAACTGTTCTACTATACC 5265
Qy 7295 GTGTTTATGACCTTCCGAGCAATGCCCCTCTATTTCTGGAGCTGTTCTATTACACG 7354
Db 5266 GAACCAATGGAATTCAGCGCGCTACAGCGCTCTATTCTCTGGAACTGTTCTACTATACC 5325
Qy 7355 CGATGATGTTGTCAGCGGTTGTTGAGGAACAGCATTTCCCGGAAGCCACCCGCTGG 7414
Db 5326 CCGATGCTGTTCTCAACGTTTGTGCTGATGAACAGAACTTCGATGAAGCAACCGTTGG 5385
Qy 7415 CTCGATGATGTCGGAACCCGCGCGGCGATGTTAAACGGGTGCTGCGAGATTAACAC 7474
Db 5386 CTGAATATGCTGGAGTCCATCCGTTTATTTGTCACGGCCAGATTCAGAACTACAG 5445
Qy 7475 TGAATGTCCTGCTGGAGGAGGACACCGGCTGGAAACGACTCGCGCTGGACTCCATT 7534
Db 5446 TGGAACTCGCGCGCTTCTGGAAGACACAGTTGGAACTGATCTTTGGATTCGCTC 5505
Qy 7535 GACCCGATGCAATAGCCAGTACGACCCCATGATTAAGGTGCGCACTTTATGTCG 7594
Db 5506 GATCTCTGAGCGGTAGCAGACGATCCAAATGCACTACAAAGTTTCAACTTTATGCGT 5565
Qy 7595 TACCTGACCTGATTTGCCGCGGTGATGCCGCTACCGGCTGCTCGAGCGGACAC 7654
Db 5566 ACCTTGGATCTATTGATAGACGCGCGGACCATGCTTTATGCCAACTGGAAACGAGATA 5625
Qy 7655 CTTAAACGAGCCCGGATGTTGTTCCAGGCGCTTGAACCTTCTGGCGCAGGAGCCCTAT 7714
Db 5626 CTCAAAGAGGAGATGTTGTTATGCAAGCGCTGCACTATTAGGTGACAACTTAT 5685
Qy 7715 ATTTCTTTGACGCCGATGTTGTCGGGTTGAACCTCGGTGACGACGACGAGGTGACG 7774
Db 5686 CTACCGCTGATGACGATGAGTATCCACGACTAGACAGAGCGCGGATATCACTACC 5745
Qy 7775 CGAGCGGATTACAGAGGCGCTGCTGGCGTGGCGGTTGTTGCTCCCGTCCCGGAGACA 7834
Db 5746 CAAATGCTCAGCAGCGCAATAGTCGCTCTCGCGCAATATATCTACACCGGACCT 5805
Qy 7835 -----CGGACGCGGAATTCCTGACGCGCTGTTCTCCCGAGCAGAAACGAGGTG 7885
Db 5806 TTATCATTTGGAGCGCTTAATACCTGACTGATCTCTTCTGCGGCAATCAATGATGATG 5865
Qy 7886 CTCAAAGGCTACTGGCAAACTTTGGCAGACGCGCTCCATAAACCCTGGCCCAACCTCTCC 7945
Db 5866 ATGATGAATTTACTGGCAGACATTAGTCTCAGAGAGTATACAATCTGCGTCAATACCTCTCT 5925

Qy	7946	ATTGACGGCCAGCGCTTTCCCTGTCCGTTCTTAGCCACGCGCTCGAACCGTCCGCCCTG	8005
Db	5926	ATCGACGGCCAGCGGTTATATCTGCCAATCTATGCCACACGCGCGGATCCGAAGCGTTA	5985
Qy	8006	CAGAGTGGCGTGTCAACAGCGGCGCAGGTGCTGCAGACTGCGGCGCGGTGATGCGG	8065
Db	5986	CTCAGCGCGCGTTGGCATTCTTCAAGTGGAGGCAAGCTACCGGAATCAITTTATGTCC	6045
Qy	8066	CTTTTACAGTTTCCCGGTCATGCTGGAGAACGCCCGGGGATGTTGAGCCTGCTGACCGGG	8125
Db	6046	CTGTGGCGTTTCCGCGACATGCTGGAAATGCGCGCGCATTGGTTAGCCAGCTCACCCAG	6105
Qy	8126	TTCCGCAACACACTGCTCGGTATTACCGAGCGTCAGGATGCGGAGGCGCTGGGCCAAACTG	8185
Db	6106	TTCCGCTCCAGTTTACAAAATATTATCGAACGTCAGGACGCGGAAGCGCTCAATGCGTTA	6165
Qy	8186	CTGCAGACCCAGGGCAGTGAACATGATACGCCAGGGCCTTCGCCAGCAGGATATAGTCCTC	8245
Db	6166	TTACAAAATCAGGCGCGCAGCTGATATTGACTAACTGAGCATTCAGGACAAAACCATT	6225
Qy	8246	GAGAAATCGATGCGGATATTGCGGCCCTGGAGGAGAGCCGCCGCGCGCAGATGCGT	8305
Db	6226	GAAGATTGGATGCCGAGAAACCGGTGTTGGAAAAATCCAAAGCGGAGCACAAATCGCGC	6285
Qy	8306	TTTGAACGTTTACAAAGTGTGTACGAGCGGCACTCAACACCGCGCAAAAACAGGCCATG	8365
Db	6286	TTTGTAGCTACGCAAACTGTACGATGAGATATCAACGCGGTGAACACCAAGCCATG	6345
Qy	8366	GACTTGTACTCAGTTGCTGCTGCTGCGCATCAACCGCGCGCTCTTTTGGCGCAG	8425
Db	6346	ACGCTACGAGGCTCCGCGCGCGGCTTACCACGGCACTTCAGGCATCCGCTCTGGCGGT	6405
Qy	8426	GCCCGGCCGATATGCTGCCCAATTTTACGGGCTGCGCGTCCGGGCTCCCGCTATGGG	8485
Db	6406	GCGCGCGCTGATCTGGTGCCCTAAACATCTTGGCTTTGCCGCTGGCGCAGCCGTTGGGG	6465
Qy	8486	GCACATTTTAAAGCCACCGCCATCGGCATCCAGGTGTCCTCCGATGCCACCCGCATATCA	8545
Db	6466	GCTATCGCTGAGGCGCAGGTTATGTGATGGAATCTCCGGAATGTTATGAACCCGAA	6525
Qy	8546	GCGGACAAAATACGCCAGTCGGAAGTGTAACGCCGTGCGCGGAGGAGTGGGAAATCCAG	8605
Db	6526	GCGGATAAAAATTAGCCAATCTGAAACCTACCGTCTGCGCGTCAGGAGTGGGAGATCCAG	6585
Qy	8606	CGTGATAGTCGCAGTCTGACGTGGCCAGATTGATGCCACGCTGGCGGCATGGCAGTG	8665
Db	6586	CGGAATATGCCGAAGCGGAATTGAAGCAATCGATGCTCAGCTCAAATCAGTCGCTGTA	6645
Qy	8666	GCCCGGAAGGGCTGAGCTGCGAATAACTTACCTTGAGACCCAGCAGACCCAGGCACAG	8725
Db	6646	GCCCGGAAGCCGCGGTAATTGCGAATAACAGTCTGGAACCCNAAGAAGACAGACCCAA	6705
Qy	8726	GCGCAGTTGGCATTCCTGCGAGTAAAGTTCAACAATACGGCTCTGTACAGCTGGCTGCGG	8785
Db	6706	TCTCAATTGGCTTCTCTGCAACGTAAGTTTCAAGCAATCAGGCGTTATACAACTGGCTGCGT	6765
Qy	8786	GGCAGGTTGTCGCGCAATTTATACCACTTATGACCTGGCAGTATCCCGCTGCCTGATG	8845
Db	6766	GGTCGACTGGCGGCGAATTTACTTCAGTTCTAAGATTGGCGCGTGGCGGTTGCCCTGATG	6825
Qy	8846	GCGCAACAGGCTCGGCAGTGGGA---TAAATTCGAGACTAGGTGTTTATCCAGCGCGGG	8902
Db	6826	GCAGAACAGGTTACCGTTGGGAACCTCAATGATGACTCTCGCGCTTCATTAACCGGGC	6885
Qy	8903	GCCTGGATGGGGCAATGCGGCTCTGCTGGCGGGGAAACCTCTGATGCTGAATCTGGCG	8962
Db	6886	GCCTGGCAGGAACTTATGCGCGTCTGCTTGCAAGTGAACCTTTGATGCTGAGCTGGCA	6945
Qy	8963	CAGATGAGCAGGCTGGCTGACGGGGGATGACGGCGCAATAGAGGTGACGCGGACGGTC	9022
Db	6946	CAAAATGGAAGCGCTCATCTCTGAAACGCGGATAAAGCGGCATTTAGAGGTTGAACCCAGTA	7005

Qy	9023	TGCTGTGCGAGGTCTATAACGACCTCGCGGAGGAT---GCGGCATCTCTCTGGCGCGAC	9079
Db	7006	TCGCTGCCGGAAGTTTATGCAAGATTACCAAAAGATAAACGGTCCATTTTCCCTGGGCTCAG	7065
Qy	9080	AAGTGTGTGAACTGGTCACTAAACGGTTCGGGCAGTGCGGGTACGAAACGAACGCGATT	9139
Db	7066	GAAATTCACAAGCTGGTGTAGTCAAGGTTTCAGGCAGTGC CGGCAGTGGTAAATAAATTTG	7125
Qy	9140	CAGATGG-----ATCAACAGCAACTCGAGGCCACCCCTGAAACTGGGCTGAC	9184
Db	7126	CGCTTCGGCGCCGCGACGACACTAAAACCTTTTGCAGGCATCAGTTTCATTCGCTGAT	7185
Qy	9185	CTCGGTATCGCAACCGATTACCCGGTCTCCCTGGGCAACATGAGGCGCATCAAAACAATA	9244
Db	7186	TTGAAAATTCGTGAAGATTACCCGGGATCGCTTGGCAAAATTCGAGTATCAACACAGATC	7245
Qy	9245	AGCGTCAGCTCCCGGGCTGGTTCGGCCCTATCAGGACGTTCGTGGGTTCTCAGCTAC	9304
Db	7246	AGCGTCACTTTGGCCCGGCTACTTGGGACCGTATCAGGATGTA CAGGCAATATTGTCTTAC	7305
Qy	9305	GGCGGAAGTATGTCTATGCCCCGGGTTGCAGCGCGCTGGCGGTCTCACACGGAATGAAC	9364
Db	7306	GGCGATAAACCCGGAATTAGCTAACGCGCTGGAAGCGCTGGCAGTTTCTCAGCGTATGAAT	7365
Qy	9365	GACAGCGGCCAAATTCCAACTGGATTCAATGACCCCGGTTACTCTCGCGTTTGAAGACTT	9424
Db	7366	GACAGCGGCCAAATTCCAGCTCGATTTCAACGATGGCAAAATTCCTGSCAATTCGAAGGCATC	7425
Qy	9425	CCAGTTGATGACACAGGACCCCTGACACTGAGCTTCCCGGATGCG-----TGAC	9472
Db	7426	GCCATTGATCA---AGGCACGCTGACACTGAGCTTCCCAAATGCATCTATGCGCGAGAAA	7482
Qy	9473	GGCAACAACAGGCGATGCTCCTCAGTCTCAGCGACAATCATCTCGATATCCGTTACACC	9532
Db	7483	GGTAAACAAGCCACTATGTTAAAAACCTTGAAAGATATCATTTTGGCATATTCGCTACACC	7542
Qy	9533	ATTA 9536	
Db	7543	ATTA 7546	

RESULT 6

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US-09-637-048C-1
; Sequence 1, Application US/09637048C
; Patent No. 6590142
; GENERAL INFORMATION:
; APPLICANT: Patel, Jim
; APPLICANT: Merlo, Donald
; APPLICANT: Herman, Rod
; APPLICANT: Roberts, Jean
; APPLICANT: Guo, Lining
; APPLICANT: Schafer, Barry
; APPLICANT: Sukhapinda, Kitisri
; APPLICANT: Owens Merlo, Ann
; TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin
; FILE REFERENCE: 50698
; CURRENT APPLICATION NUMBER: US/09/637,048C
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/148,356
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 7551
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7548)
US-09-637-048C-1

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Matches 3662; Conservative 0; Mismatches 3347; Indels 495; Gaps 31;

Qy	2510	CTGACGGATTATTTCTCGCGTTCGGTTTCCCGAGGTCAAAAAATCACTGGCGCAGCGCTG	2569	3584	AGCAATCTTTTACTCTCGGGATTATCAGCTTCAAAAAGGGTTCGCTATAGCATTTCTGTGTT	3643
Db	61	CTGACAGATATTAGCCACAGCTCTTTTAATGAATTCGCCAGCAAGTATCTGAGCACCTC	120	1132	CTTGTTCGAACGAAAGCGCTCTCTCAAGTCAATATAGAATACTCCGCAATAATCAACATTA	1191
Qy	2570	TCATGGGGAGGTCTGCTATCTGTGACGTGAGCGGAGCAGCAACGAAAGAAAACCGG	2629	3644	GAAATAGATGAAGGAAGTTAAATGATGGAT---CACAAATAGGATGAGTAGGAAGGG	3700
Db	121	TCCTGGTCCGAAACACACAGCACTTATATCATGATGTCACAAAGGACACAAAAGGATAATCGC	180	1192	AATACCGCTGATATCAGTCAACCTTTTGAATTTGGCTGACACGAGTACTTCTCTCCGGT	1251
Qy	2630	CTCACGGAATCCCGTATTTCTGGCCGGCGGAATCCCTACTGTTGATGATCGGTTCCGCTG	2689	3701	GGGGATATTACTCAACAGTAAACCTTCACTCTGATTTGAATATGATCTCTCGATATTTCATT	3760
Db	181	CTGTATGAGCGGGTATTTCTCAACGCGCAATCCCAATTAACAAATGCGGTGATCTT	240	1252	TCTTGGGCATATGCCGCCGCAAAATTTACGTTGAAGAGTATAACCAATACTCTTTCTG	1311
Qy	2690	GGAAATCGGAGGAGCGCGGAGTCGCA---GCTATGATCACTGGTTTGGCTCCCGCGCA	2746	3761	CTTAAATTAATAAAGTTATCCGCTTATACAAGGCCACGCGGCATGACCAAGCGGAATA	3820
Db	241	GCCATTCTCGCTCCCAATGCTGAACCTGATAGGCTATAACAATCAATTTAGCGGTAGAGCC	300	1312	CTAAATCTTAACAAGGCTATTCGTCTATCAGCTGCGCAGAAATTTGTCAACCCAGATTCTG	1371
Qy	2747	GACGGTTTCCCGCCCGCTCGGTGGCTCTCAATGTTCTCACTGGCGGGGTATCTGACC	2806	3821	TATCAAAATCACAATATTTCTTAATAACGGTCTCACCAATGACCATCGGGTCTCGAGTAAA	3880
Db	301	AGTCAATATGTTGGCGCGGTAGCGTTTCTTCATGTTCTCCCGCGCGCTTATTGACT	360	1372	GAAAGCATTTGTGCGCAGTGTAACTTACAACCTGGATATCAACACAGACGTTATTAGGTAAA	1431
Qy	2807	GAGCTGTACCTGAGCGAGGAGCACTGCATCCGGACACCTCGCTGTTCCGGCTGGACATC	2866	3881	ATCTTCTCGTCCGTTTACCTGATGCGTCACTACTACGCTTGTATGCTGGCCCGTCACTGATA	3940
Db	361	GAACTTTATCGTGAAGCAGCAATTTTACGCAAGTGACTCCGTTTATTATCTGGATACC	420	1432	GTTTTCTGACTAAATATTATATGACGCGTTATGCTATTCACTGCTGAAACTGCCCTGATA	1491
Qy	2867	CGCGCTCCGACCTGGCGGCTGGCCCTTAGCCAGAAATATATGACGACGAGCTCTCC	2926	3941	TTGTGCAACGGAACCAATCAGTGACCAAGCGGTTTCAGCGCGGAAACCGGCTGTTCCACCAG	4000
Db	421	CGCGGCCAGATCTCAAAATCAATGGCGCTCAGTCAGCAAAATATGATAGAAATATACC	480	1492	CTATGCAACGCGCTTATTCAACAGTTTATATGATTAATCAACCTAGACCAATTTGATCGC	1551
Qy	2927	ACCTGAGCCTGTCCAAATGAGC---TACTGTATCGCGGTATCGGGCAGCGGAAGGCTT	2983	4001	CTGTTCAACACCCACCGCTGAAACGCGCAGCTGTTTTCGAGATGATACCCCTCGAC	4060
Db	481	ACACTCTCTTTTCCAAATGAGCTGTTATTGGAAGCATTAATAACTGAATCTAACTGGAA	540	1552	CTGTTTAATACGCAATTACTGAACGCAATAATTTTCTACCGCGATGAGGAGATTGAT	1611
Qy	2984	GAGCAGCAGCGTCAGGAGCTGCTCGCGGGTATGCGCTGACCGGCTGACCCCTAT	3043	4061	TTACGCTCTGAAGCACCGGAGGATGCTTTCGCTCTCAGCGTACTGAAACGCGCATTTAAC	4120
Db	541	AACTATACTAAAGTGATGGAATGCTCTCCACTTTCCGCTCTTCGCGCGCAACGCGCTAT	600	1612	TTAAATTCAGGTAGTACCGCGCA---TTGGCGAAAAACCATACTTAAGCGTGATTTAAT	1668
Qy	3044	CACCTGGCGGTACGAGGGCGCCGCAAGCCATTCTGGTGACGACCGACGCTGATGGGG	3103	4121	ATCAGCGCTCGGGGCTTCCACGCTCTGGCAGTTGGCGCAGCGGTGACAGCAGCGCTGGG	4180
Db	601	CATGATGCTTATGAATGTCGTGAAGTTATCCAGCTACAGATCTTGACATTGAGCAA	660	1669	ATTGATGATGCTCGCTCTTCGCGCTGTAAATAATTCAGCACCATGATATAAAGATGGA	1728
Qy	3104	TTCAGCGGTAAATCCGGATGTCGGCAGCTTATGGAACCTCGCTCCATGCTGGCCATTGAA	3163	4181	T---TTAGTGTCTGTCTGACAAATATCGCGCAGCTCTACCGAGTGAACCTCTGGCTGAC	4237
Db	661	CTCAATCATCACCGGCAATTGCGGCTTGATGTCATCAAGCCCTCCCTATTGGGTATTAAAC	720	1729	AAAAATTAATAAATACTAAAGAACTTCCAAATTTATATATGGAATAATTTACTGGCAGAT	1788
Qy	3164	GCGGATATTTCCGAGAGCTGATCAGATGCTGGCGGAGAAATATGACAGACAGTTAC	3223	4238	ATCCAGCAGCTATCCGCTGGTGAAGCTGTCAAATGTTGCTGTCCGTCTCCCTTTTCAGGGG	4297
Db	721	GCTTCAATCTCGCTGAGCTATTAAATATTCTGACGAGGAGATTTACCGAAGGTAATGCT	780	1789	ATTCAATCAATTAACCAATTGATGAACCTGGATTTTACTGATTTGCCGTAGGTGAAGGAAA	1848
Qy	3224	GAAGCACTCTGGAGTAAGAATTTTGGTGATATGCTCCCTCCCTCACTGTTTATCTATGAT	3283	4298	GTGGCGCGCGCTCGCTGCTCCGATAA-----TGAGCTGACGAGTTTCTGTACCAG	4348
Db	781	GAGAACTTTATAGAAAAATTTTGGTAATATCGAACCGGCTCATTTGGCTATGCGCGAA	840	1849	ACTAATTTATCGCTATCAGTATAGTAAGCAATTTGGCTACCTGATCAGAAAACATCAATACT	1908
Qy	3284	GCACTTGCAACATTTTATGATCTTGATPACGATGAGCTAACTTCGTTATTGTCAITTAAGG	3343	4349	ACCACCACTGGCTACGGAGCAGGGCTGGACGGTCAGCGATGTTGTTCTGTGATGCTGACG	4408
Db	841	TACCTTAAACGTTATTATTAATTAAGCGATGAAGAACTTAGTCAGTTATTGTTGAAGCC	900	1909	ATTACCAGCTGGCTACATACACAGAAATGAGTGGTATTTCAGCTATTTATCATGACCTCC	1968
Qy	3344	CTGCACTTTTCAATCAAAATGAATATCTAATTAATAGTCAATTAAGTGTGCTGTAAC	3403	4409	ACGAGTAGGTAACCTGCTGACCCCGACATTTGAGAACCTGCTCGCTTCCCTGCGCAAC	4468
Db	901	AGCAATTTTGGTCAAC-----AGGAATATAGTAATAACCAACTTATTACTCCGGTA	951	1969	ACCAGCTATAACAAAAACGCTTAACGCTGAAATTTAAGAAATTTGTGATACCGTCTACCAC	2028
Qy	3404	CTGAATGAAGCACTGTTTAACTATACATCATTTATTTAAGAACCTTAGCGGGAGAC	3463	4469	GGAGTCTCGCGCGTGGAGCTGTTCCCGGAAACGCTCCCGCGCATGGCGCTCCCTTTATT	4528
Db	952	GTCAACAGCAGTGAAGCAACGGTTAAGGTATATCGGATACCCCGCAATATACAAACAT	1011	2029	GGTTTAAAGTTTTTATTAAGCAAAAGCAGATTGCTACATGTCATGCGCGCTTATATT	2088
Qy	3464	TCACAGCAGATTAACCTGAGCTTATACCTTATGGGGATGGAAACATCTTTTATAATTTTC	3523	4529	GCGCGCCCATGCGAGCTGGACGCGCACGATACGGCGAAAGCGGATGCTGTGCTTGGCGGAC	4588
Db	1012	GCATTATCAATGGATGTGGAGCTATTTCCCTTCGTTGGTGAGAAATATCGTTAGATTAT	1071	2089	GCGGCACTTGCATTTATCATCGGAAATATGTGCGCCACTCGGTACTCTCTTTGGGAGAT	2148
Qy	3524	AGCGTGTGTCAACGATATCAGAGGATAGTTTCAAACTAGGGTGGTTAGGTTCTTAACAGT	3583	4589	CAGTTGAAGCCAGAGGGGCTGACGCTGACGGAATTTATTTCTTTTGGT-----	4635
Db	1072	AAATTCAAAAATTTTATAATGCTCTTATTATTATCCATCAAGTTAAATGATAAAGAGAA	1131	2149	AAATTACAGCCCGCGCAGCGCGCAATGACAGCAGAAAAAATTTCTGGGACTGTTTGAATACT	2208

QY 4636 -----GATGAATGCCGCCCAATGACGAGCAGCGCGCCAGATGTCAGGGTTCTGC 4687
Db 2209 AAGTATACGCCGGTTTCATCGGAGCGGTAGAAACGACGAAACATATCGTTCAGTATTGT 2268
QY 4688 CAAGCCCTGTGGCAACTGGCACTGATCATCCGAGACACCGGCCCTCAGCAGCGCGAGCTG 4747
Db 2269 CAGGCTCTGGCACAATTGGAAATGGTTTACCATTCCACCGGCATCAACGAAACGCCCTTC 2328
QY 4748 ACGCTGCTGGTCAGCCGAGCGGGACGCTTCGCGACAGGATGGACCATCTGGCC---CAT 4804
Db 2329 CGTCTATTTGTGACAAAACGAGAGATGTTTGGCGCTGCAACTGGAGCAGCGCGCGCAT 2388
QY 4805 GACCTCGCGCGCTTCGCGACACTTACGCGTTCATGCGCTCGTTAACCGCAGCGCGCAGC 4864
Db 2389 GATGCCCTTCACTGATTATGTGACACGTTTTTGGGATGGTGAACCCACTAGCGGAA 2448
QY 4865 CATGCGGGGAGGTCTGACCGCACTTGAGACGGGAGAACTGTCTGTCAGCCCTGTGGCC 4924
Db 2449 AAAGCGTCTCGGTGCTAGCGGCATTTGAAGCTTAACCTGTTAACGGCAGAAACAATGGCT 2508
QY 4925 CGGGCCCTGTCAGAAATG-----AGCAGGATGTGACCGGCCCTTGGCGGAG 4972
Db 2509 GATGCCATGAATCTTGATCTAATTTGCTGTTGCAAGCCAGTATTCGAAGCACAATAATCAT 2568
QY 4973 GTGAGGGGGCGGTGAACAGGACAAACAGCGTGTTCACCTCTGGGAGAGGTGGACCCAG 5032
Db 2569 CAACATCTCCCGAGTAATCCAGAAATGCGTCTCTGTTGNCATCTATCAATACT 2628
QY 5033 GCTGAGCAGTGTGTCAGATGAGTGAACCTGTCCATTAACGCCATCCGGTCTGCGTAGC 5092
Db 2629 ATCTGCAATGGGTTAATGTGCAACAATGAATGTGCGCCACAGGGCGGTTCCGCT 2688
QY 5093 CTGATGTCCTGAGTACATCAATGTGTCGATGACAGTGCACCGTGTGACAGCCAGTGG 5152
Db 2689 TTGGTGGCGGTGATTATTAATCAATCAATGAAGAGA---CACCGACCTATGCCAGTGG 2745
QY 5153 CAGGTGGTATCCGCTCTGTCAGGCGGGCTGMAAGCAGCAGAGCTCGCGCTGCAC 5212
Db 2746 GAAGACGGCAGCGGTATTAACCGCGGGTTGAATTCACACAGGCTAATACATTACAC 2805
QY 5213 GATTATCTGGAGAGGGGACAGCAGCGCCCTTTGCGTATTTATGCGTAATCT--- 5268
Db 2806 GCTTTTCTGGATGAATCTCGCAGTGCAGCATTAAGCACCTACTATATCCGTCAAGTCGCC 2865
QY 5269 --GGCACCGAATGATGTCGCGCGGATGACCTCTTCGGGTATCTGCTGCTGATAT 5326
Db 2866 AAGGCAGCGCGCTATTAAGCCGTGATGACTTGTATCAATCTACTGATGATAAT 2925
QY 5327 CAGGTGTGACCAAGGTAAAAACCAACCGCATTTGCGAGGCCATCGCCGGCATACGGCTG 5386
Db 2926 CAGGTTTCTGCGCAATAAACCCACCGGATCGCGAGGCCATGGCCAGTATTCACCTG 2985
QY 5387 TATATCAACCGGGCCCTTAAACCGAATAGAACTCAGCGCCATGGCAGAGTGAAGGGCGT 5446
Db 2986 TACGTCAACCGGGCATTTGAAATATGTGAAGAAATGCCAAATTCGGGGGTATCAGCCGC 3045
QY 5447 CAGTTTTTCACTGACTGGGATAGTTCAACAAACGTTACAGCACCTGGCGGGCGCTCA 5506
Db 3046 CAATCTTTTATCGACTGGGACAAATACAATAACGCTACAGCACCTGGCGGGGTGTTCT 3105
QY 5507 GAGCTGGTTTACTATTCGGGAAATCTACCTCGACCCCGACCGTCCGTATCGGGCAGACCGC 5566
Db 3106 CAATAGTTTACTACCCGGGAAACTATATTGATCCGACCATGCGTATCGGACAAACCAA 3165
QY 5567 ATGATGGAACCGTGTGCTGTCGTGTCAGCCAGAGCATGATCAACCGCGATACCGTGGAG 5626
Db 3166 ATGATGGAGCATTAAGTCAATCCGTCAGCCAAAGCCAAATTAACCGCCATACCGTGGAA 3225
QY 5627 GATGCCCTTAAACCTTATCTGACCAAGTTTGAAGAGATGGCCAACTGAACTGAACTGACG 5686
Db 3226 GATGCCCTTATGCTTTATCTGACATCGTTTGAACAGTGGCTAACTTAAAGTTATTAGC 3285
QY 5687 GGATATCACGATAACGCCAGCATGACGCGGGGACTACATGTTGTTGTTGGTGGCAGCATC 5746

Db 3286 GCRATACGATPAATATTAATTAACGATCAAGGCTGACCTATTTATCGGACTCAGTGAA 3345
QY 5747 ACAGATCAGACTAACTGGTACTTGGCGCAGCGCAACACAGCAAAATCCAGACTCAATG 5806
Db 3346 ACTGATCGCGTGAATATTTATTTGGCGCAGTGTGATCAGTAATTCACAGCGGTAA 3405
QY 5807 ATGCCCGGATGCTGACCGGATGGACAAAATTAATCTGCGGAATGATCCGTTGGTCA 5866
Db 3406 TTGCGGGCTAAATGCGCTGGAGTGAATGGGCATAAAATTTGATGTCCTAAATTAACCTTATAAA 3465
QY 5867 GATCTTGTGCTCGGTGTTTCAACAGTCCGCTTTATGCTCTGGGTGCAAGA--- 5922
Db 3466 AGCACTATCCGTCAGTGATATATAATCCCGCTGTATCTGCTCTGGTTGGAACAAAG 3525
QY 5923 -----GAATCAGTCTGCTGATACGGAGGAGAGACAGCAACCAACGACGAGAGC 5974
Db 3526 GAGATCACCAACACAGACAGGAAATAGTAAGATGCTATCAAACTGAACCGGATATCGT 3585
QY 5975 TACAGCTGAACTGTGTTCCGGCGCTACGACGCTACATGAGTTCGCCGTTCCCGTGTGTT 6034
Db 3586 TATGAACATAAATTTGGGCATATCCGCTATGATGACCTTGGATACGCAATCACCTTT 3645
QY 6035 GACATTACCGCAACATGCG-----ATTTCGGAAACGAGGCGCATGCTGACCTGT 6088
Db 3646 GATGTCAATAAATAATTCGAGCTAAAACGAGGAAATAAGAGCGCCGAGCTCTAT 3705
QY 6089 AATCCC---CTGACTGAGCAGCTCTATGCGCGTTTTACTCCGTCACGACGAAACGGA 6144
Db 3706 TGTGCGGTTTCAAGGTGAAGTACGTTGCTGCTGATGTTTATAAACCAACAGACACA 3765
QY 6145 CTTTGATTAACGCTCAGCTGATTTCTGTGGAATGATGATGAGCT----- 6189
Db 3766 CTAGATAGTTATAAAGCGCTTCAATGCAAGGACTATATATCTTTGCTGATATGGCATCC 3825
QY 6190 --AAATGTCATCTCAGATATAGGGATTTTAAAGCG-----TCAGTCAACGAATTAAT 6241
Db 3826 AAGATATGACCCAGACAGACAGCAATGTTTATCGGTAATAGCTATCAACAATTTGAT 3885
QY 6242 ACGACACTGAGAAATTTATTAATAATGTTTTTTCAGACCTTCGCTTAATTTAT----- 6295
Db 3886 ACCAATAATGTGAGAAGTGAATTAACCGCTATGACAGGATTAAGATTCCTTCCTCG 3945
QY 6296 -TTTCTCAGTCAACGAGTTTAAATGATGATGTTAT-----CCACAGC 6337
Db 3946 GTAAGTACCGTAAAGACTATGGTTGGGAGATTAATTAACCTCAGCATGTTATTAACGGA 4005
QY 6338 GATTTCTCACTCTTTAATCTAAAACTACAAGTACTGTTTTTAC----- 6381
Db 4006 GATATTCCAACTATCAATTAACAAAGCCGATCAAGTGATTTAAAAATCTATATCTACCA 4065
QY 6382 TAATGAAGATTCCTCTCTTTTGAACCCAGAGCTTCATATTAAGCAAAATGTTTCGTGTT 6441
Db 4066 AAAATTAAGAATTTATTCATAATGGATATGAAGGACGAAAGCGCAATCAATGCAATCTGATG 4125
QY 6442 TGTGATGACTGCTGCGCATCGCACCTCAATCTACCATAGAAAATTCGTTTCAGCGAGGAT 6501
Db 4126 AATAAATATGGCAAACTAGGTGATAAATTTATGTTTATATCTAGCTTGGGGTCAATCCA 4185
QY 6502 AGAATTTGAGGAAATTAATTTTATGACGGCCAGCGCCGCGGATTTGACGGATTTGT 6561
Db 4186 AATAACTCGTCAATTAAGCTCATGTTTACCCCGTCTATCAATATAGCGGAAACCACT 4245
QY 6562 GG-----GAGTGGATGTTTCTAAATTCAAAAGTATAC 6592
Db 4246 GGACTCAATCAAGGGAGACTACTATTCACCGTGACCACTTATCCATCTAAAGTAGAA 4305
QY 6593 CAGGTGCGGAAAGAGAGCTGCTCACTGTAAAAATCTTATTCGTCACCTGCGCTAGT 6652
Db 4306 GCTTGATTCCTGGAGCAAAACGTTCTCTAACCAACCAAAATGCCGCCATTTGGTATGAT 4365
QY 6653 GGTTCGTGATGTTATTTATGATTCATCAATAAATATCTTACGCGGAATTTTGTGAGAT 6712

Db 4366 TATGCTACAGACTCTCTGAATAAACCAGGATGATCTTAAGCAATATATCTTTATGACTGAC 4425
Qy 6713 AARATGATAACCGCTTTAAATTAGCGGAGTACATCAAAAGTTAA----- 6757
Db 4426 AGTAAAGGACTGCTACTGATGTCTCAGGCCAGTAGAGATTAATCTGCAATTTCTCCA 4485
Qy 6758 -----TACGTGTGCTCTATTTGGCTCTCAA 6781
Db 4486 GCAAAAGTTCAGATAATAGTCAAGCGGTGGCAAGGCAAACTTTTACCGCAGATAAA 4545
Qy 6782 GATTTTGGAGTGTAAGTGTCTCATGCCGGCACTTCAGATATATGAATTAATTCGATGAT 6841
Db 4546 GATGTCTCCATTCAGCCATCACCTAGCTTTGATGAAATGAATATCAATTTAATGCCCTT 4605
Qy 6842 ATCATACTGACATCCGGCGTAATGGGACTGAAATTAATCC-----TGG 6886
Db 4606 GAAATAGACGGTTCGTGCTGAAATTTTATTAACAACCTCAGCCAGTATGATGTTACTTTT 4665
Qy 6887 CTTTCCGCTGAATGATATATGATAAGCTGAGTCTGCAATCCGGGAAATAATCTTTTCAAC 6946
Db 4666 ACCGCAITTTGGAGAGATGGCGCAAACTGGTTATGAAAGTTTCAGTATTTCTGTACC 4725
Qy 6947 ACBAATCGTGAGTTTTACGGTTAATACAGTATATTTGTTGAAGATGATTTGACGTG 7006
Db 4726 CTCAGGTAAAGTACCGATAATGCCCTGACCCTGACCATAATGAAATGGTGGCAATAT 4785
Qy 7007 ACGTTTACGTTACCGCTGTCGATCAGATAAAGTGTGTCGCCGCCCGGACGGCATA 7066
Db 4786 ATGCAATGGCAATCCTATCGTACCGCTGAAATACTCTATTGCGCCGCCAGTTGGTTGCA 4845
Qy 7067 TTAACCGTCAITTCGAAACATTA----- 7088
Db 4846 CGCGCCACCACCGAATCGATACAAATTTCTGATGATGAAACTCAGATATTCAGGAACCG 4905
Qy 7089 ----- 7088
Db 4906 CAGTTAGGCAAAAGTTTCTATGCTACGTTGCTGATACCTCCCTATACCTATCAACTCAT 4965
Qy 7089 -ATAATCACACTCCGTTATCGGATTAAGTAAATAACGGTGGCGGAGTATATTCGT 7147
Db 4966 GGTGATGAACGTTGGTTAAGCTTTATCAACATGTTGTTGATAATTAATTCACATATT 5025
Qy 7148 TTCACTCGGGTAACGATGTGGCGCTTATTGCGCTCAACCCCTCTTTGCGCCCAACTG 7207
Db 5026 ATCTATTACGGCAGCTAAACAGATACAAATATATAACATCAATTTATTCTCTTGAT 5085
Qy 7208 GTGACCGGGGGAATACCGGATTGACCAATCTT----- 7243
Db 5086 GATGTCCCATTTGAATCAAGATTATCAGCCAAAGTTTATATGACCTTCAAGAAATACCA 5145
Qy 7244 ----- 7243
Db 5146 TCAGATGGTACTGGTGGGCGCTCACTTTGTTAGATGATATAAGGAATAGTAACAATA 5205
Qy 7244 -----TCCATGGAGACCCAGAGGCTTACCGAACCGCCCTGGAAGAGGGAGTGT 7294
Db 5206 AACCTAAATCCATTTTGACCCATTTTGAGAGCGTCAATGTCTGATATATATAGTAGC 5265
Qy 7295 GTGTTTATGACTTCTCCGAGCAATGCCCTCTATTCTTGGGAGCTGTTCTATTACAG 7354
Db 5266 GAACCAATGGATTTACGCGCGCTTAACAGCGCTCTATTCTTGGGAACTGTTCTACTATACC 5325
Qy 7355 CCGATGATGTTGTTCCAGCGTTGTTGACGAACAGCACTTCCGGGAAGCCACCGCTGG 7414
Db 5326 CCGATGCTGTTGCTCAACGTTTCTGATGAACAGAACTTCGATGAAGCAACCGTTGG 5385
Qy 7415 CTGCAGTATGTCTGGAACCGCGCGGCACTGTGTAAACGGGTGCTGCAGAAATTACAC 7474
Db 5386 CTGAAATATGTCTGGAGTCCATCCGGTTATTTGTCACGGCCAGATTCAGAACTACAG 5445
Qy 7475 TGGAAATGCTCGCTCGGAGGAGGACACCGGCTGGAAACGACTCGCGCTGGACTCCATT 7534
Db 5446 TGGAACTGCGCGCTTACTTGGAAAGACACCAAGTTTGGAAACAGTATCTTTGGATTCCGTC 5505

Qy 7535 GACCCGATGCAATAGCCAGTAGTACGCCCATCGATTACAAAGTTCGCCACCTTTATGTCG 7594
Db 5506 GATCTGACGCGTAGCAGCAGCAGATCCAAATGCACTACAAAGTTTCAACTTTTATCGGT 5565
Qy 7595 TACCTGACACTGTGATTGGCCGCGGTGATGCCGCTTACCGGTGCTCGAGCGGACACC 7654
Db 5566 ACCTTGGATCTATTGATAGCACCGCGGACCATGCTTATCGCCAACTGGAACGAGATACA 5625
Qy 7655 CTTAAAGAGCCCGGATGTTGTTACGTCAGGCCCTCGAACCTTCTGGGCGAGAGCCCTAT 7714
Db 5626 CTCAGCAAGCGAAGATGTGTATATGCAAGCGCTGATCTATTAGGTGCAAAACCTTAT 5685
Qy 7715 ATTTCTTTGACCGGACTGTTGCGGCTTGACCTGGGTGACGACGACCGAGGTGACG 7774
Db 5686 CTACCGCTGATGACGACATGGAGTATCCACGACTAGACAGACCGCGGATATCACTACC 5745
Qy 7775 CGACGGGATTACACAGGAGGCCCTGCTGGCGTGGCGGTTGGTGGCCGCTCCCGAGACA 7834
Db 5746 CAAATGCTCACGACAGCGCAATAGTCGCTCTGCGCAGAAATATACCTACACCGCACCT 5805
Qy 7835 -----CGGACGGGAATTCCTGACGGCACTGTTCTCTCCGACGAGAAAGAGGTG 7885
Db 5806 TTATCATTTGGCAGCGCTAATACCTGACTGATCTTCTCTGCGCAAAATCAATGAAGTG 5865
Qy 7886 CTCAAAGGCTACTGCGCAAACTTTGGCACAGCGGCTCCATAACCTGGCCACACCTCTCC 7945
Db 5866 ATGATGAATTTACTGGCAGACATTTAGCTCAGAGAGTATACAATCTGGGTATAACCTCTCT 5925
Qy 7946 ATTGAGGCGCAGCGCTTTCCCTGCTGCTAGCCCAACCGCTCCGAACCGTCCGCCCTG 8005
Db 5926 ATCGACGGCAGCGCTTATCTGCCAATCTATGCCACACCGGCCGATCCGAAGCGTTA 5985
Qy 8006 CAGAGTCCGCTCTCAACAGCGCGAGGTTGTCAGCACTGTCGCGCGCGGTGATGCCG 8065
Db 5986 CTCAGCGCGCGCTTGGCACTTCTCAAGGTGAGGCAAGTACTACCGAATCATTTATGTCC 6045
Qy 8066 CTTTACAGTTTCCGCTCATGTGGAGAACCGCCGGGGGATGCTGCTGTCGACCGG 8125
Db 6046 CTGTGGGCTTCCGCGACATGCTGGAATAATGCGCGGCGCATGTTAGCAGCTCACCCAG 6105
Qy 8126 TTCCGCAACACACTGCTCGGTATTACGAGCGTCAAGATGCGGAGGCGCTGGGCCAAACTG 8185
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Qy 8186 CTCAGACCCAGGCAAGTGAATGATACGCGAGGCTTTCGCCAGCAGGATACGTCCTC 8245
Db 6166 TTACAAATATCAGGCCCGCGAGCTGATATTGACTTAACCTGAGCATTCAGGACAAACCAT 6225
Qy 8246 GAGGAATCGATCGCGATATTGCGCCCTGAGGAGAGCGCCGCGCGCGCAGATCGCT 8305
Db 6226 GAAGAATTGGATGCCGAGAAACCGGTGTTGGAATAATCCAAACGGGAGCACAATCGCG 6285
Qy 8306 TTTGAAACGTTTACAAAGTTGTACGAGGCGGACGCTCAACACCGCGCAAAAACAGGCCATG 8365
Db 6286 TTTGATAGCTACGGCAAACTGTACGATGAGATATCAACGCGGTGNAACCAAGCCATG 6345
Qy 8366 GACTTGATCCTCAGTTGCTCGGTGTCGGCATCAACCGCCCGCTCTTTTGGGCGAG 8425
Db 6346 ACCTACGAGCGTCCGCGCGCGGCTTACACGCGCATTCAGGCAATCCCTCTGCGCGGT 6405
Qy 8426 GCGCGCGCGATGCTGCCAATATTACGGGCTGCGCGCTCGGGGCTCCCGCTATGGG 8485
Db 6406 GCGCGCGGCTGATGTGTGCTTAACATCTTCGGCTTTGCGGCTGGCGGACCGCTTGGGG 6465
Qy 8486 GCACTATTTAAAGCCACCGCATCGCATCCAGGTGCTCTCCGATGCCACCCGCATATCA 8545
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Qy 8546 GCGGACAAAATCAGCCAGTCGGAAGTGTACCGCGCTGCGCGGAGGAGTGGGAAATCCAG 8605
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RESULT 8
US-10-435-835-1
; Sequence 1, Application US/10435835
; Patent No. 6717035
; GENERAL INFORMATION:
; APPLICANT: Patelli, Jim
; APPLICANT: Merlo, Donald
; APPLICANT: Herman, Rod
; APPLICANT: Roberts, Jean
; APPLICANT: Guo, Lining
; APPLICANT: Schafer, Barry
; APPLICANT: Sukhapinda, Kitisri
; APPLICANT: Owens Merlo, Ann
; TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin
; FILE REFERENCE: 50698
; CURRENT APPLICATION NUMBER: US/10/435,835
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 60/148,356
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 7551
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7548)
US-10-435-835-1

Query Match 4.5%; Score 848.8; DB 4; Length 7551;
Best Local Similarity 48.8%; Pred. No. 2.6e-225;
Matches 3662; Conservative 0; Mismatches 3347; Indels 495; Gaps 31;

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DB 1909 ATTACCACTGGCTGACATACACAGAGTGGAGTGTATTTCCAGCTATTTATCATGACCTCC 1968
QY 4409 ACGCAGTACGCTACCTGCTGACCCCGACATTCAGAACTCTGCTGCTCCCTCGCGCAAC 4468
DB |||||
DB 1969 ACCAGCTATAACAAAACGCTAACCGCTGAATTAAGAAATTTGCTGGATACCGTCTACCA 2028
QY 4469 GGACTGTGGGCGGTGAGCTGTTCCCGGAAACGCTCCCGCGAGTGGCGCTCCCTTTTATT 4528
DB |||||
DB 2029 GGTTTACAGGTTTGTATAAGACAAAGCAGATTTGTACATGTCATGGCGGCTTATT 2088
QY 4529 GCGCCCGCATGAGCTGAGCGCACCGGATACGGCGAAGGCGATGCTGATCTGGGCGGAC 4588
DB |||||
DB 2089 GCGGCCACCTTGCAATTTATCATCGGAAATGTTCGCCCACTCGGTACTCTTTGGGCAGAT 2148
QY 4589 CAGTTGAAGCCAGAGGGGCTGACCTGACGGAATTTTATTTCTTTTGGT----- 4635
DB |||||
DB 2149 AAGTTACGCCCGGACGGCGCAATGACAGCAGAAATTTCTGGACTGGTTGAATACT 2208
QY 4636 -----GATGAATGCGCGCCCAATGACGAGCAGCGGCGGCAAGATGGCAGGGTTCTGC 4687
DB |||||
DB 2209 AAGTATACCGCGGTTTCATCGGAAGCGGTAGAAACGCGAGGAACATATCGTTCAATTTGT 2268
QY 4688 CAAGCCCTGTGGCACTGACACTGATCATTCGGAGCACCAGCGCTCAGCAGCGCGAGCTG 4747
DB |||||
DB 2269 CAGGCTCTGSCAAATTTGAAATGGTTTACCAATTCACCGCGCATCAACGAAACGCGCTC 2328
QY 4748 ACGCTGCTGTGACGACGCGGAGCGTTCGCGACAGATGGCACCACATCTGCCC---CAT 4804
DB |||||
DB 2329 CGTCTATTGTGAACAAACAGAGATGTTTGGCGCTGCAACTGAGCAGCGCGCGCGCAT 2388
QY 4805 GACCTGCGGCGCTTCGCGACATTPACGCTGTTTTCATGCGCGTCTGTTAACCGCAGCGCAGC 4864
DB |||||
DB 2389 GATGCCCTTTCACTGATTATGCTGACACAGTTTTCGGGATTGGGTGAACGCACTAGGCGAA 2448
QY 4865 CATGCCGGGAGGTCTGACGCACTTTGAGACCGGAGAACTGTGCTGAGCCCTGCTGGCC 4924
DB |||||
DB 2449 AAAGCGTCTCTGCTGCTGAGCGCAATTTGAAGCTAACTCGTTAAACGCGAGAACTGGCT 2508
QY 4925 CGGSCCTGTACAGATG-----AGCAGGATGTGACCGGCGCTTTGGCGCAG 4972
DB |||||
DB 2509 GATGCCATGAATCTTTGATGCTAAATTTGCTGTGTGCAAGCCAGTATTCAGGACCAAAATCAT 2568

QY 4973 GTAGGGGGGCGGTGAACAGGCAACACAGCGGTGTTCCACTCTCTGGAGAGGTGGAACGAG 5032
DB |||||
DB 2569 CAACATCTTCCCCAGTTAACTCCAGAAAATGCGTCTCTCTGTTGGACATCTATCAATACT 2628
QY 5033 GCTGAGCAGTGGCTGGACATGAGTGAGACCCCTGTCCATTTAGCCCATCCGGTCTGGCTAGC 5092
DB |||||
DB 2629 ATCTGCAATGGGTTAATGTGCGCAACAATTTGAATGTGCGCCCAACAGGGGCTTTCCGCT 2688
QY 5093 CTGATTCGCCCTGAAGTACATCAATGTCTCGATGACAGTGCACCGTGTGTACAGCCAGTGG 5152
DB |||||
DB 2689 TTGGTGGGCTGGATTAATTTCAATCAATGAAGAAGAG---CACCGACTATGCCAGTGG 2745
QY 5153 CAGGTGTTATCCGCTCTGCTGCGAGCGCGGTGAAAGACGACAGAGCTCGCGCTGCAC 5212
DB |||||
DB 2746 GAAAAACGCGCAGCGGTATTAAACCGCGGTGTAATTTCAACAACAGGCTAAATACATTACAC 2805
QY 5213 GATTATCTGAGAGGGGACACAGCAGCGCCCTTTGTGGGTATTATCTGCGTAAATCT--- 5268
DB |||||
DB 2806 GCTTTTCTGGATGAATCTCGCAGTGGCGCATTAAGCACCTACTATATATCCGTTCAAGTCGCC 2865
QY 5269 --GGCACCGCAACATGGTATCCGGCGCGATGACCTCTTCGGGTATCTGCTGCTGGATAAT 5326
DB |||||
DB 2866 AAGCAGCGCGGCTATTAAAGCGGTGATGACTTGTATCAATACTTACTGATTGATAAT 2925
QY 5327 CAGGTGTGACGAGGTAAACCAACCGCATTCGCGAGGCGCATTCGCGGATACCGGCTG 5386
DB |||||
DB 2926 CAGGTTTCTGGGCAATAAACAACCGGATCGCGAAGCCATTGCCAGTATTTCAACTG 2985
QY 5387 TATATCAACCGGCGCTTAAACGGAAATAGAACTCAGCGCCATGCGAGAGGTGAGGGGCGT 5446
DB |||||
DB 2986 TAGCTCAACCGGCGATTGGAAAATGTGGAAGAAAATGCCAATTCGGGGGTATTACAGCGC 3045
QY 5447 CAGTTTTCCTGACTGGGTATCGTTCAACAAAGTTTACAGCACTCGGCGGGGTCTCA 5506
DB |||||
DB 3046 CAATTTCTTATGACTGGGACAAATCAATAAAGCTTACAGCACTTGGGCGGGTGTTC 3105
QY 5507 GAGCTGTTTACTATTCGGGAAACTACTCGAACCGGCTCGGTATTCGGGCGACACGCG 5566
DB |||||
DB 3106 CAATTAGTTTACTACCGGAAACTATTTGATCCGACCATGCGTATTCGGCAACCAAA 3165
QY 5567 ATGATGACACCTGCTGCTGAGTGTGTCAGCAGAGCAGTATCAACCGCGATACCGTGGAG 5626
DB |||||
DB 3166 ATGATGACCATTTACTGCAATCCGTGAGCAAGCCAAATTAACGCGGATACCGCTGAA 3225
QY 5627 GATGCTTTTAAACCTATCTGACCACTGTGACAGATTTGACGAGTTCGCACTGACCTGAC 5686
DB |||||
DB 3226 GATGCTTTTATGCTTATCTGACATCGTGTGAAACAGTGGCTAATCTTAAAGTTATTAGC 3285
QY 5687 GGATATCACGATAACCGCAGCATGACGAGGAGCTACATGCTATGTGGGTGCGAGCATC 5746
DB |||||
DB 3286 GCATATCACGATAATATTATTAACGATCAAGGCTGACCTATTTTATCGGACTCAGTGAA 3345
QY 5747 ACAGATCAGACTAATCTGGTATCTGGCGAGCGCCAAACACAGCAAAATTCGAAGCTCAATG 5806
DB |||||
DB 3346 ACTGATGCGCGTGAATATTATTGGCGCAGTGTGATCAGAGTAAATTAACAGCGGTAAA 3405
QY 5807 ATGCGCGGAACTCTGGACCGGATGGACAAAATTAACCTGCGGATGAATCCGTGGTCA 5866
DB |||||
DB 3406 TTCGCGGCTAATGCTGGAGTGAATGGCATAAAATTTGATTTGCAATTAACCCCTTATAAA 3465
QY 5867 GATCTTGTGCTGCTGTTTTCACAGTTCGCGCTTATCTGCTGCTGGGTGCAAGA--- 5922
DB |||||
DB 3466 AGCACTATCCGTCAGTGATATAAATCCGCGCTGTATCTGCTCTGTTGGTGGAAACAAAG 3525
QY 5923 -----GAATCAGTCTGCTGATACGGAGCAGAGACGACAAACCAACGACGACAGAGC 5974
DB |||||
DB 3526 GAGATCACCACAAACAGACAGGAAATAGTAAAGATGGCTATCAAACTGAAACGGATTAATCGT 3585
QY 5975 TACACCTGAAACTGTGTTCCCGCGCTAGCAGGTGATGAGTGTCCCGGTGCTGCTTC 6034
DB |||||
DB 3586 TATGAATAAATTTGGCGCATATCCGCTATGATGGCATTGGAATACGCCAATCACCTTT 3645
QY 6035 GACATTACCGGCAACATCGC-----ATTTCGGGAAACGCGAGGCGCATGTGACCTGT 6088

Db 3646 GATGTCATAAATAAATATCCGAGCTAAACCTGGAATAAATAGAGCGCCGAGCTCTAT 3705
 QY 6089 AATCCC-----CTGACTGAGCAGCTCTATTCGCGGTTTTACTCCGTCACACGAAAGCCGA 6144
 Db 3706 TGTGCCGGTTATCAAGGTGAAGTACGTTGCTGGTGATGTTTATTAACCAACAAGACACA 3765
 QY 6145 CTTTGATAACGCTCAGCTGATTTCTGTGGATTAAGTATGACGCT----- 6189
 Db 3766 CTAGATAGTTATATAAAGCGTTCAATGCAAGGACTATATATCTTTGCTGATGCGCATCC 3825
 QY 6190 --AAATGTCATCTCAGATATAGGATTTTAAAGCG-----TCAGTCACGAATTTAAT 6241
 Db 3826 AAAGATATGACCCCAAGACAGACAAATGTTTATCGGGATAATAGCTATCAACAAATTTGAT 3885
 QY 6242 ACGAGCACTGAGAAATTTTATTAATAATGTTTTTTTCAGACCTTTCCGCTAATTAT----- 6295
 Db 3886 ACCAATAATGTCAGAGAGTGAATAACCGCTATGCGAGAGGATTTATGAGATTCCTTCCTCG 3945
 QY 6296 -TTTGTCAGTGCACAGGTTTAAATTTGATGATGTTAT-----CCACAGC 6337
 Db 3946 GTAAGTAGCCGTAAGACTATGTTTGGGGAGATTATTAACCTCAGCATGGTATATAACGGA 4005
 QY 6338 GATTTCTCACTCCTTAATCTTAACTTAACTACAAGTACTGTTTTTAC----- 6381
 Db 4006 GATATCCAACTATCAATTAACAAGCGCATCAAGTGAATTTAAATCTATATCTCACCA 4065
 QY 6382 TAATGAAGATTCCTCTCTTTTGACGCCAGAGCTTCATATTTACAGCAAAATGTTTCGTGTTT 6441
 Db 4066 AAATTAAGATTTATCATATGATATGAAGGACAGAGCGCAATCAATGCAATCTGATG 4125
 QY 6442 TGTGTACTGCTGGCATCCCACTCAATCTACATAGAAATTTGTTTCAGCGAGGAT 6501
 Db 4126 AATAAATATGCAAACTAGTGTAAATTTATTTGTTTATTAATGTTTACTAGCTTGGGGGTCAATCCA 4185
 QY 6502 AGAATTTGAGAAATTAATTTTATGAGCCAGGCGCGCGGAGTTTGACCGAATTTGT 6561
 Db 4186 AATACTCTGCAATAAGCTCATGTTTACCCCGTCTATCAATATAGCGGAACACAGT 4245
 QY 6562 GG-----GAGTGGATGTTTCTAATTCAAAGTATAC 6592
 Db 4246 GGACTCAATCAAGGAGACTACTATTCACCGTGACACCACTTATCCATCTAAAGTAGAA 4305
 QY 6593 CAGTCCGAAAGAGCAGTTGTTGTCACGTAAATCTTATTCGTCAGTCCGCTGAT 6652
 Db 4306 GTTGGATTCCTGGAGCAAAACGTTCTTAACCAACCAATGCGCCATTTGTTGATGAT 4365
 QY 6653 GGTTCCTGTTGATTTATTTGATTCATCAATAAATACTTCAGCGGAAATTTTGTGAGAT 6712
 Db 4366 TATGCTACAGACTCTCTGAATAAACCGGATGATCTTAAGCAATATATCTTTATGACTGAC 4425
 QY 6713 AAAATGATAACCGCTTTAATTTAGCGGAGTACATCAAAAGTTAAT----- 6757
 Db 4426 AGTAAAGGAGCTGCTACTGATGTTCTCAGGCCAGTAGAGATTAATACTGCAATTTTCTCCA 4485
 QY 6758 -----TACGTGTCGTCTATTGGCTCTCAA 6781
 Db 4486 GCAAAAGTTTCAATAATAGTCAAGCGGTGGCAAGGACAACTTTTACCGGATATAA 4545
 QY 6782 GATTTTTGGAGTGAAGTCCCTCATGCGCACTTCAGATATATGAATTAATCATGATGAT 6841
 Db 4546 GATGTCCTCAATTCAGCCATCACCTAGCTTTTATGATGAATGAATTAATTAATGATGCTT 4605
 QY 6842 ATCATACTGACATCGGGGTTAAATGGGACTGAAATTAATTC-----TGG 6886
 Db 4606 GAAATAGACGGTTCTGGTCTGAAATTTTATTAACCACTCAGCCAGTATGATGTTACTTTT 4665
 QY 6887 CTTTCGCTGAATGATATGATAAGCTGAGTCTGCAATCCGGAATAATCTTTTCAAC 6946
 Db 4666 ACCGATTTGGGGAGTAGCGCGCAACTGGGTTATGAAAGTTTCAAGTATTCCTGTTACC 4725
 QY 6947 ACCAAATCGCTGAGTTTACCGTTTAAATACAGTGAATTTGTTGAAGATGAGTTTGACGTG 7006

Db 4726 CTCAGGTAAGTACCGATAATGCTGACCTGACCTGACCACTAATAAGAAATGGTGGCAATAT 4785
 QY 7007 AGTTTTAGTTTCAACCGCTGTCATCAGAAATACGTCGTGCTGGCGCCGCGGACGCCATA 7066
 Db 4786 ATGCAATGGCAATCTCATCGTACCGCTGAATCTCTATTTGCCCCGACGTTGTTGCA 4845
 QY 7067 TTAAACCGTCATTTGAAAACTTA----- 7088
 Db 4846 CGCGCCACCAACCGGAATCGATACAAATCTGAGTATGGAATCTCAGAAATTTACGGAACCG 4905
 QY 7089 ----- 7088
 Db 4906 CAGTTAGGCAAAAGTTTCTATGCTACGTTGCTGATACCTCCCTATAAACCTATCAACTCAT 4965
 QY 7089 -ATAATGACACTTTCGTTTATCGATTACGTAAATAACGCTGGCGCGCAGTATATTCGT 7147
 Db 4966 GGTGATGAACGTTGTTTAAAGCTTTATATCAAAACATGTTGTTGATAAATTTACATATT 5025
 QY 7148 TTCACCTGCGGGTAAACGATGTCGCTTATTCGCTTCAACACACCTCTTTGCGCCGCAACTG 7207
 Db 5026 ATCTAATCAGGCGCAGTAAACATAAATAAATACATCAATTTATTTCTCTCTGAT 5085
 QY 7208 GTCGACCGGGCGAATACCGGGATGACACCTTT----- 7243
 Db 5086 GATGTCCTCAATGCAATCAAGATTTATCAAGGTTTATATGACCTTCAAGAAATCAACCA 5145
 QY 7244 ----- 7243
 Db 5146 TCAGATGCTACCTGCTGGGGCCCTCACTTTGTTGAGATGATAAAGGAATAGTAACAATA 5205
 QY 7244 -----TCCATGGAGACCCAGAGGCTTTACCGAACCCGCTCGGAAGAGGGAGTGTAT 7294
 Db 5206 AACCCTAAATCCATTTGACCCATTTTGAGAGCGTCAATGTCCTGAATAATATTAGTAGC 5265
 QY 7295 GTGTTTATGGAATCTTCGCGGACCAATGCCCTCTATTTCTGGAGCTGTTCTATTACAG 7354
 Db 5266 GAAACCAATGGATTTACGCGCGCTTAAAGCCTCTATTTCTGGAACTGTCTTACTATACC 5325
 QY 7355 CCGATGATGCTGTTCCAGCGGTTGTTGAGGAACAGCACTTCCCGGAAGCCACCCGCTGG 7414
 Db 5326 CGATGCTGCTGCTCAAGCTTTGCTGATGAACAGAACTTCGATGAACCCACCGTTGG 5385
 QY 7415 CTGCAATGATGCTGGAACCCGCGGACGTTGGTAAACGGGGTGTGTCAGAAATTHACACC 7474
 Db 5386 CTGAATATGCTGAGTCCATCCGTTTATTTGTCACCGGCAGATTCAGAACTACCAG 5445
 QY 7475 TGGAAATGCTGCTGCGTGGAGGACACCGCTGGAACAGCTCCGCGTGGACTCCATT 7534
 Db 5446 TGGAACTGCGCGCGTTACTTGGAAAGACACAGTTGGAACAGTATCTTTGGATTCCGTC 5505
 QY 7535 GACCCCGATGCAATAGCCAGTACGACCCCATGCAATTACAAGTCCGCCACCTTTATGTCG 7594
 Db 5506 GATCTGACGCGGTAGCAGACGATCCAAATGCACTACAAGTTTCAACTTTTATGCGT 5565
 QY 7595 TACCTCGACCTGCTGATTTGCGCGGTGATGCGCCTACCGGCTGTGAGCGGGACACC 7654
 Db 5566 ACCTTGGATCTATTGATAGCAGCGCGGACCAATGCTTATCGCCAACTGGAACAGATACA 5625
 QY 7655 CTTAAACGCGCGGATGTTAGCTCCAGGCCCTGAACTCTTGGCGGACAGCCCTAT 7714
 Db 5626 CTCACGAAGAGATGTTGATATGCAAGCGCTGCACTCTATTAGTGACAACTTAT 5685
 QY 7715 ATTTCTTTGACCGGCTGCTGCGGTTGACCTTGGGTGACGACGACGAGGAGTGAAG 7774
 Db 5686 CTACCGCTGAGTACGATGAGTATCCAGACTAGACAGAGCCCGGATATCACTACC 5745
 QY 7775 CGACGGGATTAACAGAGGCGCTGCTGCGCGGTGCGCGGTGTTGTCGCTCCCGGACACA 7834
 Db 5746 CAAAATGCTCACGACAGCGCAATAGTCGCTCTCGCGGCAATATACCTACCGCGGACCT 5805
 QY 7835 -----CGGACGGGAATTCCTGACGGCACTGTTCTCTCCGACGACGAGAGCGGTTG 7885
 Db 5806 TTATCATTTGCGAGCGCTAATACCTGACTGATCTCTTCTCTGCGCAATCAATGAAGTG 5865

; FEATURE:									
; OTHER INFORMATION: Description of Artificial Sequence:hemicot tcda									
US-09-637-048C-3									
Query Match									
Best Local Similarity 4.3%; Score 815.2; DB 4; Length 7577;									
Matches 3641; Conservative 0; Mismatches 3368; Indels 495; Gaps 31;									
QY	2510	CTGACGGATTATTCCTGGGTTCTGTTTCCCGAGGTCAAAAAATCACTGGCGACGCTG 2569							
DB	66	CTCACTGACATCTCCACAGCTCTCTTCAAGAGTTCAGACAAACAAGTCTCTGAGCACCTC 125							
QY	2570	TGATGGGAGAGTCTGCTATCTGTACGTACGGCCGACGACGACGACGACGACGACG 2629							
DB	126	TCTGTGTCGAGACCCATGACCTCTACATGACGCTCAGCAGCTCAGAGGACGACGAG 185							
QY	2630	CTCACCGAATCCCGTATCTGGCCGCGGAATCCCTACTGCTGAATGCGGTTGCGCTG 2689							
DB	186	CTCTAGAGCTAGGATCTCAAGAGGGCTAACCCCACTCCAGAACGCTGTCCACCTC 245							
QY	2690	GGAATACGGCAGGCA---GCCGCGAGTCGCGAGCTATGATGACTGTTGGCTCCCGCA 2746							
DB	246	GCCATCTTGGCTCCAAACGCTGAGTTGATTGGTTACAACAACCAAGTTCTCTGGCAGAGCT 305							
QY	2747	GACGTTTCCGCGCCGCTCGGTGGCTCCATGTTCTCACGGCGGCTATCTGACC 2806							
DB	306	AGCCAGTACGTGGCTCTGGTACAGTCTCTCTCCATGTTACGCCAGCGCTTACCTCACT 365							
QY	2807	GAGCTGTACCGTGAGGCGAAGACCTGCATCCGCGACACCTCGCTGTTCCGGCTGGACATC 2866							
DB	366	GAGTTGTACCGGAGGCTAGNACCTTCATGCTTCTGACTCCGCTACTACTTGGACACA 425							
QY	2867	CGGCGTCCGACCTGGCGGCTGGCCCTTAGCCAGATAATATGACGACGAGCTCTCC 2926							
DB	426	CGCAGACGACCTCAAGAGCATGGCCCTCAGCCCAACAGAACATGACATCTGAGTTGTCC 485							
QY	2927	ACCTGAGCTGTCCAAATGAGTACTGTATCGCGGTATCGGCGAGCGGAGGCTTGAC 2986							
DB	486	ACCTCTCTCTTGAGCAACGAGTCTCTTGAGTCCATCAAGACTGAGCAAGTTGGAG 545							
QY	2987	GAGCAGC---GTCAAGGAGCTGCTCGCGGATATCGCTGACCGGCTGACCCCTAT 3043							
DB	546	AATACACCAAGGTCTAGAGATGCTCTCCACCTTCAGACCAAGCGGTGCACTCCATAC 605							
QY	3044	ACTGGCGCTACGAGGCGCGCGCAAGCCATTTCTGGTGACGACCGCGCTGATGGG 3103							
DB	606	CATGATGCCCTACGAGAACGTCAGGAGGTCTATCCAACTTCAGACCCCTGCTTGACAA 665							
QY	3104	TTCAAGCGTAAATCCGATGTGGCGCAGCTTATGACCCCTGCCATGCTGGCCATTGAA 3163							
DB	666	CTCAAGCTTCTCAGCCATTGCTGGTTGATGACACGAGCATCTTCTCGGTATCAAC 725							
QY	3164	GCGGATATTTACGCGAGCTGTATCAGATATCGCCGAGAAATTAACGACAGAGTTAC 3223							
DB	726	GCTTCCATCTCTCTGAGTTGTTCAACATCTTGACTGAGGAGTCACTGAGGCGCAACGCT 785							
QY	3224	GAACCACTCTGGATAGATTTGTTGATATGCTCCCTCCCTCCTCAGTCTTCTTATGAT 3283							
DB	786	GAGGAGTTGTACAGAGAGACTTCGGCAACATGAGCCAGCCTCTCTTGCAATGCTCTGAG 845							
QY	3284	GCACTTGCAACATTTTATGATCTTGATTACGATGAGCTAACTTCTGTTTATTTGTTCAATGAGG 3343							
DB	846	TACCTCAAGAGGTACTCAACTCTCTGATGAGGAGCTTCT-----CAATTCAATT 896							
QY	3344	CTGACATTTTCAATCCAAACATGAATACTAATTAATAGTCAATTAAGTGTGTTACT 3403							
DB	897	GGCAAGGCTTCCAACTTCGCTCAACAGGAGTACAGCAACACCAAGCTCATCACTCCAGTT 956							
QY	3404	CTGAATGAAGCACTGGTTTAAATAACTATATCATCATTTATTAAAGACGCTAGGCGGAGAC 3463							
DB	957	GTGAATCTCTGTATGGCAGTGTGAAGTCTACCGCATCAACGTGAGTACACCAACAAC 1016							
QY	3464	TCACAGCAGATTAAACCTGAGCTTATACCTTATGGGATGGAAACATATCTTTATAATTTC 3523							

DB	1017	GCCTACCAATGATGATGTTGTTGCCATTCGGTGGTGAACATCAGACTTCAGCTAC 1076							
QY	3524	AGCGTGGTGTCAACGATATCAGAGATAGTTTCAAACCTAGGCTCGTTAGTTCTAACAGT 3583							
DB	1077	AGTTTCAAGAAGTCTTACAAAGCCTCTACCTCTCCATCAAGTTGAACGACAGAGGAG 1136							
QY	3584	AGCAATCTTTTACTCTGGGATATCAGCTTCAAAAGGGTTCGCTATAGCATTCCTGTT 3643							
DB	1137	CTTGTGAGGACTAGGGTCTCTCAAGTGAACATTTGAGTACTCTGCGCAACATCAACCTC 1196							
QY	3644	GAATAGATAGAGAAAGTTAAATCATGGAT---CACAATAGGATTCAGTAGGAAAGG 3700							
DB	1197	AACACAGCTGACATCTCAACCATTCAGATTGGTTTGACAGAGTCTTTCCTCTGGC 1256							
QY	3701	GGGGATATTTACTCAACAGTAACTTCACTCTGATGTAATATGATCTCGCGATATTCATT 3760							
DB	1257	TCTTGGGCTACGCTGACGCAAGTTCACTGTGAGGAGTACCAACAGTACTCTTTTCTCTC 1316							
QY	3761	CTTAATTAATAAAGTTATCCGCTATACAGGCGACGGGATGACCAACGCGGAAATA 3820							
DB	1317	TTGAAGCTCAACAGGCAATTCGTCTCAGCAGAGCCACTGAGTTGTCTCCACCATCTTG 1376							
QY	3821	TATCAAAATCACCAATATTTCTTAATAACGCTCTCACCATTTGACCATCGGTCCTGATGATA 3880							
DB	1377	GAGGCAATGTGAGGCTCTCTCAACCTTGACATCAACACATGATGTCTTGGCAAG 1436							
QY	3881	ATCTTCTGGTCCGTACCTGATGCTCATCTATCAGCTTGATGTGGCCGCTCAGTGATA 3940							
DB	1437	GTCTTCTTCTCACCAAGTACTACATGCAACGCTACGCGCATCCATGCTGAGACTCATCTATC 1496							
QY	3941	TTGTGCAACGGAAACCATCAGTGACAGGCTTTCAGCGGCAAAACGCGCTGTTTCACACG 4000							
DB	1497	CTCTGCAAGCAACCATCTCTCAACGCTCTAGACAAACAGCTTCCAGTTCCAGG 1556							
QY	4001	CTGTTCAACACCCCGCTGAACGCGCAGCTGTTTCTGAGATGATACCCCTTCGAC 4060							
DB	1557	CTCTTCAACACCTCTCTCTTGAACGCGCAGTACTTCTCCACTGCTGATGAGGAGATTGAC 1616							
QY	4061	TTACGCTCTGAAGCACCGGAGTGTTCCTGCTCAGCGTACTGAAACGCGCATTTTAC 4120							
DB	1617	CTCAACTCTGGTCTCCAC---AGGTGACTGGAGAAAGACCATCTTGAAGAGGCGCTTCAAC 1673							
QY	4121	ATCAGCGCTCGGGCTTTCACGCTCTGCGAGTTGGCGAGCGTGACAGCAGCGCTGG- 4179							
DB	1674	ATTGATGATGCTCTCTCTCTCTCTCTTGAAGATCACAGATCAACGACAGGATGSC 1733							
QY	4180	--GTTTGTGCTGCTGACAAATATCGCGCACTCTACCGAGTGAACCTCTCTGGCTGAC 4237							
DB	1734	AAGATCAAGAACAACTTGAAGAACCTTTCACACCTCTACATTTGGCAAGTTGCTTGCAGAC 1793							
QY	4238	ATCCAGCACTATCCGCTGGTGGCTGTCAATGTTGCTGCTCTCCCTTTTCAGCGG 4297							
DB	1794	ATCCACCAACTCACCATTGATGAGTTGAGCTCTTGTCTCATTTGAGTGGGCAAG 1853							
QY	4298	GTGGCGCGCGGCTCGCTGTCCGATATGAG-----CTGACGCGAGTTTCTGTACCAAG 4348							
DB	1854	ACCAACTCTCTGCAATCTCTGACAGCAGTTGGCAACCTCATAGGAAGTTGAACACC 1913							
QY	4349	ACCACCACTCTGCTCAGGAGCGGGCTGGAAGGTCAGCGATGTTTCTGTGATGCTGACG 4408							
DB	1914	ATCACCTCTCTGGCTTCCACCCAGAGAGTGTCTCTTCTTCAACTCTTCAATCATGACAGCAG 1973							
QY	4409	AGCAGTACGGTACCTGCTGACCCCGCATTTGAGAACTGTCTCGCTTCCCTTTCGCGCAAC 4468							
DB	1974	ACCTCTCAACAGACCTCTCTCTGTAGATCAAGAACTCTTGGACACAGTCTACCAAC 2033							
QY	4469	GGAAGTCTGGCGCGTGTGTTTCCGGAACAGCTCCCGGGGATGGCGCTCCCTTTATT 4528							
DB	2034	GGTCTCCAAGGCTTCGACAGGACAGGCTGACTTGTCTTCACTCATGTGCTCCCTACATT 2093							
QY	4529	GCAGCGCATGAGCTGGACCGCACGATACGCGAAGGCGATGCTGACTTGGCGGAC 4588							

Db 2094 GCAGCCACCCCTCCAACTCTCTCTGAGAAAGTGGCTCACTCTGTCTTGTCTGGGCTGAC 2153
Qy 4589 CAGTTGAAGCCAGAGGGGCTGACGCTGACCGAAATTATTTCTTTTGGTGATGAATCCGCC 4648
Db 2154 AAGCTCCAACTGGTGATGGTGGCCATGACTGCTGAGAAGTTCTGGGACTGGCTCAACACC 2213
Qy 4649 CAAA-----TGACGAGCAGCGGGCCGACATGGCGAGGTTCTGCG 4687
Db 2214 AAGTACACACGAGGCTCTCTGAGGCTGTGAGACTCAAGAGCACATTTGTGCAATACTGC 2273
Qy 4688 CAAGCCCTGTGGCACTGGCACTGATCATCCGAGCAGCCGCTCAGCAGCGGAGGTG 4747
Db 2274 CAGGCTCTTGACAGTTGGAGATGGTATACCACTCCACTGGCATCAACGAGAACGCTTTC 2333
Qy 4748 ACGCTGCTGGTCAAGCCGCGGAGCTTCCGCAAG--ATGGCACCATCTGCCCAT 4804
Db 2334 AGACTCTCTGTCACCAAGCCTGAGATGTTGGTGTGCCACAGGTGCTGACCTGTCTCAT 2393
Qy 4805 GACCTGCCGCGCTTGGCGACATTAACGCGTTTTATGCGCGTCTGTTAACCGCAGCGGAGC 4864
Db 2394 GATGCTCTCTCCCTCATCATGTTGACCAAGTTGGTGAAGTGGTCAAGCTCTTGGTGAG 2453
Qy 4865 CATGCCGGGAGGTCTGACCGCACTTGAGACCGGAGAACTGTGCTGACGCCCTGCTGGCC 4924
Db 2454 AAGGCTTCTCTGCTTGGCTGCTTCCGAGCCAACTCCCTCACTGCTGAGCAACTTGTCT 2513
Qy 4925 CGGCGCTCTCACAGAAATGACAGATGTGACCGCGCTTGGCGAGGTGAGGGGGCC 4984
Db 2514 GATGCCATGAACCTTGATGCCAACTCTTGTCTCAAGCTTCCATTCAGCTCAGAACCA 2573
Qy 4985 GGTGAACAGGACA-----ACAGCGTGTTCACCTCTGGGAAGAGGTGGACAG 5032
Db 2574 CAACACCTCCCACTGTCACTCCAGAGAACGTTCTCTCTGCTGACCTCCATCAACACC 2633
Qy 5033 GCTGAGCAAGTGGTGAGCATGAGTGAGACCTGTGCTCAATTAAGCCATCGGCTGGCTAGC 5092
Db 2634 ATCTCCAAATGGGTCAACGCTGGCTCAGCAACTCAACGCTGGCTCCCAAGGTTGTCTGCT 2693
Qy 5093 CTGATTGCCCTGAAGTACATCAATGTGTCGATGACAGTGCACCGTTGTACAGCCAGTGG 5152
Db 2694 TTGGTGGTCTTGACTCATCTCA-----GTCCATGAAGGAGACCAACCTACGCTCAATGG 2750
Qy 5153 CAGGTGGTATCCGCTCTGCTGAGCGCGGCTGAAAAGCAGCCAGAGCTCGGCGCTGCAC 5212
Db 2751 GAGAAACGAGCTGGTGTCTTGAAGTCTGCTGCTCACTCCCAACAGGCCAACCCCTCCAT 2810
Qy 5213 GATTATCTGAGGAGGGGACAGCAGCGGCTTTGTGGTATTAATCTGGCA 5272
Db 2811 GCTTTCTTGGATGAGTCTGCTCTGCTGCTCCACTACTACATCAGGCAAGTGGCC 2870
Qy 5273 CCGAACATGGTATCCGG-----GGCGATGACCTCTTGGGTATCTGCTGGTAAAT 5326
Db 2871 AAGGAGCTGTGCGCATCAAGTCTCGGATGACCTCAACCAATACCTCTCTCATTTGACAA 2930
Qy 5327 CAGGTGTGAGCAAGTAAAAACCAACCGCATTCGGAGGCGCATCGCGGATACAGGCTG 5386
Db 2931 CAGGTCTCTGCTGCTGCACTCAAGCAACAGGATGCTGAGGCGCATGCTTCCATCCAACTC 2990
Qy 5387 TATATCAACCGGCGCTTAAACGSAATAGAACTCAGCGCCATGGCAGAGGTGAGGGGCGT 5446
Db 2991 TACGTCAACCGGCTCTTGAGAAAGTTGAGGAGAACGCCAACTCTGGTGTCTATCTCTCGC 3050
Qy 5447 CAGTTTTTCACTGACTGGATACGTTCAAAAGTTTACAGCACTGGGGGGGCTCTCA 5506
Db 3051 CAATTTCTCATCTGGCAAGTACAAAGAGGTAATCCAAAGGTAATCCACTGGGCTGGTGTCT 3110
Qy 5507 GAGCTGGTTTACTATCCGGAAAACTACCTCGACCGAGGTCGTTATCGGGCAGACCGGC 5566
Db 3111 CAATTTGTCTACTACCCAGAGAACTACATTAACCAACCATGAGGATTTGGTCAGAACAG 3170
Qy 5567 ATGATGACACCTCTGCTGCTGTCAGCGCAGAGCATATCAACCGGATPACCGTGGAG 5626
Db 3171 ATGATGATGCTCTCTTGGCAATCTGTCTCCCAAAGCCAACTCAACGCTGACACTGTGGAG 3230

Qy 5627 GATGCTTTTAAACCTATCTGACCAAGTTGAGCAGATTTGCAATCTGAACACTGTGACG 5686
Db 3231 GATGCTTTTATGAGTACTACTCCTCTTGAGCAGAGTTGCAACCTCAAGTCACTCTCT 3290
Qy 5687 GGATATCAAGCAATACCGCAGCATGACGAGGGGACTACATGGTATGTGGGTGCGAGCATC 5746
Db 3291 GCTTACCATGACCAACATCAACAGCAAGGTCTCACTACTTCAATTTGGTCTCTCTGAG 3350
Qy 5747 ACAGATCAGACTAATCTGGTACTGGCAGCGCCAAACCAAGCAAAATTCAGACTCAATG 5806
Db 3351 ACTGATCTGGTGAAGTACTTGGAGATCCGTGGACCAAGCAAGTTCAACGATGGCAAG 3410
Qy 5807 ATGCCCGCAATGCTCGGACCGGATGACAAATAATTAACTCGCGAAATGAATCCGTGGTCA 5866
Db 3411 TTGCTGCAAAAGCTTGGTCTGAGTGCAAGATGACTGCTGCTTCAACCAATACAG 3470
Qy 5867 GATCTTGTGCTCGGTTTTTTTCAACAGTCCGCTTTATGTGCTGGGTGCAAGAGAAAT 5926
Db 3471 TCCACCATCAGACCTGTCTATCAAGAGCGCTCTACTTGTCTGGCTTGAGCAGAG 3530
Qy 5927 CAGT-----CTGCTGATAACGAGCAGAGCAGGACCAACCAACGAGAGC 5974
Db 3531 GAGATCAACCAAGCAAACTGGCAACTCCAAGGATGGTTACCAAACTGAGACTGACTACCGC 3590
Qy 5975 TACAGCTGAAAACTGCTGTTCCGCGCTACGAGGTACATGGAGTTCCTCCGCTGCTGTTCC 6034
Db 3591 TACAGTTGAAGTTGGTCTCATCCGCTACGATGCTGCTGGAACACTCCAACTCACCTTC 3650
Qy 6035 GACATTAACCGCAACATCGCATTTTCCGGAACCGAGGCGATGATGACCTGTAATCCC 6094
Db 3651 GATGTCACCAAGAGATCAGGAGTTGAAGTTGGAGAAGAACGCTGCTCCTGGTCTCTAC 3710
Qy 6095 CTGACTGAGCAGCTCTATTGGC-----GTTTTACTCCGTACACGAGCAAGCCGGA 6144
Db 3711 TGCGCTGTTTACCAAGGTGAGGACACCTCTTGGTCTATGTTCTACAAACGAGCAAGCACC 3770
Qy 6145 CTTTGTAT-----AACGCTCAGCTGATTTCT 6169
Db 3771 CTTGACTCTTACAAAGAGCTTCCATGCAAGGTCTCTACATCTTCGCTGACATGGCTTCC 3830
Qy 6170 GTGATTAATGATATGACGCTAA-----ATGCTATCTCAGATATAGGGATTTTT 6217
Db 3831 AAGGACATGACTCCAGAGCAAGCAAGCTCTACGCTGACAACTCTTACCAACAGTTCCAG 3890
Qy 6218 AAGAGCTCAGTCAAGATTTAATAACGACATGAGAAATTTAATAATATGTTTTTCA 6277
Db 3891 ACCAAACACGTCAGGCGTGTCAACCAACAGATACGCTGAGGACTACGAGATCCCAAGCTCT 3950
Qy 6278 GACCTTCCGCTAATTTTGTGTCAGTGAACGAGTTTAAATGATGATGTTATCCACAGC 6337
Db 3951 GTGAGTCTCGAAGGACTACGGCTGGGTGACTACTACCTCAGCATGGTGTACAACGGT 4010
Qy 6338 GATTTCTCACTCTTAAATCTAAACCTACAAAGTACTGTTTTTACTAATGA----- 6387
Db 4011 GACATCCCAACCATCACTACAGGCTGCTCTTCCGACCTCAAAATCTACATCAGCCCA 4070
Qy 6388 -----AGATTCTCTCTTTTGAACGAGCTTCAATATTACAGCAAAATGTTTCTGTTT 6441
Db 4071 AAGCTCAGGATCATCCAAACGCTACGAGGTGAGAGGAGGAGGAGGAGGAGGAGGAGG 4130
Qy 6442 TGTATTGATCTGCTGGCATCGCACTCAATCTACATAGAAAATTCGTTTCCAGGAGGAT 6501
Db 4131 AACAGTACGGCAAGTTGGGTGACAGTTTCTTGTCTTGTGTTGTGTTCAACCCCA 4190
Qy 6502 AGAATTTGAGAAATTAATTTTTATGAGCGCGAGGCGCGGAGTTTGTACCGATTTGT 6561
Db 4191 AACAAAGCTCCAAAGCTCATGTTCTAACCAGTCTACCAATCTCTGGCAACACCTCT 4250
Qy 6562 GG-----GAGTGGATGTTTCTTAATTTCAAAAGTATACAGGTGCGGAAAAAGAGAGTTG 6614
Db 4251 GGTCTCAACCGGGTAGACTCTTGTTCACAGGGACACCACTACCCCAAGCAAGGTTGGAG 4310

Db 6471 GCCATTGCTGAGGCTACCGGTTTACGTCATGGAGTCTCTGCCAACGTCATGAACACTGAG 6530
Qy 8546 CGGACAAATCAGCCAGTCGGAAGTGTACCGCGCTGCCGGGAGGAGTGGAAATCCAG 8605
Db 6531 GCTGACAGATCAGCAATCTGAGACTACAGAGGCGCCCTCAAGAGTGGAGATCCAA 6590
Qy 8606 CGTANTAGTGGCGAGTCTGAGCTGGCGGAGATTTGATGCCAGCTGGCGGCCATGGCAGTG 8665
Db 6591 AGGAACACGCTGAGGAGAGTGAAGCAAAATCGATGCTCAACTCAAGTCTTGGCTGTC 6650
Qy 8666 CGCGGGAAGGCTGAGCTGCAGAAACTTACCTTGAGAGCCAGCAGACCCAGGCACAG 8725
Db 6651 AGAAGGAGGCTGCTGCTCCAGAGACCTCCCTCAAGACCCCAAGAGCAAAACCCAG 6710
Qy 8726 CGCAGTTGGCATCTCTGCAGAGTAAGTTCAACAATACGGCTCTGTACAGCTGGCTGGG 8785
Db 6711 TCCAGTTGGCTTCTCCCAAGGAGTTCTCCAAACAGGCTCTCTACAACTGGCTCAGA 6770
Qy 8786 GGCAGTTGTCGGCAATTTATACAGTTCTATGACCTGGCAGTATCCCGTGGCTGATG 8845
Db 6771 GCGCGTTGGCTGGCATCTACTTCCAATTTCTACGACCTTGTGTGGCCAGGTGCTCATG 6830
Qy 8846 GCGCAACAGGCTGGCAGTGGGA--TAAATTCAGACTAGTGTGTTTATCAGCCGGG 8902
Db 6831 GCTGAGCAAGCTTACCGCTGGAGTTGAACGATGACTCCGCGAGGTTCAATCAAGCCAGGT 6890
Qy 8903 GCCTGGATGGGGCAATGCCGCTCTGTGCGCGGGAAACCTGTGATGCTGAATCTGGCG 8962
Db 6891 GCTTGGCAAGCAGCTTACGCTGGTCTCTGCTGGTGAGACCTCATGCTCTCTGGCT 6950
Qy 8963 CAGATGAGCAGGCTGGCTGACGGGGATGAGCGGCAATPAGAGGTGACGCGGACGGTC 9022
Db 6951 CAAATGGAGTGTCTCACTCAAGAGGCAAGAGGCTTTGGAGGTGGAGAGGACATG 7010
Qy 9023 TGCCTGTGCGAGTCTATACAGGCTGCG--GAGAGTGGCGATTTCTCTGCGCGAC 9079
Db 7011 TCCCTGTGAGGTCTACGCTGGTCTCCCAAGGACCAAGCTGCTATCTCTCTGCTCAA 7070
Qy 9080 AAGTGTGGAACTGGTCAGTAAGCTTTCGGGAGTGGGTGAGTGGTGAAGCAAGCAAGTGA 9139
Db 7071 GAGATTGACAAGTTGGTCAGCAAGTTCTGGTCTGCTGTTCTGGTGAACAACAATTG 7130
Qy 9140 CAGATGG-----ATCAACAGCAACTCGAGGCGCACCTTGAAACTGGCTGAC 9184
Db 7131 GCTTTCGGCGCTGTACTGACACCAAGACCTCCCTCAAGCTCTGTCTCTCTGCTGAC 7190
Qy 9185 CTCGGTATCGCAAGATTACCGGCTCCCTTGGACCATGAGGCGGATCAAAACAATA 9244
Db 7191 CTTAAGATCAGGAGGACTACCCAGCTTCCCTTGGCAAGATCAGGCGCATCAAGCAAAATC 7250
Qy 9245 AGCTCAGCTCCCGGCGTGGTCCGCCCTTATCAGGACGTCGCTGGGTTCTCAGCTAC 9304
Db 7251 TCTGTCACTCCAGCTCTCTTGGTTCATACCAAGATGCCAAGCAATCTCTCTCTAC 7310
Qy 9305 GCGGGAAGTATGGTCATGCCCGGGTTGACGCGCTGGCGGTCTCACAGCGGAATGAAC 9364
Db 7311 GGTGACAAGGCTGTTTGGCGAAGCTTGGAGGCTCTTGTGTCTCTCATGGCATGAC 7370
Qy 9365 GACAGCGGCATTTCCAACTGGATTCAATGACCCGGCTTACCTGCGGTTTGAAGACTT 9424
Db 7371 GACTCTGGTCAATTTCCAACTTGACTTCAACGATGGCAAGTTCTCTCCATTCGAGGGCAT 7430
Qy 9425 CCAGTTGATGACACAGGAGCCCTGACACTGAGCTTCCGGATGCT-----GAC 9472
Db 7431 GCCAT---TGACCAAGGAGCCCTCACCCTCTCTCTTCCCAACAGCTTCCATGCCAGAGAG 7487
Qy 9473 GCGAAACAACAGGCGAGTCTCTCAGTCTGAGCGACATCATCTCTGATATCCGGTTACACC 9532
Db 7488 GGAAGCAAGCCACCATGCTCAAGACCTTCAACGATATCATCTCTCCACATCAGGTACACC 7547
Qy 9533 ATTA 9536
Db 7548 ATCA 7551

RESULT 10

US-10-435-835-3
; Sequence 3, Application US/10435835
; Patent No. 6717035
; GENERAL INFORMATION:
; APPLICANT: Patell, Jim
; APPLICANT: Merlo, Donald
; APPLICANT: Herman, Rod
; APPLICANT: Roberts, Jean
; APPLICANT: Guo, Lining
; APPLICANT: Schaffer, Barry
; APPLICANT: Sukhapinda, Kittieri
; APPLICANT: Owens Merlo, Ann
; TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin
; FILE REFERENCE: 50698
; CURRENT APPLICATION NUMBER: US/10/435,835
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 60/148,356
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 3
; LENGTH: 7577
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(7553)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:hemicot toda
US-10-435-835-3

Query Match 4.3%; Score 815.2; DB 4; Length 7577;
Best Local Similarity 48.5%; Pred. No. 6.4e-216;
Matches 3641; Conservative 0; Mismatches 3368; Indels 495; Gaps 31;
Qy 2510 CTGACGGAATTATTCTCGGTTTCCCGAGGTCAAAAAATCACTGGCGCAGGCTG 2569
Db 66 CTCACGTGACATCTCCACAGCTCTTCAACGAGTTTCAGACAACAGTCTCTGAGCACCTC 125
Qy 2570 TCATGGGGAGAGTCTGCTATCTGTACAGTCAGCGCAGCAGCAACAGAAAGAAACCGG 2629
Db 126 TCTTGGTCCAGACCATGACCTTACCATGACGCTCAGCAGCTCAGAGGACAAAGG 185
Qy 2630 CTCACCGAATCCCGTATTTTGGCCCGGGCGAATCCCTACTGTGTAATGCGTTGCGCTG 2689
Db 186 CTCTACGAGCTAGGATCTCTCAAGAGGGCTAAACCAAACTCCAGAAACGCTGTCCACTC 245
Qy 2690 GGAATACGGCAGGCA---GCCGGCAGTCGCGATGATGATGCTGGTTGGCTCCGCGCA 2746
Db 246 GCCATCTGGCTCCAAACGCTGAGTTGATGGTTTACAAACACCAAGTTCTCTGGCAGAGCT 305
Qy 2747 GACCGTTTCGCCCGCCCGCTCGGTGGCTCATGTTCTCACCGGGGGGTATCTGACC 2806
Db 306 AGCAGTACGTGGCTCTCTGTACAGTCTCTCATGTTTACGCCAGCGCTTACTCACT 365
Qy 2807 GAGCTGTACCGTGAAGGAGAGCCTGCAATCCGAGACCTCGCTGTTTCCGGCTGGACATC 2866
Db 366 GAGTTGTACCGCGAGGCTAGGAACCTTCATGCTTCTGACTCCGTCTACTTCTGGACACA 425
Qy 2867 CGCGGTCCCGACCTTGGCGGCTGGCCCTTAGCCAGATATATAGACGAGGAGCTCTCC 2926
Db 426 CGCAGACCAAGCTCTCAAGAGCATGGCCCTCAGCCAAACAGAAATGGAATTTGAGTTGTC 485
Qy 2927 ACCCTGAGCTGTCCCAATGAGTACTGTATCGCGGTATCGGCGAGCGGAGAGGCTTGGAC 2986
Db 486 ACCCTCTCTTTAGCAACGAGCTTCTCTTGGAGTCCATCAAGACTGAGCAAGTTGGAG 545
Qy 2987 GAGCAGACG---GTCAGGGAGCTGCTCGCGGGTATCGCCTGACCGGCTGACCCCTTAT 3043
Db 546 AACTACACCAAGGTCATGGAGATGCTCTCCACCTTCAGACCAAGCGGTGCAACTCCATAC 605

QY	3044	CACTGGGCGTAACGAGGGCCGCCAAGCATTCTGTGTCAGGACCGAGCGCTGATGGG	3103	4121	ATCAGCGCCTCGGGGCTTTCCAGCTCTGGCAGTGGCCAGCGGTGACAGCAGCGCTGG-	4179	
Db	606	CATGATGCCCTACAGAAAGTCAGGAGGTCATCCAACTTCAAGACCCTGGTCTTGAGCAA	665	Db	1674	ATTGATGATGCTCTCTCTCTTCGTCTCTTGAAGATCACAGATCACAGAACAAAGGATGGC	1733
QY	3104	TTCAGCGTAATCCGGATGTGGCGAGCTTATGAGACCCCTGCCCTCCATGTCTGGCCATTGAA	3163	QY	4180	--GTTTAGTGTCTGTGACAAATATGCGCCGACATCTACCGAGTGAAATCTCTCTGGCTGAC	4237
Db	666	CTCAACGCTTCTCCAGCATTGCTGGTTGATGACACCGAGCATCTCTGTCTGGTATCAAC	725	Db	1734	AAGATCAAGAACAACTTGAAAGAACCTTTCCAACTCTATATGGCAAGTGTCTTGACAGAC	1793
QY	3164	GCGGATATTTCACCGAGCTGTATCAGATCTAGGCGGAGAAATTAAGACAGACAGTTAC	3223	QY	4238	ATCCAGACCTATCCGCTGGTGGCTGTCAATGTGTGCTGTCCGTCTCCCTTTTCAGGGG	4297
Db	726	GCCTCATCTCTCTGAGTTGTTCAACATCTTGATGAGAGATCACTGAGGCGCAACGCT	785	Db	1794	ATCCACCAACTCACCATTGATGAGTTGGACCTCTTGCTCAITGCGATCGGTGAGGCGAAG	1853
QY	3224	GRAGCACTCGAGTAAGAAATTTGGTGATGATGCCCTCCCTCACTGTTATCTTATGAT	3283	QY	4298	GTGGCGCGCGCTCGCTGTCGATAATGAG-----CTGACGCACTTTCTGTACCAAG	4348
Db	786	GAGGAGTTGTACAGAGAACTTCGGCAACATTTGAGCCAGCCTCTCTTGCATGCGCTGAG	845	Db	1854	ACCAACCTCTCTGCAATCTCTGACAGAGATTTGGCAACCTCATCAGGAAGTTGAACACC	1913
QY	3284	GCACTTGCAACATTTTATGATCTTGATTAAGATGAGCTAACTTCGTTATTTGATTAAGG	3343	QY	4349	ACCAACCTCTGCTCAAGAGCAGGCTGGACCGGTGGACGGTGGATGTGTCTGTGATGTGACG	4408
Db	846	TACCTCAAGAGGTACTACAACTTGTCTGATGAGGAGCTTCT-----CAATTCATT	896	Db	1914	ATCACCTCTCTGGCTTCAACCCAGAAAGTGTCTGTCTTCCAACCTCTTCATCATGACACAGC	1973
QY	3344	CTGGACTTTTCAATCAAAATGAATACATTAATTAAGTCAATTAAGTGTGTAACCT	3403	QY	4409	AGCGAGTACGGTACCTGCTGACCCCGACATTTGAGAACCTGCTCGCTTCCCTGCGCAAC	4468
Db	897	GGCAGGCTTCCAACTTCGGTCAACAGGAGTACAGCAACAAACAGCTCATCTCCAGTT	956	Db	1974	ACCTCTCAACAGAACCTCTCTCTGAGATCAAGAACCTTTGGACACAGTCTATCCAC	2033
QY	3404	CTGAATGAAGCACTGTTTAAATACTATACATCATTTATTAAAGAGCGCTAGGCGGAGC	3463	QY	4469	GGACTGTCCGGCGCTGAGCTGTTCCCGGAAACGCTCCCGGGGATGGCGCTCTCCCTTTATT	4528
Db	957	GTGAATCTCTGATGCACTGTGAAGTCTACCGCATCAACGTGATGATACCAAC	1016	Db	2034	GGTCTCCAGGCTTCGACAGGACAGGCTGACTTGTCTCATGTCTATGCTCCCTACATT	2093
QY	3464	TCACAGCAGATTAAACCTGAGCTTATACCTTATGGGGATGGAAATATCTTTATAATTC	3523	QY	4529	GCGCGCGCATGAGCTGGACGCCAGCGATACGGCGAAGCGGATGTGTCTGTGGCGGAC	4588
Db	1017	GCCTACCAATGATGTGTGAGTTGTTCCCATTCGGTGGTGAAGTACAGACTTGACTAC	1076	Db	2094	GCAGCCACCTCCAACTCTCTCTGAGAACTGGTCTCACTGTCTGTCTGTCTGGGCTGAC	2153
QY	3524	AGCGTGTGTCAGATATCAGAGGATAGTTTCAAACCTAGGTCGTTAGTTCCTAACAGT	3583	QY	4589	CAGTTGAAGCCAGAGGGCTGACGCTGACGGAATTTTCTTTTGTGTGATGAATCGCGC	4648
Db	1077	AAGTTCAAGAACTTCTACACGCTCTCACTCTCCATCAAGTTGAACGACAGAGGGAG	1136	Db	2154	AAGTCCAACTCTGGTATGTTGCCATGACTGTGTGAAAGTTCTGGGACTGGCTCAACACC	2213
QY	3584	AGCAATCTTTACTCTGGGATATACAGTTCAAAAAGGGTTCGCTATAGCATTCCTGTT	3643	QY	4649	CCAAA-----TGACGAGCAGCGCGGCGGACAGTGGCAGGGTTCTGC	4687
Db	1137	CTTGTCAAGACTGAGGTGCTCTCAAGTGAACATTTGAGTACTCTGCCAACATCACTTC	1196	Db	2214	AAGTACACACAGGCTCTCTGAGGCTGTTGAGACTCAAGAGCACATTTGTGCAATACTGC	2273
QY	3644	GAATAGATGAAGAAAGTTAAATGATGGAT---CACATAGGATTTGATGAGAAAGG	3700	QY	4688	CAAGCCCTGTGGAACTGGCACTGATCATCCGAGACACCGGCTCAGCAGCGCGAGCTG	4747
Db	1197	AACACAGCTGACATCTCAACCATTCGAGATTGGTTTGACAGAGCTCTTCCCTCTGGC	1256	Db	2274	CAGGCTCTTGCAAGTTGGAGATGGTCTACCACTCCACTGGCATCAACGAGAACGCTTC	2333
QY	3701	GGGGATATTACTCAACAGTAACCTTCACTGATTTGAATATGATCTCTGGATTTCAIT	3760	QY	4748	ACGCTGCTGTCAGCCAGCGCGGACGCTTCCGCAACAGG---ATGGCACCATCTGCCCAT	4804
Db	1257	TCCTGGGCTTACGCTGAGCCAAAGTTCACTGTTGAGGAGTACAAACAGTACTCTTTTCTC	1316	Db	2334	AGACTCTTCTGTCACCAAGCTGAGATGTTCCGTGCTGCCACAGTGTCTGCACCTGTCT	2393
QY	3761	CTTAAATTAATAAAGTTATCCGCTTATCAAGCCACGGGATGACCGCGGAAATA	3820	QY	4805	GACCTGCGCGGCTTCCGCACTTACGCGTTTTTCAITGCGCTCGTTAACCGCAGCGGACG	4864
Db	1317	TTGAGCTCAACAGGCAATCTCTCAGCAGAGCCACTGAGTTGTCTCCACCATCTTG	1376	Db	2394	GATGCTCTCTCCTCATCATGTTGACCAAGTTCCGCTGACTGGGTCAACGCTCTTGTGAG	2453
QY	3821	TATCAATCAACATATTCTTAATAACGCTCTCAACATGACCATGGCTCTGTAGTAA	3880	QY	4865	CATGCGGGGAGGTCTCTGACCGCACTTGAGACCGGAGAACTGTCTGTCAGCCCTGTGGCC	4924
Db	1377	GAGGCAATTGTGAGTCTGTCACTTCACTTGAATCAACATCACTGATGCTTGGCAAG	1436	Db	2454	AAGGCTTCTCTGTCTGTGGCTCTCGAGGCACTCCCTCACTCTGTCAGCAACTGTCT	2513
QY	3881	ATCTTCTGTCTGTACCTGATGCTGCTCATATCAGCTTGTATGGCCCGGTCACCTGATA	3940	QY	4925	CGGGCCCTGTCAAGAAATGAGGATGTGACCGGCGCTTGGCGCAGGTGAGGGGGGCC	4984
Db	1437	GTCTTCTCTCAAGTACTACATGCAACGCTACGCCATTCATGCTGAGACTGCACTCAT	1496	Db	2514	GATGCCATGAACCTTGATGCCAACCTCTTGTCTCAAGCTTCATTCAGCTCAGAACCA	2573
QY	3941	TTGTGAACGGAAACCATCAGTGAACGAGCGTTCAGCGGCGAAACCGGCTGTTTCAACG	4000	QY	4985	GGTGAACAGGACA-----ACAGCTGTTCACCTCTCTGGGAAGAGGTGGAACAG	5032
Db	1497	CTCTGCAACGCAACCATCTCTCAAGCTCTTCAACACACCGCTTCCAGTTGACAGG	1556	Db	2574	CAACACTCCACCTGCTCACTCCAGAGAACGCTTCTCTGTGGACCTCCATCAACACC	2633
QY	4001	CTGTTCACACCCACCGCTGAACGCGCAGCTGTTCGTGAGATGATACCCCTCTGAC	4060	QY	5033	GCTGAGCAGTGGTGGACATGATGAGACCTGTCCATTACGCCATCCGCTCTGGCTAGC	5092
Db	1557	CTCTTCAACACTCTCTTGTGAACGCGCAGTACTTCTCACTGGTATGAGGAGATGAC	1616	Db	2634	ATCTCCAAATGGGTCAACGTGCTCAGCAACTCAACGTGGCTCCACAAGGTGTCTCTGT	2693
QY	4061	TTACGCTCTGAACCGGAGGATGCTTTCCGCTCTAGCGTACTGAAACCGCATTTAAC	4120	QY	5093	CTGATTTCCCTGAAGTACATCAATGTCTCGATGACAGTGCACCGTGTGTACAGCCAGTGG	5152
Db	1617	CTCAACTCTGGCTCCAC---AGGTGACTGGAGAAAGACCATCTTTGAAGAGGGCTTCAAC	1673	Db	2694	TTGGTGGTCTTGACTACATCCA---GTCCATGAAGGAGACACCACTACGCTCAATGG	2750
				QY	5153	CAGGTGGTATCCGGTCTGTGCGAGCGCGGCTGAAAGACGACGAGAGCTCGGCGCTGAC	5212

Db	2751	GAGAACGAGCTGGTGTCTTGA	2810	Db	3831	AAGGACATGACTCCAGAGCA	3890
Qy	5213	GATTATCTGAGAGGGGAC	5272	Qy	6218	AAGAGCGTCAGTCACGAA	6277
Db	2811	GCCTTTCTTGATGAGTCT	2870	Db	3891	ACCACAAACGTCAGGCGT	3950
Qy	5273	CCGAACATGATATCCGG-	5326	Qy	6278	GACCCCTTCGCTAAATTA	6337
Db	2871	AAGCGAGCTGCTGCCAT	2930	Db	3951	GTCCAGCTCTCGAAGGAC	4010
Qy	5327	CAGGTGTCAGCAAGGTA	5386	Qy	6338	GATTTCTACTCTTAAAT	6397
Db	2931	CAGGTCTCTGCTGCAAT	2990	Db	4011	GACATCCCAACCATCA	4070
Qy	5387	TATATCAACCGGCGCTT	5446	Qy	6388	-----AGATTCCTCT	6441
Db	2991	TAGCTCAACCGCGCTT	3050	Db	4071	AAGCTCAGGATCATCA	4130
Qy	5447	CAGTTTTTCACTGACT	5506	Qy	6442	TGTTAGTACTGCTGG	6501
Db	3051	CAATTTCTCATCGACT	3110	Db	4131	AACAAGTACGGCAAG	4190
Qy	5507	GAGCTGGTTACTATCC	5566	Qy	6502	AGAAATTTGAGGAAAT	6561
Db	3111	CAACTTGTCTACTAC	3170	Db	4191	AACAACAGCTCCAA	4250
Qy	5567	ATGATGACACCTGCT	5626	Qy	6562	GG-----GAGTGG	6614
Db	3171	ATGATGATGCTCTCT	3230	Db	4251	GGTCTCAACACGGG	4310
Qy	5627	GATGCCCTTTAAAC	5686	Qy	6615	G-----TGTCAC	6631
Db	3231	GATGCCCTTCATGAC	3290	Db	4311	GCITGGATTCCTGG	4370
Qy	5687	GGATATCAAGATAA	5746	Qy	6632	TATTCGTCACCTG	6691
Db	3291	GCTTACCATGACAA	3350	Db	4371	TAGCCACAGACTCC	4430
Qy	5747	ACAGATCAGACTAC	5806	Qy	6692	TTTCAGCGGA-	6701
Db	3351	ACTGATGCTGGTGA	3410	Db	4431	TCCAAGGGCACAG	4490
Qy	5807	ATGCCCGGAATGCT	5866	Qy	6702	--TTTTTTCAGAT	6759
Db	3411	TTCCGCTGCAACG	3470	Db	4491	GCCAAGTCCAAAT	4550
Qy	5867	GATCTTGCTCGGT	5926	Qy	6760	CGTGTGCTCTAT	6817
Db	3471	TCCACCATCAGAC	3530	Db	4551	GATGTCTCCATC	4610
Qy	5927	CAGT-----CTG	5974	Qy	6818	CAGATATGAAATTA	6877
Db	3531	GAGATCACCAGCA	3590	Db	4611	GAGATGATGGTTC	4670
Qy	5975	TACAGCTGAAACT	6034	Qy	6878	AAATCTGCGCTTC	6937
Db	3591	TACAGTTGAGTTG	3650	Db	4671	ACTGCTTCGCTG	4730
Qy	6035	GACATTAACGGCA	6094	Qy	6938	CTTTTCAACACCA	6997
Db	3651	GATGTCAACAAGA	3710	Db	4731	CTTAAGGTTTCCA	4790
Qy	6095	CTGACTGACAGCT	6144	Qy	6998	TT-----TGAC	7012
Db	3711	TGCGCTGGTTAC	3770	Db	4791	ATGCAATGGCAAG	4850
Qy	6145	CTTTGAT-----	6169	Qy	7013	ACGTTACCGCTG	7072
Db	3771	CTTGACTCTTACA	3830	Db	4851	CGTGCCACCAC	4910
Qy	6170	GTGGATTAATGA	6217	Qy	7073	GTCAITTCGAA	7132
				Db	4911	CAGTTGGGCAAG	4970

QY	7133	GCGCAGTATATTCGTTTCACTCGGGGTAAAGATGTGGCGCTT-----	7174	CTTTACAGTTTCCGGTCTCGGTATTTACCGAGCGTCCGCGGATGGTGTAGACCTGTGTACCGGG	8125
Db	4971	GGTGATGAGAGGTGGTTCAAGCTCTATCAAGCAGCTGGTTGACAACTCCCAATC	5030	CTCTGGAGGTTCCTCCACATGTTGGAGAAACGCGCGTGGCATGGTCTTCCCACTCAACCCAG	6110
QY	7175	-----ATTGCGCTCAAAACACCTCTTTTGGCC-----	7199	TTTCGGCAACACACTGTCTCGGTATTTACCGAGCGTCCGAGTGGCGGCTGGGCCAAACTG	8185
Db	5031	ATCTACTCTGGTCAACTACTGACACCAACATCAACATCACCTCTTTATCCCACTTGAC	5090	TTTCGGTTCCACCTCCAGAACATCTTGGAGGCAAGATGCTTGAGGCTCTCAACGCTTG	6170
QY	7200	-----	7199	CTTCAGAACACGAGCAGCTGAGTTGATCTCTACCAACTTGTCTCATCCAGACAAAGCAATT	6230
Db	5091	GATGTCCCACTCAACAGGACTACCATGTCCAAAGTCTCATATGACCTTCAAGAAGTCTCCA	5150	GAGGAAATCGATCGCGATATTGCGCCCTGGAGGAGAGCGCGCGCGCGGAGATGCGT	8305
QY	7200	-----GCCAACTGGTTCGACGGCGGAATACCGGGATTGACACAT-	7239	GAGGAGCTTGATGCTGAGAAGACAGTCTTTGAGAAGAGCAAGCTGGTGGCCCAATCTCGC	6290
Db	5151	TCTGATGGCACCCTGGTGGGTTCACACTTGTCTCGTGATGACAAAGGGCATCGTCAACATC	5210	TTTGAAACGTTTACAAAGTGTGTACGAGGCGGAGCTCAACACCGGCGGAAAAAAGGCCATG	8365
QY	7240	-----TCTTTCCATGGAGACCCAGAGGCTTACCGAAACCGCGCTTGAAAGAGGGAGTGAT	7294	TTTCGACTCTACGGCAAGCTCTACGATGAGAACATCAACGCTGGTGAGAACCCAGGCCATG	6350
Db	5211	NAACCCAAAGTCCATCTCACCACTTTCGAGTCTGTCAAAGTCTCAACACATCTCTCT	5270	GACTGTGTA CTTCAAGTTTCTCGTGTGGGATCAACCCGCGCGCTCTTTTGGCGGAG	8425
QY	7295	GTGTTTATGAGCTTCTCCGAGGCAATGCGCTCTATTTCTGGAGCTGTTCTATTATACG	7354	ACCCCTCAGGCTTCCGACGCTGTCTACCACTGTCTCAAGCTCTCAAGCTCTCGCTTGGGTGT	6410
Db	5271	GAGCCAAATGAGCTTCTCTGTGCAACTCCTCTACTTCTGGAGTGTCTTACTATACACA	5330	GCGCGCGCGGATATGCTGCCCAATATTTACGGGCTCGGCGCTCGGGGCTCCGCTATGGG	8485
QY	7355	CCGATGATGGTGTTCAGCGGTGTTGACGAGACAGCACTTCCCGGAAGCCACCCCTGG	7414	GCAGCTGTGACCTCGTTCCAAACATCTTCGGTTTCGCTGGTGGTGGCTCCAGATGGGT	6470
Db	5331	CCAACTGCTGTGGCTCAAGGTGTGCTCATGAGCAGAACTTCGATGAGGCCAACAGGTGG	5390	GCATATTTTAAAGCCACCCCATCGGCATCCGATCCGATGTCTCTCGATGCCACCCGATATCA	8545
QY	7415	CTGCACTATGTCTGGAACCCGCGCGGCGACGCTGGTAAACGGGTGCTGCAGAAATTACAC	7474	GCCATTGTCTGAGCTACCGGTTAGCTCATGGAGTTCTCTGCCAAACGCTCATGAACCTGAG	6530
Db	5391	CTCAAGTACGTCTGGAGCCCATCTGTGTATCTGTGATGTTCAATCCAGAACTACCAA	5450	GGCGCAAAATCAGCCAGTTCGGAAGTGACCGCGTCCGCGGAGAGTGGGAAATCCAG	8605
QY	7475	TGGAATGTGCTCGCTTGAGAGAGGACACCGGCTTGAAACGACTCGCGCTGGACTCCATT	7534	GCTGCAAGATCAGCCAATCTGAGACCTACAGAAGCGCGCTCAAGAGTGGGAGATCCAA	6590
Db	5451	TGGAACGCTCAGGCCATTGCTTGAGGACACCTCTCTGGAACCTCTGACCACTTGA	5510	CGTGATGTGCGCAGTCTGACGCTGGCGCAGATTGTATGCGCAGCTGCGCGCCATGGCAGTG	8665
QY	7535	GACCCGATGCAATACCCAGTACGACCCCATGCAATTAAGGTGCGCACTTATGTG	7594	AGGAACAACCTGAGGAGAGTTGAAGCAAAATCGATGCTCAACTCAAGTCTCTTGGGTGTC	6590
Db	5511	GACCTGTGCTGTGGCTCAACATGACCCCAATGACTCAAGGTCTCCACCTTCATGAG	5570	CGCCGGAAAGGGCTGAGCTGCAGAAAACTTACTTTAGACCCAGCAGACCCAGGCACAG	8725
QY	7595	TACTCGACCTGTGATTGCGCGGTGATGCGCGCTACCGCTGTCTGAGCGGAGACAC	7654	AGAAAGGAGGCTGTCTCTCCAGAAAGCTCCCTCAAGACCCAAACAGCAGCAAAACCCAG	6710
Db	5571	ACCTTGACCTCTTGATTGCCAGAGTGACCATGCTTACCGCCAAATTGGAGGGGACAC	5630	GGCGAGTTGGCATTCCTGCAGAGTAAAGTTCAACAATACCGCTCTGTACAGCTGGCTGCGG	8785
QY	7655	CTTAAAGAGCCCGGATGTGTTAGTTCAGGCGCTGAAACCTTCTGGGGGACGAGCCCTAT	7714	TCCCAAGTTGGCTTTCCTCCAAAGGAAGTTCTCCAAACAGGCTCTCTACAACTGGCTCAGA	6770
Db	5631	CTCAAGAGGCAAGATGTGTACATGCAAGCTCTCCACCTCTTGGGTGACAAAGCCATAC	5690	GGCAGGTTCTCGCCCAATTTATTACAGTTCTATGACCTGGCAGTATCCCGCTGCTGTATG	8845
QY	7715	ATTTCTTTGAGCCGACTGTGTCGGGTTGACCTCGGTGACGACCGAGGAGTGACG	7774	GGCCGCTTGGCTGCCATCTACTTCCAAATCTAGACCTTGTGTGGCAGGTTGCCTCATG	6830
Db	5691	CTCCCACTAGCACCACTTGGTCCGACCCAGGTTGGAACGCTGCTGTGACATCAACACT	5750	GGCCAAACAGGCTTGGCAGTGGGA---TAAATTCGAGACTAGGTGCTTTATCCAGCGGGG	8902
QY	7775	CGACGGGATTACAGGAGGCGCTGTGGCGGTGCGCGGTGGTGGCGCGCTCCCGAGACA	7834	GCTGAGCAAGCTTACCGCTGGGAGTTGAACGATGACTCCGCGCAGGTTCTCAAGCCAGGT	6890
Db	5751	CAGAACGCTCATGACTCTGCCATTTGTCTCTCAGGCAAGAACATCCCACTCTGCTCCA	5810	GCTTGAATGGGGCAAAATGCCCGTCTGTGGCGGGAAACCTGTATGCTGTATCTGGCG	8962
QY	7835	C-----GGACGGGAATTCCTTGAACGCACTGTTCTCCCGCAGCAGAAAGAGTG	7885	GCTTGGCAAGGCACTTACGCTGTCTCTTGTGTGAGACCCCTCATGTCTCTCTTGGCT	6950
Db	5811	CTCTCCCTCAGATCTGTAAACCTCTACTGACTTGTTCCTCCACAGATCAACGAGGTC	5870	CAGATGGAGCAGGCTGGCTGACGCGGGATGACGCGGCAATAGAGGTGACGCGGACGGTGC	9022
QY	7886	CTCAAAGGCTACTTGGCAAACTTGGCACAGCGGCTCCATAACCTTGGCCACACACTCTCC	7945	CAATGGAGGATGCTCACCTCAAGAGGACAGAGGGCTTTGGAGTTGGAGAGGACAGTCT	7010
Db	5871	ATGATGAATCTATGGCAAACTTGGCTCAAGGGTCTAACAACCTGACACAACTCTCC	5930	TGCTGTGCGAGGCTCTATACAGCTTCGC---GGAGATGGCGCATTTCTCTTGGCGGAC	9079
QY	7946	ATTGACGGCAGCGCTTTCCCTGTCCGTCTACGCCACGCGGTTCGAAACCGTCCGCGCTG	8005	TCCCTTGTCTGAGTCTACGCTGTCTCTCCAAAGGACCAACGCTCATTTCTCTTGGCTCAA	7070
Db	5931	ATTGATGGTCAACCACTTACCTCCCAATCTACGCCACACCACTGACGCCAAAGGCTCT	5990	GAAGTGGTGGAACTGGTCACTAAGTTCGGCAGTTCGGGTACGAAAGACAGGATTA	9139
QY	8006	CAGAGTGGCTGTCAACAGCGCGCAGGGTGTCTGAGCACTGCGCGCGCGGTGTATGCGG	8065	GAGATTGACAAGTTGGTTCAGCAAGGTTCTGTGTTCTGTGTTCTGGTGAACAAACTTG	7130
Db	5991	CTCTCTGCTGCTGTGGCTACCAAGCCAAAGGTGGTGGCAAGCTCCAGAGTCTTCTATGTC	6050	CAGATGG-----ATCAACAGCAACTCGAGGCCACCCCTGAAACTGGCTGAC	9184

Db 7131 GCTTTGGCGCTGGTACTGACACCAAGACCTCCCTCCAAAGCTCTGTCTCCTTGGCTGAC 7190
Qy 9185 CTCGATATCGGCAACGATTACCCGGTCTCCCTTGGCAACCATGAGCGCATCAACAATA 9244
Db 7191 CTCAGATCAGGAGGACTCCAGCTTCCCTTGGCAAGATCAGCGCATCAAGCAATC 7250
Qy 9245 AGCGTACGCTCCCGGCGCTGGTGGGCCCTTATCAGGACGTCCTGGTGGTCTCAGCTAC 9304
Db 7251 TCTGTACCCCTCCAGCTCTCTTGGTCCATACCAAGATGTCCAAGCAATCTCTCCTAC 7310
Qy 9305 GCGGAAGTATGGTATATGCCCGGGGTTGACGCGGCTGGCGGCTCTACACGGAATGAAC 9364
Db 7311 GGTGACAAGGCTGGTGGCGAAGCGTTGCGAGGCTCTTGTGTCTCTCATGGCATGAAC 7370
Qy 9365 GACAGCGCCCAATTCCTCAACTGATTTCAATGATCAACCGGCTTACCTGCGTTTGAAGGACTT 9424
Db 7371 GACTCTGTCAATTCCTCAACTTGAATTTCAACATGATGGAAGTCTCTCCCAATTCGAGGCAAT 7430
Qy 9425 CCAGTTGATGACACAGGACCTCTGACACTGAGCTTCCCGGATGCT-----GAC 9472
Db 7431 GCCAT---TGACCAAGGACCTCTCCTCTCTCTTCCCAACGCTTCCATGCCAGAGAG 7487
Qy 9473 GCGAAACACAGGCGATCTCTCAGTCTGAGCGACATCATCTGCAATCCGTTACAC 9532
Db 7488 GGAAAGCAAGCCATGCTCAAGACCTCAAGCATATCATCTCTCCATCCAGTACAC 7547
Qy 9533 ATTA 9536
Db 7548 ATCA 7551

RESULT 11

US-09-637-048C-6
; Sequence 6, Application US/09637048C
; Patent No. 6590142
; GENERAL INFORMATION:
; APPLICANT: Patel, Jim
; APPLICANT: Merlo, Donald
; APPLICANT: Herman, Rod
; APPLICANT: Roberts, Jean
; APPLICANT: Guo, Lining
; APPLICANT: Schafer, Barry
; APPLICANT: Sukhapinda, Kitisri
; APPLICANT: Owens Merlo, Ann
; TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin
; FILE REFERENCE: 50698
; CURRENT APPLICATION NUMBER: US/09/637,048C
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/148,356
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 7621
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:hemicot tcda
; OTHER INFORMATION: fused to the modified 15 kDa zein endoplasmic
; OTHER INFORMATION: reticulum signal peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(7614)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)
; OTHER INFORMATION: n can be a, t, g, or c
US-09-637-048C-6
Query Match 4.3%; Score 815.2; DB 4; Length 7621;
Best Local Similarity 48.5%; Pred. No. 6.5e-216;
Matches 3641; Conservative 0; Mismatches 3368; Indels 495; Gaps 31;

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Db 127 CTACTGACATCTCCACAGCTCTTTCAACGAGTTTCAACAACAGTCTCTGAGCACCTC 186
Qy 2570 TCATGGGAGAGGTCTCTATCTGTACAGTCAAGCGCAGCAGCAACAAGAAAGAACCGG 2629
Db 187 TCTTGGTCCGAGACCCATGACCTCTACATGACGCTCAGCAAGCTCAGAGGACACAACAGG 246
Qy 2630 CTCACCAATCCCGTATTTCTGGCCGCGGCGAATCCCTACTGGTGAATGCCGTTGCGCTG 2689
Db 247 CTCTACAGGCTAGGATCTCTCAAGAGGCTAAACCAACATCCAGAAACGCTGTCCACCTC 306
Qy 2690 GGAATACGGCAGGCA---GCCGGCAGTCGCGACTATGATGACTGTTGGTTCGCCGCGCA 2746
Db 307 GCCATCTTGGCTCCAAACGCTGAGTTGATTGTTTACAACAACAGTCTCTGCGCAGAGCT 366
Qy 2747 GACCGTTTCGCCGCCGCCCGCTCGTGGCTTCCATGTTCTCACCGGCGGCGATCTGACC 2806
Db 367 AGCCAGTACGTGGGCTCTCTGTACAGTCTCTCCATGTTTCAGCCCGCGCTTACTCACT 426
Qy 2807 GAGCTGTACCGTGAAGGCGAAGGACCTGCATCCGAGACCTCGCTGTTCCGCGCTGGACATC 2866
Db 427 GAGTTGTACCGCGAGGCTAGGAACTTCTGCTTCTGACTCCGCTCTACTACTTGGACACA 486
Qy 2867 CGGCGTCCCGACCTTGGCGCGCTTGGCCCTTAGCCAGAAATATATGGACGACGAGCTCTCC 2926
Db 487 GCGNAGCACACCTCAAGAGCAGTGGCCCTCAGCCNACAGAAACATGGACATTTGAGTTGTC 546
Qy 2927 ACCCTGAGCCTGTCCTCAATGAGCTACTGTATCGCGGTATCGGGGCGAGCGGAGGCTTGCAC 2986
Db 547 ACCCTCTCTTGAACACGAGCTTCTCTTGGAGTCCATCAAGACTGAGAGCAAGTTGAG 606
Qy 2987 GACGACGCG---GTCAGGAGCTGCTCGCGGGTATCGCCTGACCGCGCTGACCCCTTAT 3043
Db 607 AACTACACCAAGGTCATGAGATGCTCTCCACCTTCAGACCAACGCGTGCAACTCCATAC 666
Qy 3044 CACTGGCGGTACGAGGCGGCGCCGCAAGCCATTCGTGTGAGGACCGCGACGCTGATGGG 3103
Db 667 CATGATGCTTACGAGAACGTCAGGAGGTATCCACTTCAGAACCTTGGTCTTGGAGCA 726
Qy 3104 TTCAGCGTAAATCCGATGTGGCGACCTTATGGACCTCGCTCCATCTGCTGGCCATGAA 3163
Db 727 CTCAACGCTTCTCCAGCCATTTGCTGTTGATGACCAAGGATCTTCTGCTGGTATCAAC 786
Qy 3164 GCGGATTTTCAACGAGCTGTATCAGATACTGCGCGAAGAAATTCAGACAGAGCTTAC 3223
Db 787 GCCTCCATCTCTCTGAGTTGTTTCAACATCTTGACTGAGGAGATCACTGAGGGCAACGCT 846
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Db 847 GAGGAGTTGTACAAGAAAGAACTTCGGCAACATTTGAGCGAGCTCTCTTGCATGCGCTGAG 906
Qy 3284 GCACCTGCAACATTTTATGATCTTGTATGATGAGCTAACTTCTGTTATTTGTCAATTAAGG 3343
Db 907 TACCTCAAGAGGTACTACAACCTTGTCTGATGAGGAGCTTCT-----CAATTCAAT 957
Qy 3344 CTGACCTTTTCAAAATCCAAATGAATGATCTACTATTAATAGTCAATTAAGTGTGTAAT 3403
Db 958 GGCAAGGCTTCCAACTTCGCTCAACAGGAGTACAGCAACACCAAGCTCATCACTCCAGTT 1017
Qy 3404 CTGAATGAAAGCACTGGTTTTTAATAACTATACATCATTTATTTAAGAACGCTAGGCGGAGAC 3463
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3584 AGCAATCTTTACTCTCGGGATTATCAGCTTCAAAAAGGGTTCGGTATATGACATTCCTGTT 3643
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3644 GAAATAGATGAAGAAAGTTAAATGATGGAT---CACAAATAGGATTTGAGTAGGAAGG 3700
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3761 CTTAAATTAATAAAGTTATCCGCCCTATACAAGGCCACGGGCAATGACCAAGCGGGAATA 3820
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1378 TTGAGCTCAACAAGGCAATTCGTCTCAGCAGAGCCACTGAGTTGTCTCCACCATCTTG 1437
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3821 TATCAATCAACCAATATCTTAATAACGGTCTCACCAATGACCAATCGGTCCTGAGTAA 3880
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Qy
4238 ATCCAGACCTATCCGCTGGTGAAGTCAATGTTGCTGCTCCCTCTCCCTTTTCAGCGG 4297
Db
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4298 GTGGCGCCGCGCTCGTGTCCGATAATGAG-----CTGACGCGAGTTTCTGTACCAG 4348
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4349 ACCACACCTGTGCTACGGAGCAGGGCTGGAACGGTACGGATGTTCTTGATGCTGACG 4408
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4409 ACCAGTACGGTACCTCTGACCCCGACATTTGAGAACCTGCTCGCTTCCCTCCGCAAC 4468
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2095 GGTCTCCAGGCTTCGACAAAGGACAAGGCTGACTTGTCTCATGTGCTGCTCCCTACATT 2154
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4529 GCGCCGCCATGACGTGAGCGGACCGGATACGGGAGGCGATGCTGACTTGGGGGAC 4588
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4589 CAGTTGAAGCCAGAGGGGCTGAGCTGACCGAAATTTATTCTTTTGTGATGAATCGCGCC 4648
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Qy
4649 CCAAA-----TGACGAGCAGCGCGGCCAGATGGCAGGGTTCTGC 4687

2275 AAGTACACACACAGGCTCTCTGAGGCTGTTGAGACTCAAGAGCAATTTGCAATCTGCG 2334
Qy
4688 CAAAGCCCTGTGCAACTGCACTGATCATCCGAGCACCGGCTCAGACAGCGCGAGCTG 4747
Db
2335 CAGGCTCTTGCACAGTTGGAGATGGTTACCACTCCACTGGCATCAACAGAACGCTTTC 2394
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4748 ACGCTGCTGTCAGCCAGCGCGGACGCTTCCGACAGG---ATGGCACCATCTGCCCAT 4804
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4805 GACCTGCGGGCTTTCGACATTAACGGCTTTTCAATGCGCTTGTAAACCGCAGCGGACG 4864
Db
2455 GATGCTCTCTCTCATCATGTTGACAGGTTCCGCTGACTGGGTCAACGCTCTTGGTGAG 2514
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4865 CATGCGGGGAGTCTGACCGCACTTGAGACGGGAGAACTGCTGTCAGCCCTGCTGGCC 4924
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4925 CGGGCCCTGTCACAGAAATGAGCAGGATGACCGGGCCTTGGCGCAGGTGAGGGGGCC 4984
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5033 GCTGAGCAGTGGCTGACATGATGAGACCTGTCATTAACCCATCCGCTCTGGGTAGC 5092
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2695 ATCTCTCAATGGGTCAACGTGGCTCAGCAACTCAACGTGGCTCCCAAGAGTGTCTGT 2754
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5093 CTGATTGCGCTCAAGTACATCAATGTCTCGATGACAGTGCACCGTGTGTACAGCCAGTGG 5152
Db
2755 TTGTCGGTCTTGAATACATCA---GTCCATGAAGGAGACACCACTTACGCTCAATGG 2811
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5153 CAGGTGTTATCCGGTCTGTGAGCGCGGCTGAAAGCAGCAGCAGAGTCTCGGCGCTGCAC 5212
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5273 CCGAATCATGGTATCCGG-----GCGCGATGACCTCTTCGGGTATCTGCTGTGATAAT 5326
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5327 CAGGTGTACCAAGGTAATAAACCCCGCATTTGGAGGCGCATCCCGCGCATACGGCTG 5386
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5387 TATATCAACCGGGCCCTTAACGGATAGAACTCAGCGCATGACAGAGGTGAGGGGGCGT 5446
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5447 CAGTTTTTCACTGACTGGGATACGTTCAACAAACGTTTACAGCACTTGGGGGGCGCTCA 5506
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3112 CAATTCTTCACTGACTGGGCAAGTACACAGAGGTACTTCCACTGGGCTGGTGTCTCT 3171
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5507 GAGCTGTTTATCTATCCGGAATACTACCTCGACCCGACGGTCCGTTATCGGGGAGACGGC 5566
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3172 CAACTTGTCTACTACCCAGAGAACTACATTGACCCCAACCATGAGGATTTGGTCAGACCA 3231
Qy
5567 ATGATGGACACCTGCTGCTGCTGTCAGCAGAGCAGTATCAACCGCATACCGTGGAG 5626
Db
3232 ATGATGGATGCTCTTGTGCAATCTGTCTCCAAAGCAACTCAACGCTGACATGTGGAG 3291
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5627 GATGCTTTTAAACCTTATCTGACCACTTTGAGCAGATTGCCAATCTGAACACTGTGACG 5686
Db
3292 GATGCTTTCATGAGCTACCTCACCTCTTCGAGCAAGTTGGCAACCTCAAGGTCACTCT 3351
Qy
5687 GATATCAAGATHAACCCGAGCATGACGCGGGGACTACATGTTATGTTGGTTCGAGCATC 5746

Db 3352 GCTTACCATGACAAACATCAACACGACCAAGGCTCTACCTACTTTCATTGGTCTCTCTGAG 3411
Qy 5747 ACAGATCAGACTAACTGCTACTGGCGAGCGCCCAACACAGACAAAATCCCAAGACTCAATG 5806
Db 3412 ACTGATGCTGGTAGTACTACTGAGATCCGTGGACACACGAAGTTCAACGATGGCAAG 3471
Qy 5807 ATGCCCGGAATGCTCGGACCGGATGACAAAAATTAACCTGCGGAATGAATCCGTGGTCA 5866
Db 3472 TTCGCTGCAACACGCTTGGCTGAGTGGCACAAAGATTGACTGCCCTCATACCCATACAG 3531
Qy 5867 GATCTTGTGCTCGGTGTTTTCAACAGTGCCTTTTATGCTGCTCGGTGCGAAGAAAT 5926
Db 3532 TCCACCATCAGACCTGTGCATCTCAAGAGCGGCTCTACTTGTCTGGCTGTGACAGAAG 3591
Qy 5927 CAGT-----CTGTGATACGGGAGCAGAGACGACGACAAACACGACGACAGC 5974
Db 3592 GAGATCACCAGCAAACTGGCAACTCCAGGATGGTTACCAAACTGAGACTGACTACCGC 3651
Qy 5975 TACAGCTGAACACTGTCTCGGCGGTACGACGGTACATGAGTTCCCGGTTGCTGTTTC 6034
Db 3652 TACGAGTTGAAGTTGGGCTCATACCGCTACGATGGTACCTGGAACACTCCAATCACCTTC 3711
Qy 6035 GACATTACCGCACATCGCATTTCCGGAACGACGAGCATGATGACCTGTAATCCC 6094
Db 3712 GATGTCAACAGAAAGATCAGCGAGTTGAAGTTGAGAAGAACCGTGTCTCTGGTCTCTAC 3771
Qy 6095 CTGACTGAGCAGCTCTATTGGC-----GTTTTACTCTCCACGACGACGCGGA 6144
Db 3772 TGCCTGGTTACCAAGGTGAGGACACCTCTTGGTCAATGTTCTACACCGACGACAGACC 3831
Qy 6145 CTTTGTAT-----AACGCTCAGCTGANTTCT 6169
Db 3832 CTTGACTCTTACAAGAACGCTTCATGCAAGGCTCTTACATCTTTCGCTGACATGGCTTC 3891
Qy 6170 GTGATTAATGATGACGCTAA-----ATGTCACTCAGATATAGGATTTTT 6217
Db 3892 AAGCAGATGACTCCAGAGCAAGCAACGCTACCGGTGACAACTCTTACCAACAGTTTCGAC 3951
Qy 6218 AAGAGCGTCAGTCAACGAATTAATACGAGCACTCAGAAAATTAATTAATATGTTTTTCA 6277
Db 3952 ACCAACAGTCAGGCGTGTCAACACAGATACGCTGAGGACTACGAGTCCCAAGCTCT 4011
Qy 6278 GACCTTCCGCTAATTTTGTGTCAGTGCAACGAGTTTAAATGATGATGATATCCACAGC 6337
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Qy 6338 GATTTCTCACTCTTAATCTAAACTACAGTACTGTTTTTACTAATGA----- 6387
Db 4072 GACATCCCAACCATCAACTACAGGCTGCCCTCTTCCGACCTCAAAATCTACATCAGCCCA 4131
Qy 6388 -----AGATTCTCTCTTTTGACGCCAGAGCTTTCATATTACAGCAAAATGTTTCGTTT 6441
Db 4132 AAGCTCAGGATCATCCACAGGCTACAGGGTCAAGAGGAAACAGTGCACCTTGATG 4191
Qy 6442 TGTTAGTACTCTGGCATCGCACTCAATCTACATAGAAAAATTCGTTCAGGCAGGGAT 6501
Db 4192 AACAAAGTACGCAAGTTGGGTGACAAGTTCAATTCTGTACACCTCTCTTGGTGTCAACCCA 4251
Qy 6502 AGAATTTGAGGAATTAATTTTATGAGCGCAGCGCCGCGGGATTTGACGGATTTGT 6561
Db 4252 AACAAAGCTCCAAACAGCTCATGTTCTACCCAGTCTTACCAATACTCTGCGCAACACCTCT 4311
Qy 6562 GG-----GAGTGGATGTTTCTAATTAACAAAGTATACAGGTCGGAAGAAAGACAGCTTG 6614
Db 4312 GGTCTCAACCGGTAGACTCTGTTCCACAGGGACACCCTTACCCAGCAAGGTGGAG 4371
Qy 6615 G-----TGTCACGTAAATATCT 6631
Db 4372 GCTTGGATTTCTGTGTCNAGAGGTCCCTCAACCAACGAGACGCTGCCATTGGTATGAC 4431
Qy 6632 TATTCGCTACTGGCGTTAGTGGTTCTGTTGAGTTATTTATGTTTCAATAAATAATAC 6691
Db 4432 TACGCCACAGACTCCCTCAACAGACCTGATGACCTCAAGCAGTACATCTTTCATGACTGAC 4491

Qy 6692 TTCAGCGAA----- 6701
Db 4492 TCCAGGGCACGCCACTGATGTCTCTGGTCCAGTGGAGATCAACACTGCAATCAGCCCA 4551
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Db 4552 GCCAAGGTCCAAATCATTTGTCAGGCTGGTGGCAAGGAGCAAACTTTTACAGCTGACAAAG 4611
Qy 6760 CGTGTCTCTATTGGCTCTCAAGATTTTTTGA--GTGTAAGTCTGCTCATGCGCGCACTT 6817
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Qy 6998 TT-----TGACGTGACGTTT 7012
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APPLICANT: Patell, Jim
APPLICANT: Merlo, Donald
APPLICANT: Herman, Rod
APPLICANT: Roberte, Jean
APPLICANT: Guo, Lining
APPLICANT: Schafer, Barry
APPLICANT: Sukhapinda, Kitisari
APPLICANT: Owens Merlo, Ann
TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin
CURRENT APPLICATION NUMBER: US/10/435,835
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: US 60/148,356
PRIOR FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 7621
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence.hemicoct tcda
OTHER INFORMATION: fused to the modified 15 kDa zein endoplasmic
OTHER INFORMATION: reticulum signal peptide
FEATURE:
NAME/KEY: CDS
LOCATION: (4)...(7614)
FEATURE: unsure
NAME/KEY: (1)
OTHER INFORMATION: n can be a, t, g, or c
us-10-435-835-6

Query Match 4.3%; Score 815.2; DB 4; Length 7621;
Best Local Similarity 48.5%; Pred. No. 6.5e-216;
Matches 3641; Conservative 0; Mismatches 3368; Indels 495; Gaps 31;

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Qy 2570 TCATGGGGAGAGTCTGCTATCTCTACAGTCAGGCGGACGACGACGACGACGACGCG 2629
Db 187 TCCTGGTCCGAGAGCCCATGACCTCTACATGACGCTCAGCAAGCTCAGAGGACACAGG 246
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Qy 2690 GGAATACGGCAGGCA---GCCGGCAGTCGACGCTATGATGACTGGTTTGGCTCCCGGCA 2746
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Db 367 AGCCAGTACGTGGCTCTCTGGTACAGTCTCTCCATGTTTCAGCCAGCGCTTACCTCACT 426
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Db 427 GAGTTGTACCGGAGGCTAGAACTTCTGCTTCTGCTCTGCTACTTGGACACA 486
Qy 2867 CGGCGTCCCGACCTGGCGGCTGGCCCTTAGCCAGAAATATATGACGACGAGCTCTCC 2926
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Db 667 CATGATGCTTACGAGAACGTCAGGAGGTCTCAACTTCAAGACCTCTGGTCTTGAGCAA 726
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Db 727 CTCACGCTTCTCCAGCCATTGTGTGGTTGATGACCAAGGATCTTGTCTGGTATCAAC 786
Qy 3164 GCGGATATTTACCGGAGCTGTATCAGATCTGSCCGAAGAAATTTAGCAGACAGATTAC 3223
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Db 907 TACCTCAAGAGGTACTACAACCTTGTCTGATGAGGAGCTTTCT-----CAATTCATT 957
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Qy 3404 CTGAATGAAAGCACTGGTTTTAAATAACTATATCATCATTTATTTAAGAACGCTAGGCGGAGAC 3463
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Db 1855 ATCCACCAACTCAACCATGATGATGATGAGCTCTTGTCTCATTTGCACTCGGTGAGGCAAG 1914
QY 4298 GTGGCGCGGCTCGTGTCCGATAATGAG-----CTGACGCACTTCTGTACACAG 4348
Db 1915 ACCAACTCTCTGCAATCTCTGACAGAGTTGGCAACCTCATCAGGAAGTTGAACACC 1974
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QY 5687 GATATCAAGATAACCGCAGATGACGAGGGAATACATGTTGTTGTTGTTGTTGTTGTTGTTG 5746
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Qy 8186 CTCAGACCCAGGCGAGTGAACCTGATACGCCAGGCGCTTCGCCAGCAGGATACGTCCTC 8245
Db 6232 CTCAGAACAGGAGCTGAGTTGATCCTCACCACTTTGTCCATCCAAAGACAGACATT 6291
Qy 8246 GAGGAATCGATCGGATATTTGCCGCTCGAGGAGAGCGCGCGCGCGAGATGCGT 8305
Db 6292 GAGGAGCTTGATGCTGAGAGAGACAGTCTTTGAGAGAGCAAGCTGCTGCTGCCAATCTCGC 6351
Qy 8306 TTTGAAGTTTAAAGCTTGTAGAGGCGGAGCTGAAACACCGGCGAAGAAACAGGCGATG 8365
Db 6352 TTTGACTCTTACCGCAAGCTCTAGATGAGAACATCAACGCTGTTGAGAACCAAGGCGATG 6411
Qy 8366 GACTTGTACCTCAGTTGCTCGGCTGCTGGCATCAACGCGCGCTCTTTTGGCGGAG 8425
Db 6412 ACCCTCAGGCTTCCGAGCTGCTCACACATGCTGTCCAGCCTCTGCTTGGCTGGT 6471
Qy 8426 GCGCGGCGGATGCTGCCCAATATTTACGGGCTGGCGGTCCGGTCCGGGCTCCCGCTATGG 8485
Db 6472 GCAGCTGCTGACCTGTTCCAAACATCTTCGGTTTCGCTGGTGGTCCAGATGGGT 6531
Qy 8486 GCACTATTTAAAGCAACCGCATCGGATCCAGGTGCTCTCGATGCGACCCGCAATCA 8545
Db 6532 GCCATTTGCTGAGGCTACCGGTTACGTATGAGAGTTCTTGCCAAACGTCATGAACACTGAG 6591
Qy 8546 GCGGCAAAATCAGCAGTCGGAAGTGTACCGCGCTCGCGGAGGAGTGGGAATCCAG 8605
Db 6592 GCTGAACAGATCAGCAATCTGAGACTCAGAAAGCGCGCTCAAGAGTGGAGATCCAA 6651
Qy 8606 CGTATAGTGGCAGTCTGACGTGGCGCAGATTGATGCCAGCTGGCGGCGCATGGCAGTG 8665
Db 6652 AGGAAACACGCTGAGCAGAGTTGAAGCAATCGATGCTCAACTCAAGTCTTGGCTGTC 6711
Qy 8666 GCGCGGAGGCGCTGAGCTGAGAAACCTTACCTTGAGACCCAGCAGACCCAGGCAAG 8725
Db 6712 AGAAGGAGGCTGCTGCTCCAGAGACCTCCCTCAAGACCCCAAGAGGCAAAACCCAG 6771
Qy 8726 GCGCAGTTGCACTTCTGACAGATGAATCAACAAATACGCTCTGTACAGCTGGCTGGCG 8785
Db 6772 TCCAGTGGCTTCTCCAAAGAGATGCTCCAAACAGGCTCTTACAACTGGCTCAGA 6831
Qy 8786 GCGAGTGTGCGCCATTTATTAACAGTTCTATGACTGGCAGTATCCGCTGCTGATG 8845
Db 6832 GCGCGCTTGGCTGCCATCTACTTCCAATTTCAAGACCTTGTGCTGGCAGGTGCTCATG 6891
Qy 8846 GCGCAACAGGCTGGCAGTGGG---TAAATTCGAGACTAGTTCGCTTTATCCAGCCGGG 8902
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Qy 8903 GCTGATGGGGCAATGCGGCTGCTGCGCGGGAACCTGATGCTGATCTGGCG 8962
Db 6952 GCTTGGCAAGCACTACGCTGCTCTCTGCTGGTGAGACCTCACTGCTCTCTTGGCT 7011
Qy 8963 CAGATGAGCAGGCTGCTGCTGACGCGGGATGAGCGGGCAATAGAGGTGACGCGGACGCT 9022
Db 7012 CAAATGGAGATGCTCACTCAAGAGGCAAGAGGCTTTTGGAGTGGAGAGGACAGTC 7071
Qy 9023 TGCCTGTGAGGCTCTATACAGCTGCG---GGAGGATGCGGCTTCTCTGCGCGGAG 9079
Db 7072 TCCCTTGTGAGTCTACGCTGCTCTCCAAAGGCAAAAGGTCATTTCTCCCTTGTCTCAA 7131
Qy 9080 AAGTGGTGAACCTGCTCAGTAACGCTTGGGAGTGGCGGATGCGGAAGCAACGATTA 9139
Db 7132 GAGATTGACNAAGTTGGTCAGCAGGTTCTGGTTCTGCTGGTTCTGGTAACAACAATTG 7191
Qy 9140 CAGATGG-----ATCAACAGCAACTCAGAGCCACCTCGAAACTGGCTGAC 9184
Db 7192 GCTTTGGGCGCTGGTACTGACACCAAGACCTCCCTCCAAAGCCTCTGCTCTTCTGGCTGAC 7251

Qy 9185 CTCGGTATCGGCAACGATTTACCCGGTCTCCCTTGGCAACCATGAGGCGCATCAACAATA 9244
Db 7252 CTCNAAGATCAGGAGGACTTACCAGCTTCCCTTGGCAAGATCAGGCGCATCAAGCAATC 7311
Qy 9245 AGCGTCACGCTCCCGCGCTGCTGGCGCCTATCAGGACGTCGCTGCGGTCTTCAGCTAC 9304
Db 7312 TCTGTACCCCTCCAGCTCTCTTGGTCCATACAGATGTCCAGCAATCTCTCTCTAC 7371
Qy 9305 GCGGAAGTATGCTCATGCCCGGGTTGACGGCGCTGGCGGTCTCACACGGAATGAAC 9364
Db 7372 GGTGACAAGGCTGGTTTGGGAAAGGTTGCGAGGCTCTTGTCTCTCATGGCATGAAC 7431
Qy 9365 GACAGGCGCAATTCCAACTGGATTTCAATGACCCGCTTACTGCGGTTCGAGACTT 9424
Db 7432 GACTCTGGTCAATTCCAACTTGACTTCAACGATGGCAAGTTCTCTCCATTCGAGGCAAT 7491
Qy 9425 CCAAGTTGATGACACAGGAGCCTGACACTGAGCTTCCCGGATGCT-----GAC 9472
Db 7492 GGCAT---TGACCAAGGACCTTCCCTCTCTTCCCAACGCTTCCATGCCAGAGAAG 7548
Qy 9473 GCGAAACAAACAGCGGATGCTCTCTAGTCTGAGCGACATCATCTGCAATTCGTTACACC 9532
Db 7549 GGAAGCAAGCCACCATGCTCAAGACCTCAACGATATCATCTCCACATCAGGTACACC 7608
Qy 9533 ATTA 9536
Db 7609 ATCA 7612

RESULT 13
US-09-817-514A-7
; Sequence 7, Application US/09817514A
; Patent No. 6639129
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 7512
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
US-09-817-514A-7

Query Match 4.1%; Score 781.2; DB 4; Length 7512;
Best Local Similarity 60.2%; Pred. No. 2e-206;
Matches 1356; Conservative 0; Mismatches 878; Indels 18; Gaps 3;
Qy 7301 ATGAGCTTCTCCGAGCCCAATGCCCTCTAATTTCTGGAGCTGTTCTATTAACGCGGATG 7360
Db 5257 ATGAGTTTCTCTGGCGCCAAATGCTCTATTTCTGGAACTGTTCTATTACACGCGCATG 5316
Qy 7361 ATGGTGTTCAGGGTGTGTCAGGACAGACTTCCCGGAAGCCACCGCTGGCTGGCAG 7420
Db 5317 ATGATGGCTCATCGTTGTTGTCAGGAACAGAAATTTGATGCGGCGAACCATTGGTTCCGT 5376
Qy 7421 TATGCTCGAAACCCCGCGGCGACGTGGTAAACGGGGTCTGTCAGAAATTTACACCTGGAAT 7480
Db 5377 TATGCTCGAGTCCATCCCGTTATATCGTTGATGGTAAATTTGCTATCTACCACTGGAAC 5436
Qy 7481 GTCCGCTCGCTGGAGAGGACACCGGCTGGAAACGACTCCCGCTGGACTCTCATTTGACCCC 7540
Db 5437 GTGCGACCGCTGGAAGAGACACCCAGTTGGAATGCAACAACTGGACTCCACCGATCCA 5496

APPLICANT: Schoonover, Sue
APPLICANT: ffrench-Constant, Richard
APPLICANT: Rocheleau, Thomas A.
APPLICANT: Blackburn, Michael B.
APPLICANT: Hey, Timothy D.
APPLICANT: Merlo, Donald J.
APPLICANT: Orr, Gregory L.
APPLICANT: Roberts, Jean L.
APPLICANT: Strickland, James A.
APPLICANT: Guo, Lining
APPLICANT: Ciche, Todd A.
APPLICANT: Sukhapiinda, Kitiseri
TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow AgroSciences Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,567B
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.93804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 7515 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..7515
US-08-851-567B-11

Query Match 4.1%; Score 781.2; DB 4; Length 7515;
Best Local Similarity 60.2%; Pred. No. 2e-206;
Matches 1356; Conservative 0; Mismatches 878; Indels 18; Gaps 3;

QY 7301 ATGGACTTCTCCGGAGCCAAATGCTTCTTCTGGAGCTGTCTTATTACAGCCGATG 7360
DB 5257 ATGGAATTCCTCGGCCAAATGCTTCTTCTGGAACTGTCTTATTACAGCCGATG 5316
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5377 TATGCTCGGAGTCCATCCGGTTATATCGTTGATGGTAAATTTGCTATCTACCACCTGGAAC 5436
7481 GTCCGTCCTCGAGGAGACACCGGCTGGAAAGACTCCCGCTGGACTCCATTTGACCC 7540
5437 GTCCGACCGCTGGAAGAACACACCAAGTTGGAATGCACAACTGGACTCCACCGATCCA 5496
7541 GATGCAATAGCCAGTACGACCCCATGATCAATCAAGTGCACACCTTTATGCTGACCTC 7600
5497 GATGCTGTAGCCCAAGATATCCGATGCACTCAAGTGGCTTACCTTTATGGCAGCTTG 5556
7601 GACCTGCTGATTCGCCCGCGTGATGCGCTACCGCTGCTCGAGCGGACACCCCTTAAC 7660
5557 GATCTGCTAATGCGCGTGTGATGCTGTCTTACCGCCAGTTAGAGCGTGATAGTTGGCT 5616
7661 GAGGCCCGGATGTGTAGCTCAGGCCCTGAACCTTCTGGGCGACGAGCCCTATATTTCC 7720
5617 GAAGCTAAATGTGGTATATACACAGCGCTTAATCTGTGGGTGATGAGCCACAAGTGATG 5676
7721 TTTGACGCGACTGTGTGCGCGTTGACCTGTGGGTGACGACGCGCAGCGAGGTGACGACGC 7780
5677 CTGAGTACGACTTGGCTTAATCCAATTTGGGTATGCTGCTTCAAAAACCAACACAGCAG 5736
7781 GATTACAGGAGG-----CCCTGTGCGCGTGC GCGCGGTGTGTGCGCGCTCCCGAGACA 7834
5737 GTTGTGTCAGCAAGTGCTTACCAGTTGCGTCTCAATAGCAGGTTAAAAACCCCGTTGCTA 5796
7835 CGGACGGCGAATTCCTGACGCGACTGTTCTCCCGCAGCAGCAACGAGGTGCTCAAGGC 7894
5797 GGAACAGCCCAATTCCTGACCGCTTATTCCTGCGCGCAAGAAATAGCAAGCTCAAGGC 5856
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5857 TACTGGCGGACACTGGCGCAGCGTATGTTTAATTTACGTCAATCTGTGATTGACGCG 5916
7955 CAGCGCGTTTCCCTGTCCGTCTACGCCAGCGCTCGAAACCGCTCGCGCTCGAGAGTGCC 8014
5917 CAGCGCTCTCTCTGCGCGTGTATGCTAAACCGCGGTGATCCAAAGCTTTACTGAGTGG 5976
8015 GTCGTCAACAGCGCGAGGCTGCTGACGACACTGCGCGCGCGGTGATGCGGCTTTACAGT 8074
5977 GCGGTTTCAAGTCTTCAAGGGGAGCGCGACTTTCGCGAAGCGCGCTGACTATTACCAGC 6036
8075 TTTCCCGGTCTATGCTGGAGAAACCGCCGGGGGATGGTGAGCTGCTGACCGGGTTTCGGCAAC 8134
6037 TTTCCCTCAATGCTAGAGGGGCA CGGGGCTTGGTTAACCACTTATACAGTTTCGGTAGT 6096
8135 ACACGTGCTGGTATTACCGAGCGT CAGGATGCGGAGGCGCTGGCCAAACTGTGCGAGACC 8194
6097 TCACATTATGGGGTACAGTGAGCGT CAGGATGCGGAGGCTATGAGTCAACTACTGCAAAAC 6156
8195 CAGGCGAGTGAAGTATATACCGCGCGCTTCGCCACAGCAGGATAACGCTCTCGAGGAAATC 8254
6157 CAAGCCAGCGAGTTAATCTGACCACTGACCACTGATGATGAGGAGTAAACCAATTCGAGAGCTG 6216
8255 GATGGGATATTTCGCCCGCTGGAGGAGAGCGCGCGCGCGCGAGATGGGTTTGAACGT 8314
6217 GATTGGGAAAAAACCGCGCTTCAAGTCTCTTTAGCTGGAGTGCAACACGGTTTGACAGC 6276
8315 TACAAAGTGTGTGTA CAGGCGGAGCGTCAACACCGCGGAAAAACAGGCCCATGAGCTTTGATAC 8374
6277 TATAGCAACTGTATGAGGAGAAACATCAACGCGAGGTGAGCAGCAGCGCTGGCGTTACGC 6336
8375 CTCAGTTCGTCCGTGCTGCGCATCAACCGCGCGCTCTTTTTCGCGGAGCGCGCGCC 8434
6337 TCAGAACTGTCTATGAGTCTCAGGAGCGCAGAGTTTCCTGATGCGAGCGCGGTGTT 6396
8435 GATATGCTGCCCAATATTTTACGGGCTGCGCGCTGCGGGGCTCCCGCTATGGGCACTATTT 8494

Db 6397 GATATGGCACCAGATATCTTCGGCCTGGCTGATGGCGCATGCAATATGCTGCTATTGCC 6456
Qy 8495 AAAGCCACCGCATCGGCATCCAGTGTCTCCGATGCCACCCGCATATACGGGACAAA 8554
Db 6457 TATGCCATCGTGGAGGTATGAGTGTCTTCCAGATGTTGATCGGAGAAA 6516
Qy 8555 ATCAGCCAGTCCGAAGTGTACCGCGTCCGGAGAGTGGGAAATCCAGCGTGAATG 8614
Db 6517 GTTCTCAGTCCGAATATATCGCGTCCCGCTCAAGAAATGAAATTCAGCGTGAACA 6576
Qy 8615 GCGCAGTCTGAGTGGCGCATGATGCCAGTGGCGGCATGCGCGGCA 8674
Db 6577 GCACAGCGGAGATTAACAGGTAAACCGCACTGGAATCAGTCTATTTCGCGGTAA 6636
Qy 8675 GGGCTGAGTGCAGAAATCTTACCTTGAGACCCAGCAGACCCAGGACAGCGCGCAGTTG 8734
Db 6637 GCCGCTGAATGCAAAAGAGTACTGAAACCCAGCAGCTCAGGCGCAGCAACTT 6696
Qy 8735 GCATTCCTGAGAGTAAGTTCACAAATACGGCTCTGTACAGTGGCTGGCGGGCAGTTG 8794
Db 6697 ACTTCTTAAAGACCAATTCAGTAATCAAGCGTTATATAGTTGGTTACGAGGCGTTG 6756
Qy 8795 TCCGCCATTTATACAGTCTATGACCTGCGAGTATCCGCTGCTGATGGCGCAACAG 8854
Db 6757 TCAGTATTTATTTCCAGTCTATGACTTGGCCGTATCACGTTGCCCTGATGGCAGCAA 6816
Qy 8855 GCCTGGCAGTGGGA---TAAATTCGAGACTAGTGGTCTTATCCAGCGGGGCGCTGGATG 8911
Db 6817 TCCTATCAATGGGAAGCTATGATTAATTCATAGCTTTGTCAACCGGTGCAATGCAA 6876
Qy 8912 GGGGCAATGCGGTCTGCTGGCGGGGAAAACCTGTATGCTGAATCTGGCGCAGATGGAG 8971
Db 6877 GGAACCTTACGCGCGTATTGTGTGAGAGCTTTGTATACAAATCTGGCACAATGSA 6936
Qy 8972 CAGGCTGCTGACGGGGATGACGGGCAATAGAGTGACGCGGAGCTTGCCTGTG 9031
Db 6937 GAGGCATATCTGAAATGGGAATCTCGCGCTTTGGAAGTAGAACACCGGTTTCAATGGCA 6996
Qy 9032 GAGGTCTATACAGCCTCGCGGAGATGCGGCTTCTCTGCGCGCAAGGTGGTGSA 9091
Db 6997 GTGGTTATGATTCAGTGAAGGTAAATGATCGTTTAAATTTAGCGGAACAATACCTGCA 7056
Qy 9092 CTGCTCAGTAAACGTTTCGGGAGTTCGGGTTACGAAAGCAACGGAATACAGATGATCAA 9151
Db 7057 TTATTTGATTAAGGGGAGGAAACAGCAGGAATTAAGAAATGGTTTATCATTTGGCTAAT 7116
Qy 9152 CAGCAATCTGAGGCCACCTGAAACTGGCTGACCTCGTATCGGCAAGATTAACCGGTC 9211
Db 7117 GCTATCTGTAGCTTCGGTCAAAATGTTCGACTTGAACCTGGGAAACGGATTTATCCAGAC 7176
Qy 9212 TCCCTTGG-----CACCATGAGCGCATCAAAACAAATAAGCGTCACGCTCCCGGCG 9262
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Qy 9263 CTGCTCGGCGCCTATCAGGAGCTCCGTCGCTCTCAGCTACGCGGAAGTATGGTCA 9322
Db 7237 TTGTTTGGGCTTATCAGGATGTTTCAAGTATGCTCAGCTATGTTGGCAGTACTCAATG 7296
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Qy 9443 ACCCTGACACTGAGCTTCCGAGTGTGACGGCAAAACAGGCGGATGCTCTCAGTCTG 9502
Db 7417 ACATGAATCTTCAATTTCCGAATGCTACCGCAAGCAGGAAGCAATATTCGCAACTATG 7476
Qy 9503 AGCAGATCATCTCGATATCCGTTACACAT 9534
Db 7477 AGCGATATTTTGGCATATTCGTTATACCAT 7508

RESULT 15

US-09-637-048C-2
; Sequence 2, Application US/09637048C
; Patent No. 6590142
; GENERAL INFORMATION:
; APPLICANT: Patell, Jim
; APPLICANT: Merlo, Donald
; APPLICANT: Herman, Rod
; APPLICANT: Roberts, Jean
; APPLICANT: Guo, Lining
; APPLICANT: Schafer, Barry
; APPLICANT: Sukhapingda, Kitiieri
; APPLICANT: Owens Merlo, Ann
; TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin
; FILE REFERENCE: 50698
; CURRENT APPLICATION NUMBER: US/09/637,048C
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/148,356
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 2
; LENGTH: 7515
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7512)
US-09-637-048C-2

Query Match 4.1%; Score 781.2; DB 4; Length 7515;

Best Local Similarity 60.2%; Pred. No. 2e-206;
Matches 1356; Conservative 0; Mismatches 878; Indels 18; Gaps 3;

Qy 7301 ATGAGCTTCTCCGGAGCCAAATGCCCTCTATTTCTGGAGCTGTTCTTATTACACGCCGATG 7360
Db 5257 ATGATTTCTCTGGCCCAATGCTCTATTTCTGGGAATGTTCTTATTACACGCCGATG 5316
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Db 5377 TATGCTCGGAGTCCATCCGGTTATATCGTTGATGTTAAATTTGCTATCTACCACTGGAAC 5436
Qy 7481 GTCCGTCGCTGGAGGAGACACCGGCTGGAAACGACTCGCGCTGGACTCCATTGACCCC 7540
Db 5437 GTGGACCGCTGGAAGAGACACAGTTGGAATGCACAACTGGACTCCACCGATCCA 5496
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Qy 7835 CGGACGCGGAATTCCTCTGAGCGCACTGTTCTCCCGCAGCAGAAACGAGGTGCTCAAGGC 7894

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 QY 8435 GATATGTCGCCAATATTTACGGCTGCGCGTGGCGTCCGCTATGCGGACATTTT 8494
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 QY 8495 AAAGCCACCGCATTCGATCCAGGTGCTCCGATGCGCACCGCATATCAGCGGCAAA 8554
 Db 6457 TATGCCATCTGCTGACGATTTAGTGAAGTCTTTCGCAAGATGTTGATGCGGAGAA 6516
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 Db 6517 GTTGTCTCAGTCGGAATATATCGCGCTCGCGCTCAAGATGGAAATTCAGCGTGACAA 6576
 QY 8615 GCGCAGTCTGAGTGGCGAGATTTGATGCGCGCTGCGCGCATGCGAGTGGCGCGGAA 8674
 Db 6577 GCAAAAGCGGAGATTAACAGTGTAAACGCGCAACTGGAATCACTGTCTATTCGCGTGA 6636
 QY 8675 GCGGCTGAGCTGCAGAAATCTTACCTTTGAGACCCAGCAGACCCAGCAGCGCGAGTTG 8734
 Db 6637 GCGCTGAATGCAAAAGTACCTGGAACCCAGCAGCTCAGGCGAGGCAACTT 6696
 QY 8735 GCATTCCTGCAAGTAAAGTTCAACAATACGCGCTCTGTACAGCTGGCTGCGGGCGAGTTG 8794
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 QY 8795 TCCGCCATTTATACAGTTCTATGACCTGGAGTATCCGCTGCGCTGATGGCGCAACAG 8854
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 QY 8912 GGGGCAAAATCCGCTGCTGCGCGGGGAAACCCCTGATGCTGAATCTGGCGAGATGGAG 8971

Db 6877 GGAACCTACCGCGCTTATTTGTGTGGAGAAGCTTTGATACAAAATCTGCACAAAATGGA 6936
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 Db 6937 GAGGCATATCTGAAATGGGAATCTCGCGCTTTGGAGTAGAACGACGCTTCAITGGCA 6996
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 QY 9152 CAGCAACTCAGCGCCACCTGAAACTGCTGAGCTCGGTATCGGCAACGATTAACCGGTC 9211
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Search completed: January 27, 2005, 05:49:12
 Job time : 1755 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 06:07:24 ; Search time 75282 Seconds
(without alignments)
11895.606 Million cell updates/sec

Title: US-10-070-489A-1

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 segs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
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- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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DEFINITION Sequence 1 from Patent WO0116305.
ACCESSION AX092884
VERSION AX092884.1 GI:13444936
KEYWORDS Serratia entomophila
SOURCE Serratia entomophila
ORGANISM Serratia entomophila
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Serratia.
REFERENCE 1
AUTHORS Glare,T.R., Hurst,M.R. and Jackson,T.A.
TITLE Nucleotide sequences encoding an insecticidal protein complex from Serratia
JOURNAL Patent: WO 0116305-A 1 08-MAR-2001;
New Zealand Pastoral Agriculture Research Institute Limited (NZ)
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Db	2161	AACTCAACAAACAGGACTATGTCGGCCGGGAACGAGTTTTCAGCTGGACCCGGGCCA	2220
Qy	2221	ATGGGAAGTCTCTTCCGCACTGATTTCCGCGACGCGAAGCTGAAACGGGTGTTGTTGAGA	2280
Db	2221	ATGGGAAGTCTCTTCCGCACTGATTTCCGCGACGCGAAGCTGAAACGGGTGTTGTTGAGA	2280
Qy	2281	AACCTGGTGCATAAACCTTTTGGACGCTACCCAAAGATGAAGATAACACCGCTACTGAG	2340
Db	2281	AACCTGGTGCATAAACCTTTTGGACGCTACCCAAAGATGAAGATAACACCGCTACTGAG	2340
Qy	2341	CGTGGCGCAACAAATGAATAAATGACTGTGTACGGCTGTCTTTCACACGATGGGACC	2400
Db	2341	CGTGGCGCAACAAATGAATAAATGACTGTGTACGGCTGTCTTTCACACGATGGGACC	2400
Qy	2401	ATCAACGTTAATGATGAGGCAAGACATTTATGTTAATATTTGATGATATTCTGGAGAAAT	2460
Db	2401	ATCAACGTTAATGATGAGGCAAGACATTTATGTTAATATTTGATGATATTCTGGAGAAAT	2460
Qy	2461	GATGCTCCACGAGCAGCTGTGCAAGAAACGATACAGCGGTGACGCTGACGAGTTT	2520
Db	2461	GATGCTCCACGAGCAGCTGTGCAAGAAACGATACAGCGGTGACGCTGACGAGTTT	2520
Qy	2521	ATTCTCGCTTCTGTTTCCGAGGTCAAAAAATCACTGGCGACAGGCTGTCTGGGGAGA	2580
Db	2521	ATTCTCGCTTCTGTTTCCGAGGTCAAAAAATCACTGGCGACAGGCTGTCTGGGGAGA	2580
Qy	2581	GGTCTGCTATCTGTACAGTCAGGCGCAGCAGCAAGAAAGAAAAACGGGTCTACCGAATC	2640
Db	2581	GGTCTGCTATCTGTACAGTCAGGCGCAGCAGCAAGAAAGAAAAACGGGTCTACCGAATC	2640
Qy	2641	CGTATTTCTGGCCCGGCGAATCCCTACTGTTGATTCGCTTCCGCTCGGATACGGCA	2700
Db	2641	CGTATTTCTGGCCCGGCGAATCCCTACTGTTGATTCGCTTCCGCTCGGATACGGCA	2700
Qy	2701	GGCAGCGGCGAGTCGCGAGCTATGATGACTGTTTGGCTCCCGCGCAGACCGTTTTCGCCG	2760

2701 GGCAGCGGCGAGTCGAGCTATGATGCTGGTTTGCTCCGCGCAGACCGTTTCGCCG 2760
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QY	4921	GGCCCGGCGCTCTGTCACAGAAATGAGCAGGATGTGA	CGGCGCCTTGGCGCAGGTGAGGGG	4980	6001	CTACGACGGTACATGAGGATCCCGGTGTCGTTCCGATTC	CGACATTCGCAATTTCC	6060
Db	4921	GGCCCGGCGCTCTGTCACAGAAATGAGCAGGATGTGA	CGGCGCCTTGGCGCAGGTGAGGGG	4980	6001	CTACGACGGTACATGAGGATCCCGGTGTCGTTCCGATTC	CGACATTCGCAATTTCC	6060
QY	4981	GGCCCGGTGAACAGGACAAACAGCGTGTTCACCTCT	CTGGGAAGAGGTGGACAGGCTGAGCA	5040	6061	GGAAACGCGAGGGCATGCACTGTGACCTGTAACTCC	CTGAGCAGCTCTATTGCGCGTT	6120
Db	4981	GGCCCGGTGAACAGGACAAACAGCGTGTTCACCTCT	CTGGGAAGAGGTGGACAGGCTGAGCA	5040	6061	GGAAACGCGAGGGCATGCACTGTGACCTGTAACTCC	CTGAGCAGCTCTATTGCGCGTT	6120
QY	5041	GTGGCTGGACATGAGTGAGACCTGTCCTATTCGCCAT	CCGGTCTGGCTAGCCTGATTCG	5100	6121	TTACTCCGTCACAGCAAGCGGACCTTTGATACCGCT	CAGCTGATTTCTGTGATTAATGA	6180
Db	5041	GTGGCTGGACATGAGTGAGACCTGTCCTATTCGCCAT	CCGGTCTGGCTAGCCTGATTCG	5100	6121	TTACTCCGTCACAGCAAGCGGACCTTTGATACCGCT	CAGCTGATTTCTGTGATTAATGA	6180
QY	5101	CCTGAAGTACATCAATGTGTCCGATGACAGTGCAC	CGTGTGTACAGCCAGTGGCAGGTGGT	5160	6181	TATGACGCTAAATGTCTCATCTCAGATATAGGGATTT	TTAAGAGCGTCAGTCAAGAAATTTAA	6240
Db	5101	CCTGAAGTACATCAATGTGTCCGATGACAGTGCAC	CGTGTGTGTACAGCCAGTGGCAGGTGGT	5160	6181	TATGACGCTAAATGTCTCATCTCAGATATAGGGATTT	TTAAGAGCGTCAGTCAAGAAATTTAA	6240
QY	5161	ATCCGCTCTGCTCGAGCGCGGTGAAAGACGCCAGAT	CGCGCTGCGACGATATCT	5220	6241	TACGAGCCTGAGAAATTTAATAATGTGTTTTT	TTCAGACCTTCCGCTAAATTTTGT	6300
Db	5161	ATCCGCTCTGCTCGAGCGCGGTGAAAGACGCCAGAT	CGCGCTGCGACGATATCT	5220	6241	TACGAGCCTGAGAAATTTAATAATGTGTTTTT	TTCAGACCTTCCGCTAAATTTTGT	6300
QY	5221	GGAGGAGGACACAGCAGCGCCCTTTGTGCGTATTAT	CTCGCTAATCTGSCACCGACAT	5280	6301	CAGTGCACAGGTTTAAATGATGATCTTAAATGAT	GTATCCACAGCGATTTCTCACTCCTTAATTTCTAA	6360
Db	5221	GGAGGAGGACACAGCAGCGCCCTTTGTGCGTATTAT	CTCGCTAATCTGSCACCGACAT	5280	6301	CAGTGCACAGGTTTAAATGATGATCTTAAATGAT	GTATCCACAGCGATTTCTCACTCCTTAATTTCTAA	6360
QY	5281	GGTATCCGCGCGATGACCTCTTTCGGGTATCTGCT	GTGTAATACAGGTGTCAAGCA	5340	6361	AACTACAGTACTGTTTTTACTAAATGAGATTCCT	CTCTTTTTCAGCCAGAGCTTCATAT	6420
Db	5281	GGTATCCGCGCGATGACCTCTTTCGGGTATCTGCT	GTGTAATACAGGTGTCAAGCA	5340	6361	AACTACAGTACTGTTTTTACTAAATGAGATTCCT	CTCTTTTTCAGCCAGAGCTTCATAT	6420
QY	5341	GGTAAACACACCGCATTCGCGAGGCGCATCGCG	CGCATACGCTGTATATCAACCGGCG	5400	6421	TACAGCAAAATGTTTCTGTTTGTAGTACTGCT	GTGATCGGCACCTCAATCTACCATAGA	6480
Db	5341	GGTAAACACACCGCATTCGCGAGGCGCATCGCG	CGCATACGCTGTATATCAACCGGCG	5400	6421	TACAGCAAAATGTTTCTGTTTGTAGTACTGCT	GTGATCGGCACCTCAATCTACCATAGA	6480
QY	5401	CCTTAACGGAATAGAACTAGCGCCATGGCAGAG	GTGAGGGCGGTGAGTTTTTCACTGA	5460	6481	AAATTTCTGTCAGGCGAGGATAGAAATTTGAG	GAATTTTATGCGCCAGCGCCG	6540
Db	5401	CCTTAACGGAATAGAACTAGCGCCATGGCAGAG	GTGAGGGCGGTGAGTTTTTCACTGA	5460	6481	AAATTTCTGTCAGGCGAGGATAGAAATTTGAG	GAATTTTATGCGCCAGCGCCG	6540
QY	5461	CTGGGATACGTTCAACAAAGTTACAGACCTCG	GGCGGTCTCAGAGCTGTTTACTA	5520	6541	CGCGGATTTGACGGATTTGTGGGAGTGGAT	GTGTTCTAAATTTCAAAAGTATACAGGTCG	6600
Db	5461	CTGGGATACGTTCAACAAAGTTACAGACCTCG	GGCGGTCTCAGAGCTGTTTACTA	5520	6541	CGCGGATTTGACGGATTTGTGGGAGTGGAT	GTGTTCTAAATTTCAAAAGTATACAGGTCG	6600
QY	5521	TCGCGAAACCTACCTCGACCGACGCTCCGTAT	CGGCGACACCGCATGATGACACCCCT	5580	6601	AAAAAGAGCAGTTGGTGTCACTGTAAATCTTA	TTTCCGTCACCTGGGCTAGTGGTCTGT	6660
Db	5521	TCGCGAAACCTACCTCGACCGACGCTCCGTAT	CGGCGACACCGCATGATGACACCCCT	5580	6601	AAAAAGAGCAGTTGGTGTCACTGTAAATCTTA	TTTCCGTCACCTGGGCTAGTGGTCTGT	6660
QY	5581	GCTGCGAGTCTGTCAGCCAGAGAGTATCAAC	CGCGATACCGTGGAGAGTGCCTTTAAAC	5640	6661	TGAGTTTATTTATGATTCATCAATAAATAC	TTTCAGGGAATTTTGTGTCAGATAAATGAT	6720
Db	5581	GCTGCGAGTCTGTCAGCCAGAGAGTATCAAC	CGCGATACCGTGGAGAGTGCCTTTAAAC	5640	6661	TGAGTTTATTTATGATTCATCAATAAATAC	TTTTCAGGGAATTTTGTGTCAGATAAATGAT	6720
QY	5641	CTATCTGACCACTTTGAGCAGATTCGAATCT	GTACACCTGTCAGCGGATACCGATTA	5700	6721	AAACGCTTTAAATTTAGCGGAGTACATCAAA	AGTTAATTTAGTGTCTATTGGCTCTCA	6780
Db	5641	CTATCTGACCACTTTGAGCAGATTCGAATCT	GTACACCTGTCAGCGGATACCGATTA	5700	6721	AAACGCTTTAAATTTAGCGGAGTACATCAAA	AGTTAATTTAGTGTCTATTGGCTCTCA	6780
QY	5701	CGCCAGCATGACGAGGAGTACATGTTGTTG	GGTCCGAGCATCACAGATCAGACTAA	5760	6781	AGATTTTTCGAGTGTAAAGTTCGCTCATG	CGGCACTTCAGATATATGAATTAATCGATGA	6840
Db	5701	CGCCAGCATGACGAGGAGTACATGTTGTTG	GGTCCGAGCATCACAGATCAGACTAA	5760	6781	AGATTTTTCGAGTGTAAAGTTCGCTCATG	CGGCACTTCAGATATATGAATTAATCGATGA	6840
QY	5761	CTGGTACTGCGGAGCGCCAAACACAGCAAAAT	CCAAAGATCAATGATGCCCGGAATGC	5820	6841	TATCATCTGACATCCGCGTAAATCGGACT	GAAATTAATTCCTGGCCTTCCGCTGATG	6900
Db	5761	CTGGTACTGCGGAGCGCCAAACACAGCAAAAT	CCAAAGATCAATGATGCCCGGAATGC	5820	6841	TATCATCTGACATCCGCGTAAATCGGACT	GAAATTAATTCCTGGCCTTCCGCTGATG	6900
QY	5821	CTGGACCGGATGACAAATTAATCTCGGAAT	GAAATTCCTGGTTCAGATCTGTGCTC	5880	6901	GTATAATGATAGCTCAGTCTGCAATCCG	GGAATAATCTTTTCAACACCAATTCGCTGAG	6960
Db	5821	CTGGACCGGATGACAAATTAATCTCGGAAT	GAAATTCCTGGTTCAGATCTGTGCTC	5880	6901	GTATAATGATAGCTCAGTCTGCAATCCG	GGAATAATCTTTTCAACACCAATTCGCTGAG	6960
QY	5881	GGTGTGTTTCAACAGTCCGCTTTATGTGCT	CGGTCGAAGAGAAATCAGTCTGCTGATAC	5940	6961	TTTTTACCGTTAAATACAGTGTATTTCT	GGAAGATGAGTTTTCAGCTGTTACGTTTAC	7020
Db	5881	GGTGTGTTTCAACAGTCCGCTTTATGTGCT	CGGTCGAAGAGAAATCAGTCTGCTGATAC	5940	6961	TTTTTACCGTTAAATACAGTGTATTTCT	GGAAGATGAGTTTTCAGCTGTTACGTTTAC	7020
QY	5941	GGAGGACAGAGCAACAGACAGAGAGCTACA	CGCTGAAATCTGCTTCGCGG	6000	7021	CGCTGTGATCAGATAAAGTGTGCTGCT	GCGCGCCCGGACGCGCCATATTAACCGCTCATTCG	7080
Db	5941	GGAGGACAGAGCAACAGACAGAGAGCTACA	CGCTGAAATCTGCTTCGCGG	6000	7021	CGCTGTGATCAGATAAAGTGTGCTGCT	GCGCGCCCGGACGCGCCATATTAACCGCTCATTCG	7080
					7081	AAACATTAATATGACACTTCGCTTATCG	CAATTTACGTTAAATAACGCTGCGCGCAGTA	7140

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DB 47335 CGCTACATACGGCAGACATTAGTATCTCTTATCATCAAGTAATATACACCGGAGAAT 47394

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QY	525	GCTAAATTCATGATGATAAAACGTTCCATTAATAAAATTTTCAGAAAACCTTAACACGGCAAT	584	1605	ACTTCTTAATGTTAAATGCGGTGATTTGCTTTGGCTATTGCGGTGAGATTAATTCCTGTGGCG	1664
Db	47395	GCTAAATTCATGATGATAAAACGTTCCATTAATAAAATTTTCAGAAAACCTTAACACGGCAAT	47454	48475	ACTTCTTAATGTTAAATGCGGTGATTTGCTTTGGCTATTGCGGTGAGATTAATTCCTGTGGCG	48534
QY	585	TTTATGCTGATCAGTGAATGATGTTCTCGAAAAAATAATTAATTCGACCTCTGCGCACTTAT	644	1665	TATCAATCATAAATGAAAAACAATTTGTCCTCTCTTTTATTTGCTTTTCTCAATTAATACGGC	1724
Db	47455	TTTATGCTGATCAGTGAATGATGTTCTCGAAAAAATAATTAATTCGACCTCTGCGCACTTAT	47514	48535	TATCAATCATAAATGAAAAACAATTTGTCCTCTCTTTTATTTGCTTTTCTCAATTAATACGGC	48594
QY	645	CAGATAAAACACCCCATCGGTAAGTTTATTTATTTTATTTATTAATGATTTTATTAATGAT	704	1725	GTGCGCGCTGTCCTCCATCAGGACGATGACGGGGAGTATTACTATGCGGATTTGGTCCGA	1784
Db	47515	CAGATAAAACACCCCATCGGTAAGTTTATTTATTTTATTTATTAATGATTTTATTAATGAT	47574	48595	GTGCGCGCTGTCCTCCATCAGGACGATGACGGGGAGTATTACTATGCGGATTTGGTCCGA	48654
QY	705	TTTATTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGAT	764	1785	GACGATCATTAACCTTTTCCTCTGCTGTTTATATACGAATGCGGAAATCCTTCG	1844
Db	47575	TTTATTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGAT	47634	48655	GACGATCATTAACCTTTTCCTCTGCTGTTTATATACGAATGCGGAAATCCTTCG	48714
QY	765	GGGTGATTAATTTACTTTTCTCAATTTAAATTTGTTGGTATGACCAATGTTTAGATGATGGC	824	1845	GTGCGGGGAGAAAAATGAAGATAAGTTCCCGAGGTATCGCATTAATCAAGAAGTTTCGAA	1904
Db	47635	GGGTGATTAATTTACTTTTCTCAATTTAAATTTGTTGGTATGACCAATGTTTAGATGATGGC	47694	48715	GTGCGGGGAGAAAAATGAAGATAAGTTCCCGAGGTATCGCATTAATCAAGAAGTTTCGAA	48774
QY	825	ACGGATTCATTTATGTAATAAAAGATCTAAACCTTTAGCAGCAATCCTACTTGAGGAT	884	1905	GGTCTGCGCTTACACGCTTATCGCTGCGCGCTGAGCTCTGGAATCTGCTGTTATGSCAC	1964
Db	47695	ACGGATTCATTTATGTAATAAAAGATCTAAACCTTTAGCAGCAATCCTACTTGAGGAT	47754	48775	GGTCTGCGCTTACACGCTTATCGCTGCGCGCTGAGCTCTGGAATCTGCTGTTATGSCAC	48834
QY	885	GACCTCGACAGGACTTGATTTATTTGCCATTTTTCAGAAAGGAAGATGACGGGTGATAATA	944	1965	ACGCGAGGGGTTTACAAAGGGTGACATCATCAGCTCGATGAAGCCAGACGATGCTGACA	2024
Db	47755	GACCTCGACAGGACTTGATTTATTTGCCATTTTTCAGAAAGGAAGATGACGGGTGATAATA	47814	48835	ACGCGAGGGGTTTACAAAGGGTGACATCATCAGCTCGATGAAGCCAGACGATGCTGACA	48894
QY	945	ATAAAAAAACAAAAGTATAGCCTTAGGTATCGCCGATTAATCAATCAACACTTATTTGA	1004	2025	AACGATATTACCGTATTGAAACGGGCGGTCACTCAGGCGGTGCGCGTTCCTCTGAATTCAG	2084
Db	47815	ATAAAAAAACAAAAGTATAGCCTTAGGTATCGCCGATTAATCAATCAACACTTATTTGA	47874	48895	AACGATATTACCGTATTGAAACGGGCGGTCACTCAGGCGGTGCGCGTTCCTCTGAATTCAG	48954
QY	1005	CTTTTCTTACTTCTACCGTAGCTATTAATATGATATTAATCTGTATTTTATATAA	1064	2085	TGCAATACGATCGCTGCTTTCTTTGCTTTTAAATTTGCGCAGGGGAATTTTAAACGC	2144
Db	47875	CTTTTCTTACTTCTACCGTAGCTATTAATATGATATTAATCTGTATTTTATATAA	47934	48955	TGCAATACGATCGCTGCTTTCTTTGCTTTTAAATTTGCGCAGGGGAATTTTAAACGC	49014
QY	1065	AACCACTTATGATGCTGATGCTGATTAATGATGATGATGATGATGATGATGATGATGAT	1124	2145	TCTACCTTCTTGAATAAACTCAACAAACAGGACTATGTCGGCGCCGGAAACGAGTTTTTA	2204
Db	47935	AACCACTTATGATGCTGATGCTGATTAATGATGATGATGATGATGATGATGATGATGAT	47994	49015	TCTACCTTCTTGAATAAACTCAACAAACAGGACTATGTCGGCGCCGGAAACGAGTTTTTA	49074
QY	1125	TGATCGGTGTTAATCTTTTATTTCTTCCAGTGAAGTTTTCAGGGGGAATGATTTGGGTAAT	1184	2205	CGTGGAACCCGGGCCAATGGGAAGGTCTTCCGGGACTGATTCGCGGACGCGGAAGTGAA	2264
Db	47995	TGATCGGTGTTAATCTTTTATTTCTTCCAGTGAAGTTTTCAGGGGGAATGATTTGGGTAAT	48054	49075	CGTGGAACCCGGGCCAATGGGAAGGTCTTCCGGGACTGATTCGCGGACGCGGAAGTGAA	49134
QY	1185	CATACATGCTCATTTGTTGCTTTGATGTTAAATTAACGTTTCATTTATTTATTTCTAC	1244	2265	CGGTGTTGTTTGAAGAACTGGGTGCTAAACCTTTTCCGACGCTGACCAAGATGAAGAT	2324
Db	48055	CATACATGCTCATTTGTTGCTTTGATGTTAAATTAACGTTTCATTTATTTATTTCTAC	48114	49135	CGGTGTTGTTTGAAGAACTGGGTGCTAAACCTTTTCCGACGCTGACCAAGATGAAGAT	49194
QY	1245	TGTTGTTTCTTATTTGTCGGGAACCATAGAGACTGTCGCTATGTTAATAGGAATATTGG	1304	2325	AACACCGCGTACTGAGCGGTGGCGCAACAATGAATAAATGACTGTGTACGCGCTGTCTT	2384
Db	48115	TGTTGTTTCTTATTTGTCGGGAACCATAGAGACTGTCGCTATGTTAATAGGAATATTGG	48174	49195	AACACCGCGTACTGAGCGGTGGCGCAACAATGAATAAATGACTGTGTACGCGCTGTCTT	49254
QY	1305	ACTGGTTATATGCGCAAGGTTTATCGCTGCACTCTCTGGGGCGATGGTATTCATCATTA	1364	2385	CACACCGGATGGGACCATCAACGTAATGAATGAGGCAAGACATTTATTAATTTGATG	2444
Db	48175	ACTGGTTATATGCGCAAGGTTTATCGCTGCACTCTCTGGGGCGATGGTATTCATCATTA	48234	49255	CACACCGGATGGGACCATCAACGTAATGAATGAGGCAAGACATTTATTAATTTGATG	49314
QY	1365	CGCAAGATACTTCAATTTGTTGTCAGCGGGTATTTGTTTGTCTTTTATTTACTCG	1424	2445	ATAATCTGAGAAAGTGAATGCTCCACGAGCAACCTTTTCCGAGGTAAGATACAGCGG	2504
Db	48235	CGCAAGATACTTCAATTTGTTGTCAGCGGGTATTTGTTTGTCTTTTATTTACTCG	48294	49315	ATAATCTGAGAAAGTGAATGCTCCACGAGCAACCTTTTCCGAGGTAAGATACAGCGG	49374
QY	1425	GTTTGAATTTTCAGAGAACACAGCTTCCGTTATCAACTTCTATATCCCGAATGATATAC	1484	2505	TGACGCTGACGGATTTTATTTCTCGCGTTCTGTTTCCCGAGGTCAAAAAAATCACTGGGACA	2564
Db	48295	GTTTGAATTTTCAGAGAACACAGCTTCCGTTATCAACTTCTATATCCCGAATGATATAC	48354	49375	TGACGCTGACGGATTTTATTTCTCGCGTTCTGTTTCCCGAGGTCAAAAAAATCACTGGGACA	49434
QY	1485	ATATAGAAATGACCTTGGTCCCTTTGTTACAGCGCGGTGACGGTGAAGCTTTTGTGA	1544	2565	GCTGTCTATGGGAGGTTCTGTATCTGTACAGTCAGGCGAGCAGCAAGAACAGAAAGAAA	2624
Db	48355	ATATAGAAATGACCTTGGTCCCTTTGTTTACAGCGCGGTGACGGTGAAGCTTTTGTGA	48414	49435	GCTGTCTATGGGAGGTTCTGTATCTGTACAGTCAGGCGAGCAGCAAGAACAGAAAGAAA	49494
QY	1545	TCATTATGACCAAGATAGAGAGAAATATCTTGGAGAAATACCGCCATGTTCCAAATCAT	1604	2625	ACCGGCTCACCAATCCCTTATTTCTGGCCGGGCGAATCCCTTACTGTTGTAATGCGGTTT	2684
Db	48415	TCATTATGACCAAGATAGAGAGAAATATCTTGGAGAAATACCGCCATGTTCCAAATCAT	48474	49495	ACCGGCTCACCAATCCCTGTTTCTGGCCGGGCGAATCCCTTACTGTTGTAATGCGGTTT	49554
				2685	GCCTGGGAATACGGCAGGCGACCGGAGTCGACGCTATGATGATGATGCTGTTGCTCCGCG	2744

49555	Db		GCCTGGGAATACGGCAGGAGCCGGCAGTCGACGTATGATGACTGTGTTTGGCTCCGGCG	49614
2745	Qy		CAGACCGTTTCGGCCCGCCCGCTCGGTGGCTCCATGTTCTCACCGGCGCCTATCTGA	2804
49615	Db		CAGACCGTTTCGGCCCGCCCGCTCGGTGGCTCCATGTTCTCACCGGCGCCTATCTGA	49674
2805	Qy		CCGAGCTGTACCGTGAGGCGAAGGACCTGCATCCGGACACCTCGCTGTTCCGGCTGGACA	2864
49675	Db		CCGAGCTGTACCGTGAGGCGAAGGACCTGCATCCGGACACCTCGCTGTTCCGGCTGGACA	49734
2865	Qy		TCCGGCGTCCCGACCTGGCGGGCGCTGGCCCTTAGCCAGANAATAATGACGACGAGCTCT	2924
49735	Db		TCCGGCGTCCCGACCTGGCGGGCGCTGGCCCTTAGCCAGANAATAATGACGACGAGCTCT	49794
2925	Qy		CCACCTTGAGCTGTCCAAATGAGCTACTGTATCGCGGTATCGGGGACGCGAAGGGCTTG	2984
49795	Db		CCACCTTGAGCTGTCCAAATGAGCTACTGTATCGCGGTATCGGGGACGCGAAGGGCTTG	49854
2985	Qy		ACGACGACAGCTFCAGGAGCTGCTCGCCGGGTATCGCCTGACCGGCTGACCCCTATTC	3044
49855	Db		ACGACGACAGCTFCAGGAGCTGCTCGCCGGGTATCGCCTGACCGGCTGACCCCTATTC	49914
3045	Qy		ACTGGGCGTACGAGGCGGCCCGCAAGCCATTCTGTCGAGACCCGACGCTGATGGGCT	3104
49915	Db		ACTGGGCGTACGAGGCGGCCCGCAAGCCATTCTGTCGAGACCCGACGCTGATGGGCT	49974
3105	Qy		TCAGCCGTAAATCCGGATGTGGCGCAGCTTATGGAACCTGCTCCATGCTGGCCATTGGAAG	3164
49975	Db		TCAGCCGTAAATCCGGATGTGGCGCAGCTTATGGAACCTGCTCCATGCTGGCCATTGGAAG	50034
3165	Qy		CCGATTTTACCGGAGCTGTATCAGATACCTGGCGAGAAATTACGACGACGAGTTACG	3224
50035	Db		CCGATTTTACCGGAGCTGTATCAGATACCTGGCGAGAAATTACGACGACGAGTTACG	50094
3225	Qy		AAGCACTCTGGAGTAAGAATTTTGGTGATATGCTCCCTCCCTCACTGTTATCTTATGATG	3284
50095	Db		AAGCACTCTGGAGTAAGAATTTTGGTGATATGCTCCCTCCCTCACTGTTATCTTATGATG	50154
3285	Qy		CACCTTGCACATTTTATGATCTTGATTAAGATGAGCTAACTTCGGTATTTGTCATTAAGC	3344
50155	Db		CACCTTGCACATTTTATGATCTTGATTAAGATGAGCTAACTTCGGTATTTGTCATTAAGC	50214
3345	Qy		TGGACTTTTCAAATCCAAACAATGAATACTACATTAATAGTCAATTAAGTGTGCTAACTC	3404
50215	Db		TGGACTTTTCAAATCCAAACAATGAATACTACATTAATAGTCAATTAAGTGTGCTAACTC	50274
3405	Qy		TGAATGAAGCACTGGTTTAACTATACATCATATTTAAGAACGCTAGCGGAGACT	3464
50275	Db		TGAATGAAGCACTGGTTTAACTATACATCATATTTAAGAACGCTAGCGGAGACT	50334
3465	Qy		CACAGCAGATTAAACCTGAGCTTATACCTTTATGGGATGGAACATATCTTTATAATTTCA	3524
50335	Db		CACAGCAGATTAAACCTGAGCTTATACCTTTATGGGATGGAACATATCTTTATAATTTCA	50394
3525	Qy		CGCTGGTGTCAACGATATCAGAGGATAGTTTCAAACCTAGGGTCGTTAGTCTTAACAGTA	3584
50395	Db		CGCTGGTGTCAACGATATCAGAGGATAGTTTCAAACCTAGGGTCGTTAGTCTTAACAGTA	50454
3585	Qy		GCAATCTTTACTCTGGGGATTACAGCTTCAAAAAGGGGTCGCTATAGCATTTCCGTGTTG	3644
50455	Db		GCAATCTTTACTCTGGGGATTACAGCTTCAAAAAGGGGTCGCTATAGCATTTCCGTGTTG	50514
3645	Qy		AAATAGATGAAGAAAGTTAAATGATGGGATCAATTAGGATTTGATAGAAAGGGGGGG	3704
50515	Db		AAATAGATGAAGAAAGTTAAATGATGGGATCAATTAGGATTTGATAGAAAGGGGGGG	50574
3705	Qy		GATATTACTCAACGTHAACTTCACTCTGATTGAATATGATCCTGCGATATTCATCTTTA	3764
50575	Db		GATATTACTCAACAGTAACTTCACTCTGATTGAATATGATCCTGCGATATTCATCTTTA	50634
3765	Qy		AATTAAATAAGTTTATCCGCTTATACAAGGCCACGGGCATGACCACGGCGGAAATATATC	3824

50635	AAATTAAATAAAGTTATCCGGCTTATACAGGCCACGGCGATGACCA CGCGCGAAATATATC	50699
3825	AAATCACCAATATTCTTTAAATAACGGTCTCACCAATTGACCATCGGTCCTGAGTAAAAATCT	3884
50695	AAATCACCAATATTCTTTAAATAACGGTCTCACCAATTGACCATCGGTCCTGAGTAAAAATCT	50754
3885	TCCTGGTCGGTTACCTGATGGGTCACTATCAGCTTGATGTGGCCCGGTCACTGATATTGT	3944
50755	TCCTGGTCGGTTACCTGATGGGTCACTATCAGCTTGATGTGGCCCGGTCACTGATATTGT	50814
3945	GCAACGGAAACCATCAGTGAACAGCGGTTACAGCGCGAAACCGGCTGTTTACCA CGCTGT	4004
50815	GCAACGGAAACCATCAGTGAACAGCGGTTACAGCGCGAAACCGGCTGTTTACCA CGCTGT	50874
4005	TCAAACACCCACCGCTGAAAGCGGCAGCTGTTTCTCGAGATGATATACCCCTCTGCATTTAC	4064
50875	TCAAACACCCACCGCTGAAAGCGGCAGCTGTTTCTCGAGATGATATACCCCTCTGCATTTAC	50934
4065	GCTCTGAAGACACCGAGGATGCTTTCCGTCCTCAGCGTACTGAAACGCGCATTTAAACATCA	4124
50935	GCTCTGAAGACACCGAGGATGCTTTCCGTCCTCAGCGTACTGAAACGCGCATTTAAACATCA	50994
4125	GGCCCTCGGGGCTTTCCA CGCTCTGGCAGTTGGCCAGCGGTGACAGCAGCGCTGGGTTTA	4184
50995	GGCCCTCGGGGCTTTCCA CGCTCTGGCAGTTGGCCAGCGGTGACAGCAGCGCTGGGTTTA	51054
4185	GCTGCTCTGCTGACAAATATCGCGGCCTCTACCGAGTGAATCTCTGGCTGTGACATCCACG	4244
51055	GCTGCTCTGCTGACAAATATCGCGGCCTCTACCGAGTGAATCTCTGGCTGTGACATCCACG	51114
4245	ACCTATCCGCTGGTGAGCTGTCAAATGTTGTCCTCGCTCTCCCTTTTACGCGGGTGGCG	4304
51115	ACCTATCCGCTGGTGAGCTGTCAAATGTTGTCCTCGCTCTCCCTTTTACGCGGGTGGCG	51174
4305	CGGCTCTGGTGTCCGATAATGAGCTGACGAGTTTCTGTACAGACCACTCTGGCTCA	4364
51175	CGGCTCTGGTGTCCGATAATGAGCTGACGAGTTTCTGTACAGACCACTCTGGCTCA	51234
4365	CGGACAGGGCTGGAACGGTCAAGCATGTTTCTCTGATGCTGACGACGAGTACGGTACC	4424
51235	CGGACAGGGCTGGAACGGTCAAGCATGTTTCTCTGATGCTGACGACGAGTACGGTACC	51294
4425	TGCTGACCCCGACATTTAGAAACCTGCTCGCTTCCCTGGCGAACGGACTGTGCGGCCGTG	4484
51295	TGCTGACCCCGACATTTAGAAACCTGCTCGCTTCCCTGGCGAACGGACTGTGCGGCCGTG	51354
4485	AGCTGTTCCGGAAACGCTCCCGGGCGATGGCGTCTCCCTTTATTTGCGCGCGCATGCAGC	4544
51355	AGCTGTTCCGGAAACGCTCCCGGGCGATGGCGTCTCCCTTTATTTGCGCGCGCATGCAGC	51414
4545	TGAGCGCCACGGATACGGCGAAGCGATCTGACTTTGGCGGACCAAGTTGAAGCCAGAGG	4604
51415	TGAGCGCCACGGATACGGCGAAGCGATCTGACTTTGGCGGACCAAGTTGAAGCCAGAGG	51474
4605	GGCTGACGCTGACGGAAATTTATCTTTTGTGTGATGTAATGCCGCCCAATATGACGACAGG	4664
51475	GGCTGACGCTGACGGAAATTTATCTTTTGTGTGATGTAATGCCGCCCAATATGACGACAGG	51534
4665	CGGGCCAGATGGCAGGGTCTTGCCAAAGCCCTGTGGCAACTGGCACTGATCCCGCAGCA	4724
51535	CGGGCCAGATGGCAGGGTCTTGCCAAAGCCCTGTGGCAACTGGCACTGATCCCGCAGCA	51594
4725	CGGGCTCAGCACGGCGAGCTGACGCTGTGTTGTCAGCAGCGCGGACGCTTCCGACAG	4784
51595	CGGGCTCAGCACGGCGAGCTGACGCTGTGTTGTCAGCAGCGCGGACGCTTCCGACAG	51654
4785	GATGGCACCATCTGCCCATGACCTGCGCGGCTTTCGCGACATTTAGCGTTTTTTCATCCG	4844
51655	GATGGCACCATCTGCCCATGACCTGCGCGGCTTTCGCGACATTTAGCGTTTTTTCATCCG	51714
4845	TGTTTAAACCGCACGGCAGCCATGCGCGGGAGTGTCTTGACCGCACTTGAGACCGGAGAAC	4904
51715	TGTTTAAACCGCACGGCAGCCATGCGCGGGAGTGTCTTGACCGCACTTGAGACCGGAGAAC	51774

Qy	4905	TGTCGTGAGCCCTGCTGCGCCGCGCCCTGTCAAGATGACAGGATGTGACCGCGCCCT	4964	5985	AACGTGCTGTTCCGCGCTACGACGGTACATGGAGTTCCTCCGCGTGTCTGTCGACATTAACCG	6044
Db	51775	TGTCGTGAGCCCTGCTGCGCCGCGCCCTGTCAAGATGACAGGATGTGACCGCGCCCT	51834	52855	AACGTGCTGTTCCGCGCTACGACGGTACATGGAGTTCCTCCGCGTGTCTGTCGACATTAACCG	52914
Qy	4965	TGGCGCAGGTGAGGGGGCGGGTGACACAGACACACAGCGTGTTCACCTCTCGGAGAGG	5024	6045	GCAACATCGCATTTCCGGAACCGCAGGGCATCATGTGACCTCTAATCCCTGACCTGAGC	6104
Db	51835	TGGCGCAGGTGAGGGGGCGGGTGACACAGACACACAGCGTGTTCACCTCTCGGAGAGG	51894	52915	GCAACATCGCATTTCCGGAACCGCAGGGCATCATGTGACCTCTAATCCCTGACCTGAGC	52974
Qy	5025	TGGACACAGGTGAGCGAGTGGCTGACATGATGATGAGACCCCTGTCAATACGCCATCCGGTC	5084	6105	AGCTCTATTGCGCGTATTACTCCGTCAACGACGACGCGGACTTTGATAACGCTCAGCTGA	6164
Db	51895	TGGACACAGGTGAGCGAGTGGCTGACATGATGATGAGACCCCTGTCAATACGCCATCCGGTC	51954	52975	AGCTCTATTGCGCGTATTACTCCGTCAACGACGACGCGGACTTTGATAACGCTCAGCTGA	53034
Qy	5085	TGGCTAGCCCTGATTGCCCTGAAGTACATCAATGTGTCGATGACAGTGCACCGTGTGTACA	5144	6165	TTTCTGTGGATTAATGATGACGCTAAATGTCTATCTCAGATATAGGATTTTAAAGAGCG	6224
Db	51955	TGGCTAGCCCTGATTGCCCTGAAGTACATCAATGTGTCGATGACAGTGCACCGTGTGTACA	52014	53035	TTTCTGTGGATTAATGATGACGCTAAATGTCTATCTCAGATATAGGATTTTAAAGAGCG	53094
Qy	5145	GCCAGTGGCAGGTGGTATCCGGTCTGCTGACGCGCGGGCTGAAAGCAGCCAGACTCGG	5204	6225	TCAGTCAACGAAATTAATACGACGACTGAGAAATTTAATTAATGTTTTTTCAGACCCCTT	6284
Db	52015	GCCAGTGGCAGGTGGTATCCGGTCTGCTGACGCGCGGGCTGAAAGCAGCCAGACTCGG	52074	53095	TCAGTCAACGAAATTAATACGACGACTGAGAAATTTAATTAATGTTTTTTCAGACCCCTT	53154
Qy	5205	CGCTGACACGATTAATCTGAGAGGGGACACAGCAGCGCCCTTTGTGCGTATTATCTGCGTA	5264	6285	CCGCTAAATTAATGTCAGTGCAACGAGTTTAATTCATGATGTTATCCACAGCGATTTCT	6344
Db	52075	CGCTGACACGATTAATCTGAGAGGGGACACAGCAGCGCCCTTTGTGCGTATTATCTGCGTA	52134	53155	CCGCTAAATTAATGTCAGTGCAACGAGTTTAATTCATGATGTTATCCACAGCGATTTCT	53214
Qy	5265	ATCTGGCACCCGAACATGGTATCCGGCGCGATGACCTCTTTCGGGTATCTGCTCTGGATA	5324	6345	CACTCCTTAATCTAAAACTACAACTGACTGTTTTTACTAATGAAGATTCCTCTCTTTTGA	6404
Db	52135	ATCTGGCACCCGAACATGGTATCCGGCGCGATGACCTCTTTCGGGTATCTGCTCTGGATA	52194	53215	CACTCCTTAATCTAAAACTACAACTGACTGTTTTTACTAATGAAGATTCCTCTCTTTTGA	53274
Qy	5325	ATCAGTGTGACCCAGGTAAAAACACCCGCAATGCGGAGGCGATCGCCGGCATACGGC	5384	6405	CGCCAGAGCTTCATATTACAGCAAAATGTTTCGTGTTTTTGTAGTACTGCTGGCATCGCCA	6464
Db	52195	ATCAGTGTGACCCAGGTAAAAACACCCGCAATGCGGAGGCGATCGCCGGCATACGGC	52254	53275	CGCCAGAGCTTCATATTACAGCAAAATGTTTCGTGTTTTTGTAGTACTGCTGGCATCGCCA	53334
Qy	5385	TGTATATCAACCGGGCCCTTAACCGAATAGAACTCAGCGCATGGCAGAGGTGAGGGGGC	5444	6465	CTCAATCTACCATAGAAAAATTCGTTTCAGCAGGGATAGAAATTTGAGGAAATTAATTTTT	6524
Db	52255	TGTATATCAACCGGGCCCTTAACCGAATAGAACTCAGCGCATGGCAGAGGTGAGGGGGC	52314	53335	CTCAATCTACCATAGAAAAATTCGTTTCAGCAGGGATAGAAATTTGAGGAAATTAATTTTT	53394
Qy	5445	GTCAAGTTTTCACTGACTGGGATACGTTCAACAAACGTTTACAGCACCTGGCGGGGGTCT	5504	6525	ATGACGCCAGCGCCCGCGGATTTGACGGATTTGTGGAGTGGATGTTTCTTAATTCAA	6584
Db	52315	GTCAAGTTTTCACTGACTGGGATACGTTCAACAAACGTTTACAGCACCTGGCGGGGGTCT	52374	53395	ATGACGCCAGCGCCCGCGGATTTGACGGATTTGTGGAGTGGATGTTTCTTAATTCAA	53454
Qy	5505	CAGAGCTGGTTTACTATCCGGAACAACTACCTCGACCGAGCGTCCGTATCGGGCAGACCG	5564	6585	AGATATACAGGTTCGGAAAGAGCAGTTGGTGTCTACTGTAAATCTTATTCGTCTACTG	6644
Db	52375	CAGAGCTGGTTTACTATCCGGAACAACTACCTCGACCGAGCGTCCGTATCGGGCAGACCG	52434	53455	AGATATACAGGTTCGGAAAGAGCAGTTGGTGTCTACTGTAAATCTTATTCGTCTACTG	53514
Qy	5565	GCATGATGGACACCTGCTCGAGTCTGTCAGCGCAGACGATATCAACCGCATACCGTGG	5624	6645	GCCTTAGTGTCTGTTGAGTTATTTATGATTCAATCAAAATAAATCTTCAGCGGAATTT	6704
Db	52435	GCATGATGGACACCTGCTCGAGTCTGTCAGCGCAGACGATATCAACCGCATACCGTGG	52494	53515	GCCTTAGTGTCTGTTGAGTTATTTATGATTCAATCAAAATAAATCTTCAGCGGAATTT	53574
Qy	5625	AGGATGCTTTTAAAAACCTATCTGACCACTGTTGAGCAGATTTGCAACACTGTCTCA	5684	6705	TGTCAGATAAAATGATAACCGCTTTAATTAGCGGCAGTACATCAAAAGTTTAATTCGTGT	6764
Db	52495	AGGATGCTTTTAAAAACCTATCTGACCACTGTTGAGCAGATTTGCAACACTGTCTCA	52554	53575	TGTCAGATAAAATGATAACCGCTTTAATTAGCGGCAGTACATCAAAAGTTTAATTCGTGT	53634
Qy	5685	GCGGATATCAGATAACGACGATGACGAGGGGACTACATGTTATGCGGTTCGAGCA	5744	6765	CGTCTATTGCGTCTCAAGATTTTGGAGTGAAGTGGTCTCATGCGGGCATCTTCAGATAT	6824
Db	52555	GCGGATATCAGATAACGACGATGACGAGGGGACTACATGTTATGCGGTTCGAGCA	52614	53635	CGTCTATTGCGTCTCAAGATTTTGGAGTGAAGTGGTCTCATGCGGGCATCTTCAGATAT	53694
Qy	5745	TCACAGATCAGACTTAACGTGCTGCGCAGCGCCACACACAGCAAAATCCAGACTCA	5804	6825	ATGAATTAATCCAGTATATCATATCAGACTCCGGCGTAAATGGGACTGAAATTAATCCT	6884
Db	52615	TCACAGATCAGACTTAACGTGCTGCGCAGCGCCACACACAGCAAAATCCAGACTCA	52674	53695	ATGAATTAATCCAGTATATCATATCAGACTCCGGCGTAAATGGGACTGAAATTAATCCT	53754
Qy	5805	TGATGCCCGGGAATCCCTGGACCGGATGGACAAAAATTAATCTCGGAATGAATCCGTGT	5864	6885	GGCTTTCCGCTGAATGGTATAATGATAAGCTGTCGCAATCCGGAATAATCTTTTCA	6944
Db	52675	TGATGCCCGGGAATCCCTGGACCGGATGGACAAAAATTAATCTCGGAATGAATCCGTGT	52734	53755	GGCTTTCCGCTGAATGGTATAATGATAAGCTGTCGCAATCCGGAATAATCTTTTCA	53814
Qy	5865	CAGATCTGTGCTCGGTGTTTTTCAACAGTCCGCTTTATGCTGCGGTGGAAGAGA	5924	6945	ACACAAATCCGTGAGTTTACCGTTAATACAGTGTATTTGTTGAAGATGAGTTGACG	7004
Db	52735	CAGATCTGTGCTCGGTGTTTTTCAACAGTCCGCTTTATGCTGCGGTGGAAGAGA	52794	53815	ACACAAATCCGTGAGTTTACCGTTAATACAGTGTATTTGTTGAAGATGAGTTGACG	53874
Qy	5925	ATCAGTCTGCTGATACGGAGCAGAGACGACCAACCGCAGCAGACTACACGCTGA	5984	7005	TGACGTTTACGTTTACCGCTGTGATCAGATAACCTCGTGTGCGCGCCCGCAGCGCCA	7064
Db	52795	ATCAGTCTGCTGATACGGAGCAGAGACGACCAACCGCAGCAGACTACACGCTGA	52854	53875	TGACGTTTACGTTTACCGCTGTGATCAGATAACCTCGTGTGCGCGCCCGCAGCGCCA	53934
				7065	TATTAACCGTCAATTCGAAACATTAATAATGACACTTCCGTTATCGCATTAACGTAATAA	7124

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53935 TATTAAACCGTCATTCCGAAACATTAAATGACACTTCCGTTATCGATTACGATTAATAATA 53994
|||||
7125 CGCGTGGCGGAGTATATTCGTTTCACTGCGGGTAAACGATGTGGCGCTTATTCGCCTCA 7184
|||||
53995 CGCGTGGCGGAGTATATTCGTTTCACTGCGGGTAAACGATGTGGCGCTTATTCGCCTCA 54054
|||||
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Db	56155	TCCGTGGGTTCTCAGCTACGGGGAAGTATGGTTCATGCCCGGGTTGCAGCGCGTGG	56214	57235	ATCAATGGATAGTGGCTGTGTTTATCTCGTGTGTTGATTATGGTGGAGCTAGCTCGGTGCT	57294
Qy	9345	CGGTCTCACAGGGAATGAACGACACGCGGCAATTCGAACTGGATTTCAATGACCCGGGTT	9404	10425	GTCTGAAGCGCGCGCTTGGCAAAACACACAGGAAGTGGGAGTGGCTGTGCTCAGGATTG	10484
Db	56215	CGGTCTCACAGGGAATGAACGACACGCGGCAATTCGAACTGGATTTCAATGACCCGGGTT	56274	57295	GTCTGAAGCGCGCGCTTGGCAAAACACACAGGAAGTGGGAGTGGCTGTGCTCAGGATTG	57354
Qy	9405	ACCTGCCGTTTGAAGGACTTCCAGTTGATGACACAGGGAACCTTGACACTCAGCTTCCCGG	9464	10485	TTTTTCCGGGTATGAGTTTGGTTTTAACTGCGGACTCGCGCGCTGTGCGCTCAGGTTTT	10544
Db	56275	ACCTGCCGTTTGAAGGACTTCCAGTTGATGACACAGGGAACCTTGACACTCAGCTTCCCGG	56334	57355	TTTTTCCGGGTATGAGTTTGGTTTTAACTGCGGACTCGCGCGCTGTGCGCTCAGGTTTT	57414
Qy	9465	ATGCTGACGGCAAAACACAGCGGATGCTCTCAGTCTGAGCGACATCATCTGCATATCC	9524	10545	GATGTTCCATTACCTTAGGTGTTCTGCGGGAGTTCCGGAGCGAATGATGCGCCAGCATT	10604
Db	56335	ATGCTGACGGCAAAACACAGCGGATGCTCTCAGTCTGAGCGACATCATCTGCATATCC	56394	57415	GATGTTCCATTACCTTAGGTGTTCTGCGGGAGTTCCGGAGCGAATGATGCGCCAGCATT	57474
Qy	9525	GTTCACACCATATCAGCTGATAGGTATCAACATAGCGAGCGCCCGGAAAGAGGCGCTGC	9584	10605	GATTTCTCGGCTGTTGCTGGAATAAGGAAAGTCTTCACTCAGTCTGCTCAGAACGT	10664
Db	56395	GTTCACACCATATCAGCTGATAGGTATCAACATAGCGAGCGCCCGGAAAGAGGCGCTGC	56454	57475	GATTTCTCGGCTGTTGCTGGAATAAGGAAAGTCTTCACTCAGTCTGCTCAGAACGT	57534
Qy	9585	GAGGAGACTGAGCATGCAAAATCATCAAGACATGGCCATTACTGCCCCACGTTGCCCTC	9644	10665	GCACCAAGTGGCTTATGAGTCGGACGGGACGCTTGTGCTTCCCGGCACTGGCATTTGGG	10724
Db	56455	GAGGAGACTGAGCATGCAAAATCATCAAGACATGGCCATTACTGCCCCACGTTGCCCTC	56514	57535	GCACCAAGTGGCTTATGAGTCGGACGGGACGCTTGTGCTTCCCGGCACTGGCATTTGGG	57594
Qy	9645	CGGGGGCGGTGCGGTCAACCGGGTCAAGGGTGATATCGCGGGCGAGGGCGCGATGGTGC	9704	10725	GTGGCAAACTTTTACCCCGCGACATTTGTGCGCATGCGCAGACGCGATATGGGCAA	10784
Db	56515	CGGGGGCGGTGCGGTCAACCGGGTCAAGGGTGATATCGCGGGCGAGGGCGCGATGGTGC	56574	57595	GTGGCAAACTTTTACCCCGCGACATTTGTGCGCATGCGCAGACGCGATATGGGCAA	57654
Qy	9705	GGGACCCCTGAGTATTCCTTTCGCGGTTAGCCCGGTGCGGGTTAGCCCCCACTCGGGC	9764	10785	GTTGAGTTGCTTCAACCTTATCAGCTTGTAGACCTTAACGGCGAAAGTGTGGTGGTAT	10844
Db	56575	GGGACCCCTGAGTATTCCTTTCGCGGTTAGCCCGGTGCGGGTTAGCCCCCACTCGGGC	56634	57655	GTTGAGTTGCTTCAACCTTATCAGCTTGTAGACCTTAACGGCGAAAGTGTGGTGGTAT	57714
Qy	9765	ACTTAATATACAGCGGCTCGGGACCGCCCTTTGGCATTTGGCTGGGGTATCGCGG	9824	10845	CCTGTATCAGGACAGCGGTGCTTGTGTTGACCTGTAACCGGTACCGGACGCGGAGTGA	10904
Db	56635	ACTTAATATACAGCGGCTCGGGACCGCCCTTTGGCATTTGGCTGGGGTATCGCGG	56694	57715	CCTGTATCAGGACAGCGGTGCTTGTGTTGACCTGTAACCGGTACCGGACGCGGAGTGA	57774
Qy	9825	TGCTGCTGTCCAGCGTTCAGCGCAACAGGACACCTACCTACGATGATCTGATGAATT	9884	10905	TCGGATGCTGTGACCTTGGGGGGCGGCTGCGGCCCTGCGCAAAATGCCCTTTTGCAATA	10964
Db	56695	TGCTGCTGTCCAGCGTTCAGCGCAACAGGACACCTACCTACGATGATCTGATGAATT	56754	57775	TCGGATGCTGTGACCTTGGGGGGCGGCTGCGGCCCTGCGCAAAATGCCCTTTTGCAATA	57834
Qy	9885	CACCGTCCGGAAGTGTGTGTGCGGCACTCACCGGCTGTGGCAACCAAGAACG	9944	10965	CAGCGCATCTCGCGGATCTTAATGGGAGTGGTGGCTGGAGTGGGTGCTTACCGCCC	11024
Db	56755	CACCGTCCGGAAGTGTGTGTGCGGCACTCACCGGCTGTGGCAACCAAGAACG	56814	57835	CAGCGCATCTCGCGGATCTTAATGGGAGTGGTGGCTGGAGTGGGTGCTTACCGCCC	57894
Qy	9945	ACGCGCGCACCTCACTACGGGATACACCGCGGAGCTTCAACGTTTCAAGTTTA	10004	11025	CGGTGTGGGGGATGATGATCGCACCCCGCGCGAGTGGTGGATTTACCCCTT	11084
Db	56815	ACGCGCGCACCTCACTACGGGATACACCGCGGAGCTTCAACGTTTCAAGTTTA	56874	57895	CGGTGTGGGGGATGATGATCGCACCCCGCGCGAGTGGTGGATTTACCCCTT	57954
Qy	10005	CCGTTACAGTACGAGGAGTGTCTCAGCGGCTTGGAGCTTGGCTGCCCGCACGAGAC	10064	11085	GTGAGCTTTGCCGTAGAATATGCGCATCCAAAAGCAGTGTCTCGCGATATCTCGGGGGC	11144
Db	56875	CCGTTACAGTACGAGGAGTGTCTCAGCGGCTTGGAGCTTGGCTGCCCGCACGAGAC	56934	57955	GTGAGCTTTGCCGTAGAATATGCGCATCCAAAAGCAGTGTCTCGCGATATCTCGGGGGC	58014
Qy	10065	AGAAACGGAATTTGGTGTATATACCTGACGACAGGTGGCTGTGCTGGGCGGAAA	10124	11145	TGGGTTAACGGAATGTTGCTTATCGGGCGCGAGTGGTGGCTCTTATTTCCGGCAAAA	11204
Db	56935	AGAAACGGAATTTGGTGTATATACCTGACGACAGGTGGCTGTGCTGGGCGGAAA	56994	58015	TGGGTTAACGGAATGTTGCTTATCGGGCGCGAGTGGTGGCTCTTATTTCCGGCAAAA	58074
Qy	10125	TGGCAGGCTCGCATCAGCAACCCACAGCCCAACACAGACGCGGTTTGGCTGATGGA	10184	11205	CGATGCTCGAATAAAGGGAGACCGTGCAGCAAAACGGAAAGACTCACTCTGCGGGTCCC	11264
Db	56995	TGGCAGGCTCGCATCAGCAACCCACAGCCCAACACAGACGCGGTTTGGCTGATGGA	57054	58075	CGATGCTCGAATAAAGGGAGACCGTGCAGCAAAACGGAAAGACTCACTCTGCGGGTCCC	58134
Qy	10185	GTCTCTCGGTATCACTTACCGGGAACAGATGTATTACCAATACCGTCCGGAAGATGTA	10244	11265	GGGGGTTGACCCACGTAACCTCGTGGCGTTTCACTGATATGGCTGGCAGTGGACAGACGA	11324
Db	57055	GTCTCTCGGTATCACTTACCGGGAACAGATGTATTACCAATACCGTCCGGAAGATGTA	57114	58135	GGGGGTTGACCCACGTAACCTCGTGGCGTTTCACTGATATGGCTGGCAGTGGACAGACGA	58194
Qy	10245	CGGTTGTACAGGCGGAGCGGACGCGCAACCGCGAGCGCGGCCCAACGTTTATCCGGT	10304	11325	TTTGAAGGAGTGGCTGCTTAATGAGTACGTTACTGGCCAAACCTGCGGGCACCGGTCTTT	11384
Db	57115	CGGTTGTGAAGGCGGAGCGGAGCGGCAACCGCGAGCGCGGCCCAACGTTTATCCGGT	57174	58195	TTTGAAGGAGTGGCTGCTTAATGAGTACGTTACTGGCCAAACCTGCGGGCACCGGTCTTT	58254
Qy	10305	GGCGGCTGCTGATACGTTACCGTACGCGGCTCGACGCTACCGCGCTGTGTGACACC	10364	11385	CGGTGAGCGGTGAATATTTCCCGGTTTTAGCCAGTCACTACGTTTAACTTAACTTACCA	11444
Db	57175	GGCGGCTGCTGATACGTTACCGTACGCGGCTCGACGCTACCGCGCTGTGTGACACC	57234	58255	CGGTGAGCGGTGAATATTTCCCGGTTTTAGCCAGTCACTACGTTTAACTTAACTTACCA	58314
				11445	GATATTTGCTGGCGGATACCGACGCTTCCGGTACCGGACCTTGATTTATTCGATGATGA	11504

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QY	13725	CCGCCAGGACCTGTATGSCCGACACGCACTTTTACGATCCGACGGGACCGGGAATGCAGGT	13784
Db	60595	CCGCCAGGACCTGTATGCCGACACGCACTTTTACGATCCGACGGGACCGGGAATGCAGGT	60654
QY	13785	TATTAACGCAAAAGGTGAACCGCGACAGGTGCTGTATACCCCGTGTTTGTGGTCAGTGCA	13844
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QY	13845	AGACGAGAAATGATACCGTTTGGGCTTAAACGACGATCCTGATCTGGGAAAGGAGGGGGGGAACG	13904
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QY	13905	GTGATGAGTCCGTCGCCCTGACAGCGGCTGCCCTGATGGAGACAAAGATGAAATATACAC	13964
Db	60775	GTGATGAGTCCGTCGCCCTGACAGCGGCTGCCCTGATGGAGACAAAGATGAAATATACAC	60834
QY	13965	TATCAGGTTTCGGCGGTTGTGCTGACAGGTGTTTATGTTTGGGGGCTTTCCCATTTGGCGT	14024
Db	60835	TATCAGGTTTCGGCGGTTGTGCTGACAGGTGTTTATGTTTGGGGGCTTTCCCATTTGGCGT	60894
QY	14025	TACACGCTCGGTTACACAGCGGCGAGATATCTCAATGCAACAAACGCGACGCGCAACAGGAA	14084
Db	60895	TACACGCTCGGTTACCAACGCGGCGAGATATCTCAATGCAACAAACGCGACGCGCAACAGGAA	60954
QY	14085	AGGGCCGATCGGTTGGCCCTCTCGGACGAGAAACCGGGAAAGAAAGTGGGAGCAGCAA	14144
Db	60955	AGGGCCGATCGGTTGGCCCTCTCTGGACGAGAAACCGGGAAAGAAAGTGGGAGCAGCAA	61014
QY	14145	CGACAGACTGACATGAACAGGTGGCTATACATGCTGAAGAAAGAACTGGCTGCTCGCGGT	14204
Db	61015	CGACAGACTGACATGAACAGGTGGCTATACATGCTGAAGAAAGAACTGGCTGCTCGCGGT	61074
QY	14205	GACGCTGCCCTGATGCTCAGCGCACTGGTCAAGCGCTTCAGCACACCGTTTACCAACCCCTC	14264
Db	61075	GACGCTGCCCTGATGCTCAGCGCACTGGTCAAGCGCTTCAGCACACCGTTTACCAACCCCTC	61134
QY	14265	CAGCGGCAACTTGGCCAGTGGTGAAACCGCGCGCTTTCGCGAGCTACCGCTATCGGTACA	14324
Db	61135	CAGCGGCAACTTGGCCAGTGGTGAAACCGCGCGCTTTCGCGAGCTACCGCTATCGGTACA	61194
QY	14325	GACGACCTCGGAGGCCAACCCCGCGCTTTGTTTTCGGAACCTGTTCCGCGCGCTGACCCAG	14384
Db	61195	GACGACCTCGGAGGCCAACCCCGCGCTTTGTTTTCGGAACCTGTTTCGCGCGCTGACCCAG	61254
QY	14385	AGACGGGAGAGCTGGCAGCGTATGCTGACAGGACAGAGTGAAATGGCAGGCTTCGCGG	14444
Db	61255	AGACGGGAGAGCTGGCAGCGTATGCTGACAGGACAGAGTGAAATGGCAGGCTTCGCGG	61314
QY	14445	CGCGCTTATCAGCGGCTACGACGAGCAGGAGCAAAAATAAGGCGGATTTAGCCGTTAAGGAA	14504
Db	61315	CGCGCTTATCAGCGGCTACGACGAGCAGGAGCAAAAATAAGGCGGATTTAGCCGTTAAGGAA	61374
QY	14505	AAGTGACGGTGTGTTTCGCGATTAATTAACAGGAGATCACATGAGACATCTCTTGTTCA	14564
Db	61375	AAGTGACGGTGTGTTTCGCGATTAATTAACAGGAGATCACATGAGACATCTCTTGTTCA	61434
QY	14565	GTAGCACCCCGTCGGTCGCGTGCTTCGACAAACCGCGGCTGTTGTTGGGGAGCTGCAGT	14624
Db	61435	GTAGCACCCCGTCGGTCGCGTGCTTCGACAAACCGCGGCTGTTGTTGGGGAGCTGCAGT	61494
QY	14625	ACTACGCCATCCGGATACACCGGAGGAGCGGACGAGCGGTATCACTTGCCATCAGCACG	14684
Db	61495	ACTACGCCATCCGGATACACCGGAGGAGCGGACGAGCGGTATCACTTGCCATCAGCACG	61554
QY	14685	ATGAGCGCGCAGCTTGTCAAAAGCCGACCCCGGTTTACACCGCGCGCTCTGACAA	14744
Db	61555	ATGAGCGCGCAGCTTGTCAAAAGCCGACCCCGGTTTACACCGCGCGCTCTGACAA	61614

QY	14745	ATTTCAGTACCTGAAATAGCCTGACCGGGACAGTACTGACAGAGCGTTCAGCGCCCGATGCGG	14804
Db	61615	ATTTACGCTACCTGAAATAGCCTGACCGGGACAGTACTGACAGAGCGTTCAGCGCCCGATGCGG	61674
QY	14805	GTACGTCGCTGGAACTGAGCGATGCGCGGGCGGGCGTTCTTCGGCCGTCACCGGGGCTG	14864
Db	61675	GTACGTCGCTGGAACTGAGCGATGCGCGGGCGGGCGTTCTTCGGCCGTCACCGGGGCTG	61734
QY	14865	GGACGGAAACGCGGTCACCGCACCTTGGCAATATGAAGACGATACCTCTCGCGGGCGGCC	14924
Db	61735	GGACGGAAACGCGGTCACCGCACCTTGGCAATATGAAGACGATACCTCTCGCGGGCGGCC	61794
QY	14925	CGCTGAGCATCACCGAGCAGTTTACCGGTGAAGCGGCCCAATATTCGGAACGCTTCGTGT	14984
Db	61795	CGCTGAGCATCACCGAGCAGTTTACCGGTGAAGCGGCCCAATATTCGGAACGCTTCGTGT	61854
QY	14985	ACGCTGGCAATACGGATGCCGAGACGATTTCTCAATCTGGCTGCCGCGAGTGTACAGTCATT	15044
Db	61855	ACGCTGGCAATACGGATGCCGAGACGATTTCTCAATCTGGCTGCCGCGAGTGTACAGTCATT	61914
QY	15045	ACGATACCGCCGACTGTGTGCAGACGGACAGCATTCGCTCCCTTGAGCGGGCGTCTCGCCG	15104
Db	61915	ACGATACCGCCGACTGTGTGCAGACGGACAGCATTCGCTCCCTTGAGCGGGCGTCTCGCCG	61974
QY	15105	TCACGGGCACTTGTGTCCCGACGCGCGGGGGCCAACTTGGATGGGTGAGATGCCTCGG	15164
Db	61975	TCACGGGCACTTGTGTCCCGACGCGCGGGGGCCAACTTGGATGGGTGAGATGCCTCGG	62034
QY	15165	CCTGGAATGACCTGTGGATGGGAGACGTTCTTCAACCGACCCACGCTGATGCGACCG	15224
Db	62035	CCTGGAATGACCTGTGGATGGGAGACGTTCTTCAACCGACCCACGCTGATGCGACCG	62094
QY	15225	GGCGCGTCTGAGCATCACCGATGCAAAAGGTAATCTGCAGCGTGTGGCATATGATGTGG	15284
Db	62095	GGCGCGTCTGAGCATCACCGATGCAAAAGGTAATCTGCAGCGTGTGGCATATGATGTGG	62154
QY	15285	CTGGGCTGCTATCGGGCAGTTGGTTGACGCTGAAGGACGCGACCGAGCAGGTCACTGTGG	15344
Db	62155	CTGGGCTGCTATCGGGCAGTTGGTTGACGCTGAAGGACGCGACCGAGCAGGTCACTGTGG	62214
QY	15345	CCTCCCTGACGTACTCGGCGCGGGGAAAAGTTGGTGGTGAAGAAACACGGCAACCGGCCGTG	15404
Db	62215	CCTCCCTGACGTACTCGGCGCGGGGAAAAGTTGGTGGTGAAGAAACACGGCAACCGGCCGTG	62274
QY	15405	TAACTCTGTATATTACAGACCGGAAACACAGCGCTGCAGCGGGATTTAAACGGAAACGTC	15464
Db	62275	TAACTCTGTATATTACAGACCGGAAACACAGCGCGCTGCAGCGGGATTTAAACGGAAACGTC	62334
QY	15465	CGTCTGGGCACTTGC CGGAGCAAAAGTCTGCAGGACCTTCGCTATACGTATGACCCGG	15524
Db	62335	CGTCTGGGCACTTGC CGGAGCAAAAGTCTGCAGGACCTTCGCTATACGTATGACCCGG	62394
QY	15525	TAGGCAACGTACTACGCTCAATACGATGCGGAAGAGACCCGCTTCTGGCGGTAAACAGA	15584
Db	62395	TAGGCAACGTACTACGCTCAATACGATGCGGAAGAGACCCGCTTCTGGCGGTAAACAGA	62454
QY	15585	AAGTGGTACCGGAGAACTGATCATCTACGACAGCTGTACACAGCTGCTCAGGCGCCACAG	15644
Db	62455	AAGTGGTACCGGAGAACTGATCATCTACGACAGCTGTACACAGCTGCTCAGGCGCCACAG	62514
QY	15645	GGCGTGAGATGCCCAATGCGGCGCAGCGGGCAACGACTTACCATCGCTACAGCCCGCC	15704
Db	62515	GGCGTGAGATGCCCAATGCGGCGCAGCGGGCAACGACTTACCATCGCTACAGCCCGCC	62574
QY	15705	TTCTTACAGACAGCTCTGCCTTACA CCAATTACAGCGGCACCTACCGTTATGACCGTGGTG	15764
Db	62575	TTCTTACAGACAGCTCTGCCTTACA CCAATTACAGCGGCACCTACCGTTATGACCGTGGTG	62634
QY	15765	GCAA CTTGACGAGATGSCCAAGTGGCCCTTGCACGACCAATAATATACGACAGACA	15824
Db	62635	GCAA CTTGACGAGATGSCCAAGTGGCCCTTGCACGACCAATAATATACGACAGACA	62694
QY	15825	TACGCTTAGTGACCGCAGCAATATGGGCGGTACTGACGACGTTGGCGGAAGTGGCGCTCAG	15884

Db	62695	TCACGGTTAGTACCCAGCAATAGGGCGGTACTGAGCACAGTTTGGCGGAAGTGCCGCTCAG	62754
Qy	15885	ATGTTGATATGCTGTTTCACTGACGAGGAGTACACAGAAAGCACTTCGACCGCGGGCAAGCAC	15944
Db	62755	ATGTTGATATGCTGTTTCACTGACGAGGAGTACACAGAAAGCACTTCGACCGCGGGCAAGCAC	62814
Qy	15945	TGTTGTGACCGCACCTGAGAACTGCAAAAGGTGACACGGTGTGCTGATGCGGGGG	16004
Db	62815	TGTTGTGACCGCACCTGAGAACTGCAAAAGGTGACACGGTGTGCTGATGCGGGGG	62874
Qy	16005	CGGACGACGCAAAAGCTATCGGTATGATCGGGCAGTCAGCGTATTTATCAAAACCGGCA	16064
Db	62875	CGGACGACGCAAAAGCTATCGGTATGATCGGGCAGTCAGCGTATTTATCAAAACCGGCA	62934
Qy	16065	CGCGCAAACTGGCAACAAGTTTACAGACACAGCGGGTAGTGACTCGCGGGGCTGGAGT	16124
Db	62935	CGCGCAAACTGGCAACAAGTTTACAGACACAGCGGGTAGTGACTCGCGGGGCTGGAGT	62994
Qy	16125	TAGGTATCATGGCAAAATGGGTGACCGGAAAGAAAGCCCTGCAAGTTTATACGGTGGCG	16184
Db	62995	TAGGTATCATGGCAAAATGGGTGACCGGAAAGAAAGCCCTGCAAGTTTATACGGTGGCG	63054
Qy	16185	AGCTGGCGGGCACAAAGTGCAGTATGCACTGGGAGATCGGCAAGCGGATGACCTCG	16244
Db	63055	AGCTGGCGGGCACAAAGTGCAGTATGCACTGGGAGATCGGCAAGCGGATGACCTCG	63114
Qy	16245	ATCAGGACTCGGTGCGTTACAGTTACGATTAACCTGTGGGACAGCCAGCTGGAGCTGG	16304
Db	63115	ATCAGGACTCGGTGCGTTACAGTTACGATTAACCTGTGGGACAGCCAGCTGGAGCTGG	63174
Qy	16305	ACAGAGGGTTTACCTTATCAGTGAGGAGAGTTCTACCGTATGCGGAAACGGCTGTTTC	16364
Db	63175	ACAGAGGGTTTACCTTATCAGTGAGGAGAGTTCTACCGTATGCGGAAACGGCTGTTTC	63234
Qy	16365	TGACGGCGCAAGTGAGTTGAGGCTGACTACAAAATATCCGATACTCAGGCAAGGAGC	16424
Db	63235	TGACGGCGCAAGTGAGTTGAGGCTGACTACAAAATATCCGATACTCAGGCAAGGAGC	63294
Qy	16425	GTACGCGACGGGGCTGGATTATACGGTTATCGGTATACAGGCAATGGGACGGCGCT	16484
Db	63295	GTACGCGACGGGGCTGGATTATACGGTTATCGGTATACAGGCAATGGGACGGCGCT	63354
Qy	16485	GGCTCTCCAGGACCGGACGGACCGTGGACGGGCTGAACCTGTCGATCGTGGCA	16544
Db	63355	GGCTCTCCAGGACCGGACGGACCGTGGACGGGCTGAACCTGTCGATCGTGGCA	63414
Qy	16545	ATAATCCCGTCACGCTGTTTGACAGCAACCGGGCGGATCAGTACTGGTCAGGAGCCAGAC	16604
Db	63415	ATAATCCCGTCACGCTGTTTGACAGCAACCGGGCGGATCAGTACTGGTCAGGAGCCAGAC	63474
Qy	16605	GATTAGTGGGGAGAGCAATTTGTTATCCGTTTACATCGCTGTTTGAAGAAATTTCTG	16664
Db	63475	GATTAGTGGGGAGAGCAATTTGTTATCCGTTTACATCGCTGTTTGAAGAAATTTCTG	63534
Qy	16665	TAGAGAAAGATTTCAATCAGCGTAAAGCAAGCTGCAATTTATCTATTTACGCGCTGG	16724
Db	63535	TAGAGAAAGATTTCAATCAGCGTAAAGCAAGCTGCAATTTATCTATTTACGCGCTGG	63594
Qy	16725	GTGAAGTGCAGCAGCAAAAGGCCATTAATTTCTAGAGAAACCAATTAACCCGGTTCCC	16784
Db	63595	GTGAAGTGCAGCAGCAAAAGGCCATTAATTTCTAGAGAAACCAATTAACCCGGTTCCC	63654
Qy	16785	TGAAGGTATCTATGTTGATTAAGCTGAGTCAATTTCTTGACCTGGCAACAGCTAGCGGTC	16844
Db	63655	TGAAGGTATCTATGTTGATTAAGCTGAGTCAATTTCTTGACCTGGCAACAGCTAGCGGTC	63714
Qy	16845	TCGTTGCCGAGTAGGACAGTGGGATGCATCAGGTGTACGTGGAAATTTATCGGCACAACA	16904
Db	63715	TCGTTGCCGAGTAGGACAGTGGGATGCATCAGGTGTACGTGGAAATTTATCGGCACAACA	63774
Qy	16905	GACCGGTGTGAGGATTTGGTTTATCCCTGTACGCTGCGAATATCTTCTGCCAATGAAA	16964

Db	63775	GACCGGTGTGAGGATTTGGTTTATCCTGTCTGTCAGCGCTGCAGAAATACTTCTGCAATGAAA	63834
Qy	16965	TTGTTAATGTCATGGATAAAATTTAAATCATCACGCCCTACACCGGGGATTTATGACATGC	17024
Db	63835	TTGTTAATGTCATGGATAAAATTTAAATCATCACGCCCTACACCGGGGATTTATGACATGC	63894
Qy	17025	ACGATATTTAAATTTCTCTGATGGAAAGGCGCATGTGCTACAGCGGAAGTAGTGAGG	17084
Db	63895	ACGATATTTAAATTTCTCTGATGGAAAGGCGCATGTGCTACAGCGGAAGTAGTGAGG	63954
Qy	17085	AAAGAGGAGTAAAGATCTAATTAATAAGGTGTTGCGAGGTGCGATCCTCCAGACCCCT	17144
Db	63955	AAAGAGGAGTAAAGATCTAATTAATAAGGTGTTGCGAGGTGCGATCCTCCAGACCCCT	64014
Qy	17145	TTGAGTATACAGCGATGATGTTTTCGCCATGGACCAAGGTGAACTTTGTTCCCTATA	17204
Db	64015	TTGAGTATACAGCGATGATGTTTTCGCCATGGACCAAGGTGAACTTTGTTCCCTATA	64074
Qy	17205	TGTTGGAAACATGACGACGATAAAGTCGTTAATGATAATGTTTCTGCGGGTGGTAGCTA	17264
Db	64075	TGTTGGAAACATGACGACGATAAAGTCGTTAATGATAATGTTTCTGCGGGTGGTAGCTA	64134
Qy	17265	GCCCGGGGCGGTTCCCGGTAGCGATGCTACATCAGGGGGAATGGACTGTTTTGCAACA	17324
Db	64135	GCCCGGGGCGGTTCCCGGTAGCGATGCTACATCAGGGGGAATGGACTGTTTTGCAACA	64194
Qy	17325	GTGAAGAACTGTTTAAATTTCTATAAATCTACAAATACACCTCTCTGAACTGTTCTTG	17384
Db	64195	GTGAAGAACTGTTTAAATTTCTATAAATCTACAAATACACCTCTCTGAACTGTTCTTG	64254
Qy	17385	AAAGTTTATGACAGAGGGAAGTAAGTCGCAACTCTCGGATGCTGAACTTCTTG	17444
Db	64255	AAAGTTTATGACAGAGGGAAGTAAGTCGCAACTCTCGGATGCTGAACTTCTTG	64314
Qy	17445	ATPAAACGACGCTGATGTAATCGTAAACGATTTCTGCTTACCCAAAGTATACAGCC	17504
Db	64315	ATPAAACGACGCTGATGTAATCGTAAACGATTTCTGCTTACCCAAAGTATACAGCC	64374
Qy	17505	CGGTGAGACATTTCTCTGCTCATTTGGGTTGTTTCTGCTCATCTGCACTGATGTTCT	17564
Db	64375	CGGTGAGACATTTCTCTGCTCATTTGGGTTGTTTCTGCTCATCTGCACTGATGTTCT	64434
Qy	17565	TCCTCATCTAAAGTCTAACGAGACATTTTATAGCAAAATGGCACTTTACGGTTATGTTCC	17624
Db	64435	TCCTCATCTAAAGTCTAACGAGACATTTTATAGCAAAATGGCACTTTACGGTTATGTTCC	64494
Qy	17625	CGTTTCAAACGACGGTCCGGATTTTACTCTGTAAATACAGACACTTCGCGGACCTGCTG	17684
Db	64495	CGTTTCAAACGACGGTCCGGATTTTACTCTGTAAATACAGACACTTCGCGGACCTGCTG	64554
Qy	17685	CGAAATTTATCCGTGCGAAAAAGCCAGCGGCGGATGGACGAAATGAACTGCA	17744
Db	64555	CGAAATTTATCCGTGCGAAAAAGCCAGCGGCGGATGGACGAAATGAACTGCA	64614
Qy	17745	GCTTCTGCTGGCTTTTTCGCGCAGCAACATGCTGATGGTTACGTGAGTTGATCGGCT	17804
Db	64615	GCTTCTGCTGGCTTTTTCGCGCAGCAACATGCTGATGGTTACGTGAGTTGATCGGCT	64674
Qy	17805	GCACCAAAAAGTCCGGAGGTCGCGCCAGATCGCGCGCAATAATCTGCTGTATGTTAT	17864
Db	64675	GCACCAAAAAGTCCGGAGGTCGCGCCAGATCGCGCGCAATAATCTGCTGTATGTTAT	64734
Qy	17865	TTCCATCACACCTGTATATCGCACTCTGGGCTTCCAGAAACCCCATACCGCACACCG	17924
Db	64735	TTCCATCACACCTGTATATCGCACTCTGGGCTTCCAGAAACCCCATACCGCACACCG	64794
Qy	17925	GTGTGATCGCTGGAAGCCCGGCGATTCACCGGCTGTGATCTGGAACATATTTGTGGACT	17984
Db	64795	GTGTGATCGCTGGAAGCCCGGCGATTCACCGGCTGTGATCTGGAACATATTTGTGGACT	64854
Qy	17985	TGATGTTTAGGAGATTGAATCGACCATTTTGGATGCTCCCTAACCATAGATCGTAGAGTTG	18044
Db	64855	TGATGTTTAGGAGATTGAATCGACCATTTTGGATGCTCCCTAACCATAGATCGTAGAGTTG	64914

Matches 5605; Conservative 0; Mismatches 1507; Indels 29; Gaps 13;			
QY	2414	ATGAGGCAACAGATTATGATATATATATGATATATCTGGAGAAAGTGAATGCTCACGA	2473
Db	1	ATGAGGCAACAGATTATGATATATGATATATCTGGAGAAAGTGAATGCTCACGA	60
QY	2474	GCACGCTGTGCAAGAAACAGATACAGCGGTGACGCTGACGAGATTTATTTCTCGCTTCG	2533
Db	61	GAACGCGAGTCTGAGGAAAGCGTACCGCAGAGACTCTGGCGGATTTTTCTCACGTTCT	120
QY	2534	TTTTCCGAGGTCAAAAAATCACTGGCGACAGCCTGTGATGGGAGAGGTCTGCTATCTG	2593
Db	121	CTCTCTGAAGTTAAAAAATCACCGGAGCAATCTGTGATGGGAGAGGTCCGCTATCTG	180
QY	2594	TACAGTCAGGCGCAGCAGNACAGAAAGAAACCGGCTCACCGAATCCCGTATTTGGCC	2653
Db	181	TACCGTCAGGCACAAAGAGGAAAGAAACCGGCTCACGTAGTCAGGTATTTCTGGCC	240
QY	2654	CGGCGGAATCCCCCTACTGGTGAATGCGTTGCGCTGGGAATACGGCAGGCGAGCGGCAGT	2713
Db	241	CGGCGCAATCCCCAGTCAGCGCGGTGCGCGCGCTGGGAATACGGCAGGCTGCAGATACC	300
QY	2714	CGCAGTATGATGACTGGTTTGCTCCGCGCAGACCGTTTCGCCCGCCCGGCTCGGTG	2773
Db	301	CGCAGCTATGATGAGTGGTTGCTCCGCTGCGGAACGTTTCAACCGGCCCTGATTCGGTG	360
QY	2774	GCCTCCATGTTCTACCGCGGCGGTATCTGACCGAGCTGTACCGTGAGGCGGAGACCTG	2833
Db	361	GCATCCATGTTTCCCGCGGCGGTATCAGACAGAGCTGTACCGTGAGGCGGAAGACCTG	420
QY	2834	CATCCGAGCACTCGCTTTCGCGCTGGACATCCGCGCTCCGACCTGGCGCGCTGGCC	2893
Db	421	CATCCGCAACGTCATGCTACCGCTGGACCAACCGCGCTTGACCTGGCACAACTGGC	480
QY	2894	CTTAGCCAGATATATGACAGCAGAGCTCTCCACCCTGAGCCTGTCCAATGAGTACTG	2953
Db	481	CTCAGCCAGAGCAATATGATAGAGAAATCACCACTTGGTCTCTCCAGTGAGCTGCTG	540
QY	2954	TATCGCGGTATCGGCGCAGGAGGCTTGACGACGACAGCGTCAGGAGCTGCTCGCC	3013
Db	541	CTCCGAGTATCGGGGAGGGAAGGATTTGACGTGACAGCGTCAGGAGTCTGCTCGCG	600
QY	3014	GGGTATCGCTGACCGCCTGACCCCTATCACTGGCGCTGACAGCGCGCCGCCAAGCC	3073
Db	601	GAGTATCGCTCACAGCCCTGTCCCGATCACACAGCGTA-TAGGCGCCCGCCAGCC	659
QY	3074	ATTCTGGTCAGAACCCGAGCTGATGGGTTGAGCGGTGAGCGGTAAATCCGAGTGGCGAGCTT	3133
Db	660	ATTCTGTGAGGTGCCCGAGCTGTGGGTTTTAGCAGGAATCCGAGCGTGGCGCAGCTT	719
QY	3134	ATGGACCTGCTCCATGCTGGCCATTGAAGCCGATATTTACCGGAGCTGTATCAGATA	3193
Db	720	ATGGGCCCTCGCTCCATGCTGGCTTTCAAGCCGATATTT-TGCGAGCTGTATCAGATA	778
QY	3194	CTGGCCGAAGAAATTACGACAGACAGTTACGAAAGCCTCTGGAAGTAAAGATTTTGGTGAT	3253
Db	779	CTGGCCGA--ACCTTAGCACACACAGACAGACGAGCGCTGGAGTAAAGATTTCTGTCAT	836
QY	3254	ATGCTCCCTCCTCAGCTGATCTATGATGCACTTGCAACATTTATGATCTTGATATAC	3313
Db	837	ATGCGTCCCTCAGCAGCTGTTATCTTATG-TCGACTTGCACGTTTTTACGATCTTCATTAC	895
QY	3314	GATGAGCTACTTCTGTTATGCTATTAAGGCTGGACTTTTCAATCCAAACATGAATAC	3373
Db	896	GATGGTCTAACTTCGTTATTTAGTTAAGCTGGACTTTTCCAAATCCAAACATGATATAC	955
QY	3374	TACATTAAATAGTCAATTAAGTGTGTAATCTCTGAATGAAGCACTGTTTTTAATACTATA	3433
Db	956	TACCTTATTATTCAAGTAAGTGTGTAACGC-GAATGAAGAACTGTTTATACAACACTATG	1014
QY	3434	CATCATTTAATAAGCTTAGGCGGAGACTCACAGCAGATTAACCTGAGCTTTATACCT	3493
Db	1015	CA-AGTTATTTAAAGATCGTTACCGGAGATTCACAGAGATTAACCATCGCTTATACAT	1073

QY	3494	TATGGGATGGAAACATATCTTTATAATTTACOGTGTCTCAACGATATACAGAGGATAGT	3553
Db	1074	TATCGGATGGAAAC-----ATAAATGGAGCGTGTCTGAGATATCAGAGGTATT	1125
QY	3554	TTCAAACCTAGGTCGTAGGTTCTAAACAGTAGCAATCTTTT-ACTCTGGGATTTATCAGCT	3612
Db	1126	TTCAAACCTACGACGCTTAGGTTCTAAACAGTAGCAATCTTTGCTCTGGGATTTATCAGCT	1185
QY	3613	TCAAAAGGGGTTCGCTATAGCAATTCCTGTTGAAATAGATAGAGAAAGTTAAATGATGG	3672
Db	1186	TCAGAAAGGGGTTCGCTATAGCAATTCCTGTTGAAATAGATAGAGAAAGTTAAATGATGG	1245
QY	3673	GATCAATAGGATTCGATAGGAAGGGGGGATTAATCTCAACAGTAAACTTCACTCT	3732
Db	1246	CATCAATAGGACAGAGTTGGAATCGGGGGTATATTAATCTC-ACAGTATACATCACTCA	1304
QY	3733	GATTGAATATGATTCCTCGCATATTTCAATCTTAAATTTAAATAAAGTTATCCGCTATACAA	3792
Db	1305	GATTCAATATGTTCTCGCATATACATTTCTTACTCGAAATAATGTTATCCGCTGTACAA	1364
QY	3793	GGCCACGGCATGACACACGGCGGAATATATCAATCAACAATATTTCTTAATAACGGTCT	3852
Db	1365	GCCACGGGCATCCCATGSCGGAATATATCAAAATCACCCATATTTCTTAATAACGGTCT	1424
QY	3853	CACCAATTGACCATGGGTCTGAGTAAATCTTCTGGTCCGTTACTGATGCGTCACTA	3912
Db	1425	CACTATTGACCATGCGTCTGAGCAAAATCTTCCAGGTTGTTACTGATGAGTCACTA	1484
QY	3913	TCAGCTTGATGTGGCCCGTCTCATGATTTGTGCAACGGAACCATCAGTGACAGCGTT	3972
Db	1485	TCAGCTTGATGTGGCCCGTCACTGGTA TTGTGCAACGACCAATCAGTGACAGCGTT	1544
QY	3973	CACGGCGAAACCGGCTGTTCAACACGCTGTTCAACACCCACCGCTGAACGGCCAGCT	4032
Db	1545	CACGGCGAAACCGGCTGTTCAACACGTTGTTCAACACCCCGCTGAAACGGCCAGCA	1604
QY	4033	GTTTTCTGACAGATGATACCCCTCGACTTACGCTCTGAAGCACCGGAGGATGCTTCCG	4092
Db	1605	GTTCTCTGGAGAGATACCGCTCGACTTACGCTCTGAAGCACCGGAGGATGCTTCCG	1664
QY	4093	TCTACGCTACTGAAACGCGCATTTAAACATCAGCGCTCGGGGCTTTCACGCTCTGGCA	4152
Db	1665	CCTCAACGTTACTGAAGCGGCTTTAAACGTCAGCGCTCGGGCTTTCACACGTTGGCA	1724
QY	4153	GTTGGCAGCGGTGACAGCAGCGCTGGGTTTACGCTCTGCTGCTGCAATATCGCGCACT	4212
Db	1725	GCTGGCTAGGGGCAACAGCAGCGCGGGTTTACCTGCTCTGCGCAATATCGCGCCCT	1784
QY	4213	CTACCGAGTGAATCTCTGGCTGACATCCAACGACCTATCCGCTGGTGAGCTGTCAATGTT	4272
Db	1785	CTACCGGTAAACTCTAGCGGATATCCATGACCTGTCGTTGGTGAGTTGGCGATGTT	1844
QY	4273	GCTGTCGCTCTCCCTTTTCAGCGGGGTGCGCGCGCTCGCTGCTCCGATAATGAGCTGAC	4332
Db	1845	GCTGTCGCTCTCCCTTTACGACAAAGGTCCGCTATCGACACCTGTCGCGATGAGCTGAC	1904
QY	4333	GCAGTTCTGTACCAAGACCAACCTGCTGCTCAGGAGAGGCTGGAACGCTGAGCGATGT	4392
Db	1905	GCAGTTTCTGTACCAAGACCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1964
QY	4393	GTTCTCTGATGCTGACGACGAGTACCGTACCTGCTGACCCCGACATTTGAGAAACCTGCT	4452
Db	1965	CTTTCTGATGCTGACAAACAGCGTACAGTACCTGCTGACCGCGAGATGCATAATCTGTT	2024
QY	4453	CGCTTCCCTCGGCAACGAGCTGTGCGGCGGTGAGCT---GTTCCCGGAAACGCTCCCGG	4509
Db	2025	CGCCAGCTCGCTCTGCTGCTGCGGAGCTTCAATTTCTTCTCTGAGCAACTGCTCCAC	2084
QY	4510	CGATGCGCTCCCTTTTATTTGCGCGCATGAGCTGAGCGGCGGAGTACCGGATCGCGAGGC	4569
Db	2085	CGAGCTGCACCACTGGTTGCGCGCTTTCACGCGAGCTGGAATTCACCGACAGTCCCGGGC	2144

Qy	4570	GATCGTGA	TTGGCGGAC	CACGTTGA	AGCCAGAGGGG	CTGACGCTG	ACGGAATTTAT	CTCT	4629				
Db	2145	AATCTGG	ACTTGGGCT	GATGCTCT	GCACACGGAA	GGGCTGACG	CTGATTTAT	TTTC	2204				
Qy	4630	TTTGGTGA	TGA--	ATGCGCGCC	CAATATG	ACGACGCGG	CCAGATG	CAGGGTTCTG	4686				
Db	2205	GCTGGT	CAATAAC	AGATGGC	AGCCGAC	GAAGAACA	ACCGCCCG	CTGCGCGGTTCTG	2264				
Qy	4687	CAAAGCC	CTGTGG	CAACTGG	CACTGATCAT	TCCGACG	ACCGGCTC	TACGACGCGAGCT	4746				
Db	2265	TCAGGTT	CTGTGG	CAATAT	TTCGCTGA	TATCCGCC	ATACCGGG	CTCAGTACGGTGAGCT	2324				
Qy	4747	GACGCTG	CTGGTCA	CGCAGCGG	AGACGCTT	CCGACAC	AGGATG	GCACCATCTGCCCA	TGA 4806				
Db	2325	GACCTGG	TGGTCA	GTTGCGG	GGCCGTTT	TCGTGCGGG	CTGGCAG	CCCTGCCCCA	TGA 2384				
Qy	4807	CCTGCCG	CGCTTCG	CGACATT	ACGCGTTT	CATGCCG	CTGTTAA	CCGACGCGCAG	CCCA 4866				
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VERSION AY220492.1 GI:32699985
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ORGANISM Yersinia frederiksenii
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1 (bases 1 to 4302)
Dodd, S. J., Glare, T. R., O'Callaghan, M., and Ronson, C. W.
Yersinia enterocolitica contains plasmid-encoded genes that show
similarity to the tc family of insecticidal toxins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4302)
Dodd, S. J.
Direct Submission
TITLE Submitted (16-JAN-2003) Biocontrol and Biosecurity, AgResearch
JOURNAL Limited, Gerald Street, Lincoln 8152, New Zealand
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ORGANISM Unknown.
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AUTHORS Kramer, V. Cary., Morgan, M. Kent., Anderson, A. Robert., Hart, H. Prim.,
Warren, G. W., Dunn, M. M. and Chen, J. Shong.
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ORIGIN

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11475 TACCAAGCACTGATTTATGCGATGAGTACCGGTTAGTCATTTATTTCAACAGAGTGG 11534

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11535 TAAATTTTCCCGAGCGCATACGCTCTTCTCGGAAAGGTGCGCTATGATCGCAC 11594

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11895 TCTGCTACGCAAGCTGCTTTATCGCCACGCGCTCTGGGACGGGACAGAAACGCGAGTTTCG 11954

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Db	12314	CGGATTTGGTTATGTTGAACAGAAAGACACGCCATCACTGGCCCAAGCAGTCGCCAGA	12373
Qy	11997	-----	11996
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Qy	11997	-----	11996
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Qy	12123	CGATTTCCGACCGCTTCACTGTGCGTTTCAGGAGAGATGACAGACATATACTCCGG-	12181
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Qy	12182	--ACGACAGCAAGACATCTGTTGTCAGCGAGCCCTGAAAGGATCCTGCTGGCGAGTGA	12239
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Qy	12240	GTTATACGTTGCGATGGAGAGCAGCGCCGATATCCCTTACAGGTCCTACTAGTCTCG	12299
Db	12794	ACTGTACGGGAGAGTGGCAGTACACAGGAAAAATTCCTTACACAGTCACTGAATTTTC	12853
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Db	12914	AGTTGAAAGCGCAACTATCATTTACGAAAGTATGCCAGCGATCCTCAATGACGCCAARA	12973
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Qy	13005	TACTATGCGCGCGCAGAGCATTTTCTGGCTACCGCTATCTTTCTGGGACAGTATTTGAC	13064
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Db	13622	GGGCAAAATCAGCTCACTTGGGATGCAAACTATTGCGTGTCAACAAACCCGGGATGC	13681
Qy	13125	CGCAGGATTTGTCACACAGCGACTATGACTGGCGCTTCTGACCGCCGCTCGGGTGAC	13184
Db	13682	GGCTGACTGACAACTCAGCCAGATATGTTGGCGTTTTCTGACCCCGTTCACTCAC	13741
Qy	13185	GGACCCCAATGATAATCTGCAGTCCGTCACCTCTGGATGCTCTGGGCGGGTGACCAACCCT	13244
Db	13742	GGATATCAACGACATCAGCACTTACACGCTGGATGACCTGGGCGGCAATCACACT	13801
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Db	14282	CGGCGCTCTGGTGACAAAAATGGA-----AGATACCAAAACGGCGCTG	14323
Qy	13623	GGCGGTACCGGAGCGGAGTATGACAAATAAGGTCTGCTCTGTTGGGTTTATCAGCC	13682
Db	14324	GGCGGTTACGGGACGCACTGAATATGCAATAAAGGACCAACCGATACGCACTTCAACC	14383
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Db 16498 CTTATTGATGCGGCGGACATCAGAACGTTGATATCAGGACAAAACTGAACTGGA 16557
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Db 17158 CGGTACTCTGCTTGA 17173

RESULT 6
BD136648
LOCUS BD136648 37948 bp DNA linear PAT 18-SEP-2002
DEFINITION Insecticidal toxin from Photobhabdus.
ACCESSION BD136648
VERSION BD136648.1 GI:23231593
KEYWORDS JP 2002504336-A/6.
SOURCE Photobhabdus luminescens
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photobhabdus.
Kramer, V.C., Morgan, M.K., Anderson, A.R., Hart, H.P., Warren, G.W.,
Dunn, M.M. and Chen, J.S.
Insecticidal toxin from Photobhabdus
Patent: JP 2002504336-A 6 12-FEB-2002;
NOVARTIS AG
OS Photobhabdus luminescens
PN JP 2002504336-A/6
PD 12-FEB-2002
PF 18-FEB-1999 JP 2000532529
PR 20-FEB-1998 US 09/027080, 20-JAN-1999 US 60/116439 PI
VANCE CARY KRAMER, MICHAEL KENT MORGAN, ARNE ROBERT ANDERSON, PI
HOPE PRIM HART,
PI GREGORY WAYNE WARREN, MARTHA MARY DUNN, JENG SHONG CHEN PC
C12N15/09, A01H5/00, A01N63/02, C07K14/24, C12N1/15, C12N1/19 PC

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PC C12P21/02, C12N15/00, C12N5/00
CC orf5
CC hph2
CC orf2
FH Key Location/Qualifiers
FT CDS (15171)..(18035)
FT CDS (23768)..(31336)
FT CDS (31393)..(35838)
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/mol_type="genomic DNA"
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Best Local Similarity 54.0%; Pred. No. 0;
Matches 6358; Conservative 0; Mismatches 4747; Indels 671; Gaps 47;
Qy 5291 CGCGATGACCTCTTCGGGTATCTGCTGCTGATAATCAGGTGTCAGCAAGGTAAACAC 5350
Db 5569 CGTGATGATCTATCAATACCTATCGTAGTATCAACTGTATTAACCGCGGTGCAAAAT 5628
Qy 5351 ACCCGATTGCGGAGGCCATCGCGGCATACGCTGTATATCAACCGGGCCCTTAACGGA 5410
Db 5629 ACAGAGATCGCTGAAGCTATCGTAGTATCAACTGTATTAACCGCGGTGCAAAAT 5688
Qy 5411 ATAGAACTCAGCCCATGCGAGAGGTGAGGGGCGTCAGTTTTTCACTGACTGGGATACG 5470
Db 5689 ATGAGGAGATACTGTCAACAGTGTCAACAGCGCTCATTTCTTCAACCACTGGGATAAA 5748
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Db	6825	TATTAACCCCAATATTTTTCGATAAATAAATTCATTTACCTGTTTATCAGTATAGTGG	6884
Qy	6597	TCGGAAAGACGAGTTGGTGTCTACTGTAAAACTTATTCGTCACCTGGCGTTAGTGGTT	6656
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Db	7365	TAGTAATGATCGTAACCTTAGCGGAGAACATTTCAAGTATTCGATTTATCAAAAAGCGGA	7424
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Db	7485	AAACTCTTGTAATTCGCTCTTAATAGCTATTATTGGCCGTCAATTAATTAATAGCCGACCAACGC	7544
Qy	7225	CGGGAATGACACCATTCCTTTCCATGGAGACCCAGAGGCTTACCGAAACCCGCCCTTGGAAGA	7284
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Qy	7285	GGGGAGTGATGTGTTT-----ATGGACTCTTCGCGAGCCAAATGCCCTCTATTTCGTG	7335
Db	7605	AGATTCTCCTGATGCTATGGAAACCAATGGACTTCACCGGCGCAACAGCCCTCTATTTCGTG	7664
Qy	7336	GGAGCTGTTCTATTACACGCGGATGATGGTGTCCAGCGGTGTGTGCAGGAAACAGACATT	7395
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Qy	7396	CCCGGAAGCACCCGCTGGCTGCAGTATGTCGTGAACCCGGCGCGGCACGTGGTGAACCG	7455
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Qy	7516	CTCGCCCTCGACTCCAAATTCACCCGATGCAATAGCCAGTCAGCCAGTACGACCCCATGATTACAA	7575
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Db	8205	CAACGAAGTATGCTGAGCTACTGTGGCAGAAACTAGAACACCGGTTGTATAACTCTGCGCCA	8264
Qy	7936	CAACCTCTCATTGAACGGCCAGCGCTTTCCCTGTCCGTCTAGCCCAACGCGCTCCGAACC	7995
Db	8265	TAACCTCTATTGATGGTCAACTTTACATTTTGCCCTATTTTTCGCAACACACGACAGATCC	8324
Qy	7996	GTCCGCCCTGCAGATGCCGTGCTCAACAGCGCGCAGGGTGTGCGAGCACTGCCGCCCGC	8055
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Qy	8056	GGTGATCGCCTTTACAGTTTCCGGTTCATGCTGGAGAACCGCCGGGGGATGTGTAGCCT	8115
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Qy	8116	GCTGACCGGGTTCGGCAACACACTGCTCGGTATTAACGAGCGTCAAGATGCGGAGCGCT	8175
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ORGANISM Photorhabdus luminescens subsp. laumondii TToI
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1
AUTHORS  Duchaud,E., Rusniok,C., Frangeul,L., Buchrieser,C., Taourit,S.,
Bocs,S., Boursaux-Bude,C., Chandler,M., Dassa,E., Deroose,R.,
Derzelle,S., Freyssinet,G., Gaudriault,S., Givaudan,A., Glaser,P.,
Medigue,C., Lanois,A., Powell,K., Siguer,P., Wingate,V.,
Zouine,M., Boemare,N., Danchin,A. and Kunst,F.
TITLE     Complete genome sequence of the entomopathogenic bacterium
Photorhabdus luminescens
JOURNAL   Nat. Biotechnol. 11 (1) (2003) In press
REFERENCE 2
AUTHORS  Duchaud,E., Frangeul,L., Rusniok,C. and Kunst,F.
TITLE     Direct Submission
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FEATURES
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 127816)
AUTHORS Waterfield,N.R., Bowen,D.J., Fetherston,J.D., Perry,R.D. and ffrench-Constant,R.H.
TITLE The tc genes of Photorhabdus: a growing family
JOURNAL Trends Microbiol. 9 (4), 185-191 (2001)
MEDLINE 21185117
PUBMED 11286884
REFERENCE 2 (bases 1 to 127816)
AUTHORS Waterfield,N.R., Daborn,P.J. and ffrench-Constant,R.H.
TITLE Genomic islands in Photorhabdus
JOURNAL Trends Microbiol. 10 (12), 541-545 (2002)
MEDLINE 22454990
PUBMED 12564983
REFERENCE 3 (bases 1 to 127816)

AUTHORS ffrrench-Constant,R.H., Bowen,D.J. and Waterfield,N.R.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2001) Biology and Biochemistry, University of
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REFERENCE 4 (bases 1 to 127816)
AUTHORS Waterfield,N.R. and ffrrench-Constant,R.H.
TITLE Direct Submission
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REMARK Sequence update by submitter
COMMENT On Jan 3, 2003 this sequence version replaced gi:16416925.
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gene
CDS

Query Match
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Qy      7361  ATGTGTTTCCACGGTGTGTCAGGAACAGCACTTCCCGAAGACCAACCCGCTGGCTGCAG 7420
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Qy	7601	GACCTGCTGATGTCGCCCGGTGATGCGCCTACCGCTGCTGAGCGGACACCCCTTAAC	7660
Db	11156	GATCAACTTATCTGCGCGCGATATGGCTATCGCGAACTGACCCGCGATCGTTGTAAT	11215
Qy	7661	GAGCGCCGATGTGGTAGCTGCAGGCGCTTGAACCTTCTGCGGACGAGCCCTATATTTCC	7720
Db	11216	GAGCCNAGATGTGATGTGCTGCTTTGGAAATGCTGGTGATGAGCCGAGATTAC	11275
Qy	7721	TTTGAAGCCGACTGGTGGCGTTGACCCCTGGGTGACGCGACGAGGAGTGACGGAGCG	7780
Db	11276	GGCAGGCCAAACAGTGGGCGCGACCGTCTCTTTCGTCGGCGGCAACACACACTGTGAAGCG	11335
Qy	7781	GATTACCAGAGCGCCTGTGCGCGTGGCGCGTGGTGGCGCTCCCGAGACAGGAGCG	7840
Db	11336	GGCTATCAACAAGACCTTACGGCGCTAGACAACGAGAGAGTTGCACTCAACCCCGCAAC	11395
Qy	7841	GGCAATTCCTGACGGCACCTGTTCTCCGCGACGACGAGGTGCTCAAAAGCTACTGG	7900
Db	11396	GCTAACTGTTGGTG--TTTGGTCTCGCGGAATATAACCGGAATCAACCGATTACTGG	11454
Qy	7901	CAAACTTTGACAGCGGCTTCCAATAACCTGCGCCACAACCTCTCCAATTGACGGCCAGCGG	7960
Db	11455	CAAAAC--TGCGTTTGGCCTTGGTTAACTTGGGCCATAATCTTTCCA--TGACGGCAACCG	11512
Qy	7961	CTTTCCTGTGCTGTACGCCACCGCGTCGGAACCGTCGCCCTGAGAGTGCGGTGCTG	8020
Db	11513	TTATCGTGTGCGAATTAACGCGAGCC--TAGATTCGGAAGCGTGTCTCAACAGTATGTA	11570
Qy	8021	AACAGCGCGAGGCTGTGACGACTGCGCGCGCGGTGATGCCGTCTTACAGTTTCCCG	8080
Db	11571	CAGCTTCTCAGGGCGGTAGTGAGTGTGCTGCCCGCACATTTGTGTTATACCGCTTCCCG	11630
Qy	8081	GTCAATGTGAGAAACCCCGGGGATGTGTGAGCTCTGACCGGGTTTCGGCAACACACTG	8140
Db	11631	GTGATGCTGAGCGGCGCCGCAATCTGTGAGCGCAATTAACCGAGTTTGGCACTCTCG	11690
Qy	8141	CTCGGTATTAACGAGGTCAGGATGCGGAGCGCTGGCCAAACTGTGTGACAGCCAGGCG	8200
Db	11691	CTCAGTATGCGAGAGCATGATGATGCGGATGMACTCACCACGTTGTACTACAGCAGGT	11750
Qy	8201	AGTGAAGTATACGAGGCTTTCGCCAGCAGGATAAGTCTCTGAGGAATTCGATCGG	8260
Db	11751	ATGGAATGCGGACACAGAGCATCCGTATTCAGCAACAGAACTGTGATGAAGTGTGCT	11810
Qy	8261	GATATTGCCCTTGGAGGAGAGCCCGCGCGCGCAGATGCTTTGAAGCTTACAAA	8320
Db	11811	GATATTGCTGATTTGCGACAGAGCCGCGCAGTGACAAATGCTGTGGAANAATCCAG	11870
Qy	8321	GTGTTGTACAGCGCGAGCTCAACAACGCGGAAAAACAGCCCATGACTTGTACCTCAGT	8380
Db	11871	CAGCTGTATACGAGGATATCAACACGAGAGAACAGCGTGCATGTCACTGTTGATGCG	11930
Qy	8381	TCGTCGCTGTGTCGGCATCAACCGCGCGCTCTTTTGGCGGAGCGCGCGCCGATG	8440
Db	11931	CGGCGAGTCACTGCTTGGCGGGGAGGGCTCTCAGTAGCAGAGGGGTGCTCACTTA	11990
Qy	8441	CTGCCCAATTTTACGGGCTTGGCGGTGCGGGCTCCCGCTATGCGGCACTATTAAAGCC	8500
Db	11991	GTTCCTCAACCTGTGCTTTCGCTTGTGGCGGAGTCTGTTGGGGGCGACACTGCTGCT	12050
Qy	8501	ACGCGCATCGGCATCAGAGTGTCTCCGATGCCACCCGATATCAGCGGACAAAATCAGC	8560
Db	12051	TCGCGCTCCGTGATGTCGCTTTCTGCGCACAGCTTCCCAATATTCCGACACAAAATCAGC	12110
Qy	8561	CAGTCGGAAGTGTACCGCGTCCCGGGGAGGAGTGGGAATCCAGCGTGTATAGTGGGAG	8620
Db	12111	CGTTCGGAAGCCCTACCGCGCGCGCTCAGGAGTGGGAATTCAGCGTGTATATGCTGAC	12170
Qy	8621	TCTGACGTGGCGAGATTGATGCCAGCTGGCGGCCATGGCAGTGGCGCGGGAAGGGCT	8680
Db	12171	GGTGAAGTCAACAATGGATGCCAGTCTGGAAGCCTGAAAATATACGCGCGGACGAGCA	12230
Qy	8681	GAGCTGCAGAAAACTTACCTTTGAGACCCAGCAGACCCAGCGCACAGCGCGAGTTGGCATTC	8740

Db	13306	TGCTACTACTGAATATACAGCAGTACTGCTGGCAATGGGTCAATTCGGGATGGGTGGCAAT	13365
Qy	9818	TCGGCGGTGCTGCTGCTCCAGCGTCTGACGGCGAACCGAGCACCTACTACGATGATCTG	9877
Db	13366	GTGGGGTTGGTTTATACAGCTTCGCTACCGCCAAAGGGCGTTCGGCACTATACGGGACAAG	13425
Qy	9878	ATGAATTCACCGGTCCGGACGGTGAAGTGTGTCGGGCACCTACACGGCTCTGGCACCC	9937
Db	13426	ATGAGTATCTCGGGCCGGATGGGAAGTGTGAGTATTGTCCGGACAGCAAGGCAAC	13485
Qy	9938	AAGAAGCAGCGCAGGCACTCTACTCTGGGATAAACCCAGCGGAAGCTTCAACGTTTC	9997
Db	13486	CAGAGCAACGCACCGCAACCTCACTGTGGGACGGTCTTGACACAGCGCGCTACTGTGTTA	13545
Qy	9998	AGGTTTACCGTTACGTAACGAGGGTAGTCTCAGCGCCCTTGAGCGTTGGCTGCCCGCG	10057
Db	13546	CCCGCTATCAGTCCCGGTGGCAAAATGCTTCGTTAGAACACTGGCAGCCACAGC	13605
Qy	10058	A-----CGAGACAGAAACGGAAATTTGGGTGTTATATACCCCTGACGGACAGGTGGCTC	10111
Db	13606	AGAGCGTAGAGAGAGAGAGCTCTTTTGGGTACTTTTACTGCGGATGTTTAGTGACCC	13665
Qy	10112	TGCTGGSCGAAATGCGCAGGCTCGCATCAGCAACCCCAAGCCCAACACAGACGCGCG	10171
Db	13666	TATTCGGTAAGCATCATCATGCAAGTATTGCTGACCCGCGAGGATGAACCCAGAAATGGCC	13725
Qy	10172	TTTGGCTGATGGAGTCTCGGTATCACTTACCGCGGAAACAGATGTTATACCAATACCGTG	10231
Db	13726	GCTGGCTGATGGAGAAACCGTCAAGCATACCGGGGAAACATATTTACTATCATATCGGG	13785
Qy	10232	CGGAAGATGATACGGTTGTGACAGCGGAGCGGACCGCGCACCCGCGAGCGCGGCC	10291
Db	13786	CAGAGACGATCTTGACTGTGATGAGCATGAATCTGCTCAGCATTCAGGTGTACGGCCC	13845
Qy	10292	AACGTTATCCGGTGGCGGCTCGTATGGTAAACCGTCAGCGCGGTCGGAACGCTACCGCGC	10351
Db	13846	ACCGTTATCTG-GCAAGTCCACTATGGCAATACTCAGCGCGGAAACCGCTTTTTCGCGG	13904
Qy	10352	TGCTGTCGACACCATCAATGGATA--GCTGGCTGTTTATCTCTGGTGTGATATGTTG	10408
Db	13905	TAAATCAGGTATCCCTGTGTAATGACTGGTGTGTTTCACTGGTATTTGATACGGTG	13964
Qy	10409	AGCGTAGCTCGGTG-----TGCTGGAAGCGCCCGCGCTGGC	10444
Db	13965	AGCGCTTATCTTCGCTGAATCCGTAACCGAATTCATGTGTCAAGAAACAATGTGCTG	14024
Qy	10445	AAACACAGGAAGTGGGAGTGGCTGTGTCGACAGGATGTTTTCGGGTATGAGTTTG	10504
Db	14025	AAAACAATGTCTGAAAAAATGGCGTTGCTCGGACAGTTTCTCCCGCTATGAATATG	14084
Qy	10505	GTTTTAACTCGGACTCGCGCTGTCGCTCAGGTTTGTATGTTCCATTACCTAGGTG	10564
Db	14085	GGTTTGAATTCGAACCCGCTGTGTGTGCGCAAGTCTGATGTTTCATCAGCTGAAG	14144
Qy	10565	TTCTGGCGGGAGTTCCGGAGCAATGATGCGGCAGCATGTAATTTCTCGCTGTGCTGG	10624
Db	14145	CGCTGGCAGGGAAGTTGCAAGAAACAACCGGCGCTGGTTCCCGCTTATTTCTGG	14204
Qy	10625	ACTACAGGAAAGTCTTCACTCAGTCTGTCGAGAAACGTGCAACGAGTGGCTTATGAGT	10684
Db	14205	ATTATGACCTGMAACAAAGGTTTCTTGTGTCGAAACCGGCCGAGACTGGCCCATGAA	14264
Qy	10685	CGGACGGAGCTCTTGTGCTTCGGCACTGGCATTTGGGTGGCAACCTTTACCCCGC	10744
Db	14265	CGGACGGTACGCCAGTGATGTCCCGCTGGAATGGATATCAACGTTGTAATCATG	14324
Qy	10745	CGACATTTGTCGGATGCGACAGCGTGACGATATGGCAAGTTGAGTTTTCCTTCAACCC	10804
Db	14325	CGGTGATCTGAACTGCGAGTCCATGCGCAGTTAGAAAAAATGAACACGTTGACGCAT	14384
Qy	10805	ATCAGCTGTAGACCTTAAACCGCGGAAGTGTGGGTATC-CTGTATCAGGACA---GC	10860
Db	14385	ACCAATTTGGTTGTTTATATGGAGAGAAATTTCCGCGTTACTTTATCAGGATCTCAG	14444
Qy	10861	GGTGCTGCTGTGTAACCGTGAACCGGTACGCCA---GTGGGGGATGATCCCGATGCTGTG	10917
Db	14445	AAAGCTGTGTGTACCGTCTCCGTAACGGATATCACTGCGAAGGAACGAATGGGTT	14504
Qy	10918	ACCTGGGGGGCGGCTCGCGCCCTCGGCAAAATTCGCCGCTTTTGCATAAACAGCGCATCTG	10977
Db	14505	ACCTATGAGGAGCGGAAACCACTGCCACATATTCGGGCACAAACAGAAAGCGCATGTTG	14564
Qy	10978	GGGATCTTAATGGGGATGGTCTGGCTGGAGTGGGTGTTTACCGCCCCCGGTGTGGCGGG	11037
Db	14565	TTGGACATCAATAGGTGAACGGGCGTCTGGATTGGGTGATTTACGGCATCAGGGTTTACGGGGC	14624
Qy	11038	ATGATGATCGCACCCCGCGCGCACTGGTTGTCAATTTTCAACCCCTCTGTCAGCTTGGCC	11097
Db	14625	TACACACATGTGACCGGAAGTGAATGGAACCTCTTTTATTCATTTCCGCTGTGCCA	14684
Qy	11098	GTAGAATATGCGCATCCAAAAGCAGTGTCTGCGGATATCTCTGGGGCTGGGTTAAACGGAC	11157
Db	14685	ATGGAATATTTCCATCCGCGAGCAAAACCTGGCTGATATTTGATGGGGCTGGGCTGCTGAC	14744
Qy	11158	ATGGTGTCTATCGGGCGCGCAGTGTTCGCCTCTATTTCCGGCAAAAACGATGGTTGGAT	11217
Db	14745	TTAGCGCTTATCGGGCAAAATAGTGTACGTGTCTGGTCAAAATAATCCGCGCAGGATGGAT	14804
Qy	11218	AAAGGGAGACCGTGCAGCAAAACGAAAGACTCACTCTGCGCGTCCCGGGGTGTGACCCA	11277
Db	14805	CGCGCTCAGATGTTATTTCTTTGTCAAATAAGACCACTGCGCGGTTCCCGGCAAAAATAAG	14864
Qy	11278	CGTACCTCGTGGCTTCAGTGATATGGCTGCGAGTGGACAGCAGCATTTGACGAGGTG	11337
Db	14865	CGTATCTTGTGCGATTCAGTGATGATGACAGGCTCCGGGCAATCATCTGCTGGGAAGTT	14924
Qy	11338	CGTGTAATGGAGTAGTGTACTTGGCCCAACCTGGGGCAGGTGCTTTCCGTCAGCGGTG	11397
Db	14925	ACGGCAAAATAGCGTGGCTACTGGCGCAACCTGGGGCAATGGAATAATTTGGTGAAGCTCTG	14984
Qy	11398	AATATTTCCGGTTTATGACAGTCACTGACTAGCTTTAAACCTGACCAAGATTTGCTGGCC	11457
Db	14985	ATGATAACAGG-CTTCCAAATTTACGGGGAACAGTTTAAACCCCAACAGACTGTATATGTA	15043
Qy	11458	GATACGACGGTTCGGGTACCA-CGGACCTGATTTATGCGATGAGTGAACGGTTAGTCAAT	11516
Db	15044	GACCTAAATGGCTCAGGACACACCGATTTTATTTATGTCGCGCAATFACCTTGAACCT	15103
Qy	11517	TTATTTCAACAGAGTGTGTAATTTTCCCGCAGCGCATACGCTCTCTTCGCGAAAG	11576
Db	15104	CTATGCCAATGAAGCGGCAATCAATTTCTGCTGAACCTCAGCGTATTTGATCTGCGCGATGG	15163
Qy	11577	TGTGCGCTATGATCGCACCTGCAAGTCTGCAAGTGGCGGATATCCAGGGCTGCGGGGTGCC	11636
Db	15164	GTACGTTTTGATGATCTTGTGCGTTACAATAGCGGATACACAAGGATTAGGGACTGC	15223
Qy	11637	TAGCCTGTACTAGCGGTCCCGCATGTCCGGCCCTCATCTCTGGGTGTGCATTTATTCGGC	11696
Db	15224	CAGCATTTATTTGACGATCCCGCATATGAAGGTGCGACACTGCGCATTTGATATGATGACCAT	15283
Qy	11697	AGACAAACCTGTTGTTGTAATGGCATGAACAATATATGGGGCCCGGCACTGCACTGCA	11756
Db	15284	ATTCAAGCCTTGGCTGCTGAAATGCCGTCAATTAACAATATGGGAACAAACCAACGCTGTA	15343
Qy	11757	CTATCCAGTTCGGTGCAGTCTTGGCTGGATGAGAAAGCGAGGCACTCGCGCGCAGGCAG	11816
Db	15344	TTATCCAGCTCTGCCAGTCTTGGCTGGATGAGAAATTTACAGGCTTCTGAATCCGGAT	15403
Qy	11817	TTCCCTGCTGCTACCTGCCATTTACATTTGATACCTCTGGCGGTTCCGTTGGTGCAGGA	11876
Db	15404	GACGTTGGTCACTTATACCGTTCCCGGTGATGTTGTTGGCGCACGAAAGTGTGGA	15463
Qy	11877	TGAGATCACCGGTAAACCGTCTGTCAGCGACGCTGCTTTTATCGCCACGGGCTCTGGGACCG	11936
Db	15464	TGAATTTCCGGTAACCGATTGACAGCCATTTATCATTTACTCATGTTGGTGGGATGG	15523

QY	11937	GCAGGAACCGAGTTCCTGGGGGTTGGTTTTGTTGATGATCAGGGATACCGATACCTTGGC	11996
DB	15524	TCCTGAAACGGGAGTTTCGTGGTTTTGGGGGGTGACGCAAACTGATATTGATTCACGGGC	15583
QY	11997	AAG-----CCAGGGTACCGCGACGAACTGAGTATGCCCTCTGTGAGCGCGAATCGTTA	12050
DB	15584	GATGGGACACAGGGGACACATGCTGAACACACCGGCACCTTCGCGACGGTTAAATTGGTA	15643
QY	12051	TGCCACGGGGTACCGGCAGTAGACGAGCGTCTGCCGGGAGAGTATTGGCAAAAAGATGC	12110
DB	15644	CGGCATGGCGTACGGGAGTGCATATCTTCTGCCCAACGGAATATTGACAGGGGATCA	15703
QY	12111	CGCGCTTTTGGCGATTTCCGACCCGTTTAC-----TGTCGGTTACAGGAGAGATGA	12164
DB	15704	ACAGGATTTCCCGATTTTACCCACGCTTTACCCGTTATGACGAAAAATCCGGTGTGA	15763
QY	12165	GCAGACATATCTCCGACGACAGCAAGACATTTCTGGTTGCAGCGCCCTCAAGAGCAT	12224
DB	15764	TATGACGGTCACGCCGAGCGACACAGGAGATATCTGTTACATCGAGCCTTAAAGGACA	15823
QY	12225	CTGCTCGCAGTGAGTTATACGGTCCGATGCGACGACCGCGCGATATCCCTTACAG	12284
DB	15824	ACGTTTACGAGTGCTGATGCGGATGATGATCTTACTTGGCGGTTACGCTTATTC	15883
QY	12285	CGTACTGAGTCTCGCCGCGAGTAGCGGTAGTTGAAGCAATGGA---GACTACCGGT	12341
DB	15884	AGTGGATGAATCCGACACCAAGTAGCTTTGTACCGGTGATGGTATCGAGCTGCCTGC	15943
QY	12342	GGTGTGCCGATGGGCGCGGAAGCGTACGTCAGTTTATGAACGTTACCAATGA-TC	12400
DB	15944	GGTACTGGTTTCGGTGGCGGAATCCCGCAATACCGATATGAAGGGGTTGTACCGATTC	16003
QY	12401	CTCAATGCCAAACAGCAGGGGTACTCCTCAGTGATGAATACGGTTTCCCACTCGCTCAGG	12460
DB	16004	CACAGTGACCAAAAGATTGCTTTAAATATGATCGTTAGGATTTCCGAGGACAATC	16063
QY	12461	TCAGTGTCAATATCAACAGCGCCTCGTCCGGCGACAATCCATATCCGGCTCTTAC	12520
DB	16064	TTGAGATTGCCTATTCCAGACGCTCCACAGCCTGAGTTCTCGCCTTATCCGATACCTGC	16123
QY	12521	CGCGAGCGTTTCCGCCAACAGTTATGACGAGCAGCAGACATATACGCTGGGGTGC	12580
DB	16124	CCGAAACACTTTTCAACGACGAGTTTCGAGCAACAGCAGATGTTCTTCGCTCT---GACAC	16180
QY	12581	AACAGACAGTCACATCACTTGTTCCTGCTCAGGGCGATTTGGTTTGGGGTGG	12640
DB	16181	GCAGCGTTTTCTTATCACCACTGAATCATGATGATTAATAGTGGATCACAGGCTTA	16240
QY	12641	CGGAGCGTCCGGGACGATGATTCACGTACTCTCGGACCAACGTCGCCGAAGGGGTC	12700
DB	16241	TGGATACCTCACGACGTGACGACGATTTTATCAAGCCGATAAAGTGCAGCGGTGGAT	16300
QY	12701	TGACGCTGGACACTGTTGGGGCCGAAAGCCTGCTCGGATAGTACGTCGGTACGC	12760
DB	16301	TTTCCCTTGAATGGTTTTCTGC-----CACAGGTCAGGAGCATTTGTTTGCCTG	16351
QY	12761	TGGCGGTACGACGCAAGTCTGTTATCTGGATTCAACAGCTTGCCACCGCTCGCTGCTC	12820
DB	16352	ATCCGACCGGATTTATCGGGACATCAGGTTGATGATATACCGGTCAGAAAGACAAAC	16411
QY	12821	CGCCATCCCGCCCAAGGTAGTTTTTATCGAAACCGCGCTGCTGGATGAGGTTATGGTCA	12880
DB	16412	CCGCTATTCTCCGCTGGTGGCATAATTGAAACCGCAGAGTTTGTATGAACGATCGTTGG	16471
QY	12881	GTTCACTGGCTGCTACATTGGGA-----TGAACATCTCGAGCAAGCCGGTTACCG	12932
DB	16472	CGGCTTTTGGAGGAGTGATGGATGAGCAGGAGCTGCAAAAACAGCTGATATGCGGGCT	16531
QY	12933	GCAATCCGATACCTTTTCCCTCGAGCGAGGAGCAGAACAGGCAATCTGTGACCCAGTG	12992
DB	16532	GGAAATCGGCAAGTGCCTTTCAGTGAAAGA---CAGATTTCCATGTCTGGTGGGACA	16589
QY	12993	TCAGGATATGTTTACCTATGCGCGCGCAGACGATTTCTGGCTACCGCTATCTCTTCGGA	13052

Db 17390 ACAGAAATATTAAACGGAAAGGCAAAAGCCCTCGCTTACGTTTCAA----- 17435
Qy 14133 TGGGACGACGACGACGACTGACATGAACAAGGTGGCTATACATCTGAGNAGAACTG 14192
Db 17436 -----ACGTAATCTGAAATAAATTGGGCAACTATGTCAAGTTGACCAAAAAAT 17485
Qy 14193 GCTGCTGCGCGTGACGCTGCGCTGATGCTCAGCGCACTGGTCAGCGCTCGACGACACC 14252
Db 17486 GCCGCGCAGGATATGTATGCCGATACCCATTAATGATCCGTTGGGGGTGNAATACG 17545
Qy 14253 GTTACCACTCTCAGCGGCAACTTGCAGTCTGTGAACCCGCGCTTTCCGAGTACC 14312
Db 17546 GTTATCAGCGCAAGCGGGTTGCGTCCGATCCCTTATTCACTCCCTGTT----- 17594
Qy 14313 GCTATCGGTACAGACGACCTCGAGGCGCAACCCGCGGTTTGTTCGCGAATGTTCCGC 14372
Db 17595 ----- 17594
Qy 14373 CGCGCTGACCGAGAGCGGAGAGCTGGCAGCGTATGCTGACAGGACCAGAGTGAATGG 14432
Db 17595 -----TGGTGTAATGAAGTTGAAATGACACTCCCG----- 17627
Qy 14433 CAGGCTGCGGGCGCGCTATCAGCGGCTTACGCAAGAGCAAAAAATAAGCGATTTA 14492
Db 17628 --TGAATGACAGCATAAAGCTCAGTGATGCCCTGTTCACTGAAACAGACATCACTCCATTTA 17685
Qy 14493 GCGTTTAAAGAAAGTGAACGTTTTCGGGATTAATATTACAGGAGATCAGATGACGA 14552
Db 17686 GGAATGAA-----TCATGAAGA 17702
Qy 14553 CATCTTGTTCAGTAGACCCCGTGGTGGTGTCTGCAACCCGCGCTGTGGTGC 14612
Db 17703 ATTTCGTTACAGCAATACGCAATCGTCACTGCTGAGCAACCGTGTGACAGAGTAC 17762
Qy 14613 GGAGCTGCGAGTACTACCGCAATCCGGATACACCGAGGAGACGAGCGGTATCACCT 14672
Db 17763 GCGAAATAGCGTGTATCGCACCCCGATACACTCAGGTAAACCGATGAACGATCACCG 17822
Qy 14673 GCATCAGACGATGAGCGGCGAGCTTGTCAAAAGCGCGACCCGCGGTTACAGCGG 14732
Db 17823 GTTATCAATATGATGCTCAAGGATCTGACTCAGAGTATGTATCCGCGATTATGAAC 17882
Qy 14733 CCGGTCTGACA-----AATTTACGTAACCTGAATAGCC 14765
Db 17883 GCCAGCAGACGCGAGTGACAAGAACGCCATTTACACCCATCTTATCTTGTCTATCAC 17942
Qy 14766 TGACCGGACAGTACTGACAGCGGTGACGCGCCGATGCGGTAGCTGCTGGAACAGCG 14825
Db 17943 TCAGTAAGAAGGCATTTGCGTACGCAAAAGTGTGATGCCGGAACCCGTCGCGCTGCATG 18002
Qy 14826 ATGCGCGCGGCGGCGTTTCTGGCGGTACCGGGGCTGGGACGGAAGCGCGGTACCC 14885
Db 18003 ATGTTGCGGCGCTGCCGTTTATGCTGTGAGCGCCCAATGG-----CGTTAGCC 18050
Qy 14886 GCACCTGGCAATATGAAGACGATACCCCTGCGCGCGCGCGCTGAGCATCACCGAGCAG 14945
Db 18051 GAACGTTTCAGTATGAAGTGATAAATCTTCGCGGACGATGCTAAAGTTACCGAGCAG 18110
Qy 14946 TTAACCGGTGAGCGCGCAAAATTAACGGAACGCTTCGTGATCGGTGCGAATACGGAATGCC 15005
Db 18111 TAAAGGAGAGAAACGCGCTGTATCACGAGCGATTTGATTTGGTTCAGGAAATACCGCGCAG 18170
Qy 15006 AGAAGATTCATCTGCGTGGCGCAGTGTGTCAGTCAATACGATACCGCGGACTGGTGC 15065
Db 18171 AAAAGGCAATAATTTGGCGCGCGCAGTGGTGGTTCATTTATGATCCACCGGAATGAATC 18230
Qy 15066 AGACGACAGCATCGCCCTGAGCGGCGTGCCTGCGCGCTGACGCGCGAGTGTCTGCCCG 15125
Db 18231 AAACCAACAGCATATTTGTTAAACAGCATACCCCTTGTCCATCACAGCAATTAGTGAAG 18290
Qy 15126 AC CGCGGGGGGCAACTGATGGGTAGAGATGCCCTCGGCTCGGCAATGACTGCTGGATG 15185
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Qy 15186 GGGAGACGTTCTTCCACCCAGACCCACGCTGATGCGACCGGCGCGTCTCTGAGCATCACCG 15245
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Db 18411 ATGCTGCCGGAACAAGCAACGATATGCTATGATGTGGCGGTCTGCTTCAAGGCACTT 18470
Qy 15306 GTTGAACGCTGAAGACGCGACGAGCAGGTCAATGTGGCCCTCCCTGAGAGTACTGCGCG 15365
Db 18471 GGTTCGCGCTGAAGGGAACAAAGAAAGTTATCGTGAATCCCTGACCTATTCGGCTG 18530
Qy 15366 CCGGGAAGAAAGTTGCTGAAGAACGCGCAACGCGGTGTGTAACCTGATATTTTACGAGC 15425
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Qy 15426 CGGAACACAGCGCTGACGGGGAATTAACCGGAACGTCCTGCTGGGACAGTTGCGCGAG 15485
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Qy 15546 ATAAACGATGCGGAAGAGACCCGCTTCTGCGGTAAACAGAAAGTGTGACGGAATAACGT 15605
Db 18711 CTAAATGATGCTGAAATTAACCGCTTTTGGCGCAACAGAAATTTGACCGGAATACTT 18770
Qy 15605 ACATCTTACAGACGCTGTACCACTGGTGCAGGCCACAGGGCGTGAGATGGCAATGCGC 15665
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Qy 15726 ACACCAATTTACAGCGCACTACCTGTTATGACCGTGTGGCAACCTGACGAGATGCGCC 15785
Db 18882 ATACGAATTTACTCTGCACTTACGATATGATCTGTTGGGGAATCTGACAGAAATGCGATA 18941
Qy 15786 ACAGTGCCTCTGCCAGCAATAAATATTAACAGACATCAACGTTAGTGAACGAGCA 15845
Db 18942 A-----TTACGATCAACCGTAATACTATAACAACGAACATGACCGTTTCAGATCAAGCA 18997
Qy 15846 ATAGGCGGTACTGACGAGCTTTGGCGGAAGTCCGTCAGATGTTGATGATGCTGTTCACTG 15905
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Qy 16026 GGTATGATCGGGCAGTACGCTATTAATAAACCCGCGACGCGGCAACTGCGCAACAG 16085
Db 19178 GTTATGATGACAGACGCTGAGCTGCAATTAAGACTCATATTAGGAAGACAGGTAAACAGTG 19237
Qy 16086 TTTACAGACAGCGGTGTGTAACCTGCGCGGCTGGAGTTAGCTATCATGCGCAATTTGGCG 16145
Db 19238 AGCAATATCAGCGAACAATTTATTTGCCAGAGCTGGAATGGCGCACGATATAGCGCA 19297
Qy 16146 TCACGGAATAAAGAAACCTGCAAGTTATTAACGGTGGCGAGCTGGGCGGCAACAAGTGC 16205
Db 19298 ATACATTAAGAGTTTTTTCAGGTCATCACTGTGCGTGAAGCGGGTCAGGCAACAAGTGC 19357
Qy 16206 GGTATTCGACTGGGAGATCGGACGCGGATGACCTCGATGAGGACTCGGTGCGTTACA 16265
Db 19358 GGGTGTGCTAATTTGGGAAACAGGCAAAACCGCGCGGATATCAGCAATGATCAGCTGCGCTACA 19417

Qy	16266	GTATACGATACCTGGTGGGAGCAGCAGCTGGAGCT-GGACAGAGAGGTTACCTTTATC	16324
Db	19418	GTATGCAACCTGATGGCAGTAGCGGCTGGAAATGGGACAGTACCGGCAGATCATT	19477
Qy	16325	AGTCAGGAGAGTCTACCGCTATGGCGGACCGCTGTTCTGACGGCGCGAAGTGGATT	16384
Db	19478	AGTCAGGAAGAATATTACCCCTATGGGGGACCGCCG-TGTGGCGACCCGAAATCAGTCA	19536
Qy	16385	GAGCTGACTACAAAATATCCGATATCTCAGGCAAGGAGCGTGACGGCGCGGCTGGAT	16444
Db	19537	GAAGCTGATTACACAACCGCGGTATTCTGGCAAGAGCGGATGCAACAGGGTTGAT	19596
Qy	16445	TATTACGGTATCGGTATTACCGACCATGGCAGCGCGCTGCTCCACGACCCCGCA	16504
Db	19597	TACTACGGCTATCGTTATTATCAATCTGACAGCGCATGGTTGAGTGTAGATCCTGCC	19656
Qy	16505	GGCAGCTGACCGGCTGAACCTGTTCCGATGGTGGGATATATCCGTCACGCTGTTT	16564
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AE017135/c			
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DEFINITION	Yersinia pestis biovar Medievallis str. 91001 section 9 of 16 of the complete genome.		
ACCESSION	AE017135	AE017042	
VERSION	AE017135.1	GI:45436743	
KEYWORDS			
SOURCE	Yersinia pestis biovar Medievallis str. 91001		
ORGANISM	Yersinia pestis biovar Medievallis str. 91001		
REFERENCE	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.		
AUTHORS	Song, Y., Tong, Z., Wang, L., Han, Y., Zhang, J., Pei, D., Wang, J., Zhou, D., Han, Y., Pang, X., Zhai, J., Chen, P., Qin, H., Wang, J., Li, S., Guo, Z., Ye, C., Du, Z., Lin, W., Wang, J., Yu, J., Yang, H., Wang, J., Huang, P., and Yang, R.		
TITLE	Submitted (24-APR-2003) The Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences, No. 20, Dongdajie Street, Fengtai District, Beijing 100071, People's Republic of China		
JOURNAL	Direct Submission		
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gene	HLVAMKALRQQGIDKFTHVEKGLPEEVIPIDLAEHLNAGVVVVLGTLGRTGLSAAFIG NTHVINDNLKDLLAIKPEGFTCPIEGNEQBDAAE"		
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Db	88026	CACGGTAAACGGCGTGGTGAACACGATACATACGAGCCGAGACGCAACGCTTGACCGGC	87967	Qy	16523	AACCTGTTCCGATGTCGGGAATATCCCGTCAACGCTGTTTACACAGACGGCGGATC	16582
Qy	15449	ATTAAACGAAAGTTCGCTCTGGCAGCTTGGCGGACAAAGTGTGTCAGGACCTTGGC	15508	Db	86895	AACCTGATTTGATGTAGGAATTAACCCAAACATCTCTCCATGACAGTAATGCTTAATA	86836
Db	87966	ATCCGACGAGCGGTGAGCGGACATGCAATCCGGAACGAAAGTGTCTCAGGACTTGGC	87907	Qy	16583	AGTACTGGTCAGGAGCCAGACGATTAGTGGGGGAAGCATTTCTTCATCCGTTACACATG	16642
Qy	15509	TATACGTTATGACCCGCTAGGCAACGTAATCAAGTGTCAATCAATGCGGAAGAGACCCGC	15568	Db	86835	CGTGAAGGACAGAGTCCAGGAAATTTAGTGGGGGAAGCCTTTGTGATCTTTACATATG	86776
Db	87906	TATGATGATGATCCCGTGGCAACGTCGAGGATCAGAAACGACGAGAAAGAACCCGC	87847	Qy	16643	CTGTTTTTGAAGAATTTCTGTAGAGAGAAAGATTTCAATGAGCGTAAAGGAGCTGGC	16702
Qy	15569	TTCTGGCGTAAACAGAAAGTGTACCGGAGAAATAGTACATCTACGACGCTGTACCA	15628	Db	86775	TCGGTCTTTGAACGATATCCATTTGAAGAGATATGCAATGAGCGTAAAGGAGCGGT	86716
Db	87846	TTCTGGCGCAACAGAAAGTGTGCGCGGACATGCAATCCGGAACGAAAGTGTCTACG	87787	Qy	16703	ATTATATCTATTTACGGCTGGTGAAGTGCAGCAGCAAAAGGCCATATATTTCTAG	16762
Qy	15629	CTGTCAGCCCAACAGCGGTGAGATGGCCAAATGCGCGGACGAGGCAACGACTTACCA	15688	Db	86715	ATTATATCTATTTAGCCTGGGTGAAGTGCAGCAGCAAAAGGCCATATATTTCTAG	86656
Db	87786	TTGCTCAGCGCCACCGCGCGGTGATGTTGAACGCGGACGAGGCGCGACGCTGCT	87727	Qy	16763	AAAACCATTAACCCCGGTTCCCTGAAGGCTATCTATGGTGATAAAGCTGAGTCAATCTT	16822
Qy	15689	TCGCTACAGCCCGCTTCTTACAGACAGCTCTGCTTACCAATTAACAGCGCACCTAC	15748	Db	86655	AAAACATTTAAACCCCGATCCCTGAAGGCTGCTATGAGATTAAGCCGAGCTGCTCTT	86596
Db	87726	TCC-----GCCACCTTCTATAGAGTTCCGCATATACAACTACACCCACACCTAT	87673	Qy	16823	GGACTGGCAAAAAGTGTGGTCTCTGTTGGCCGCTTGGCGGTGAATGCTCTGGTGTG	86536
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Db	87672	ACCTACGATACCGCGGTAACTGACGACGATCCGACACA--CCCGGCAACCGGCAGT	87616	Qy	86535	CAGGGGTTTATGCGTACAAACAGACCAAGCGGGGAGGNTTGGTTTATCTCTGCGAGC	86476
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Qy	15869	GCGAAGTCCGTCAGATGTTGATATGCTGTTGATGTCAGTGCAGAGTCAACAGAGAC	15928	Db	17003	TACACCGGGAATGATGATGATGATTTATTTAAATTTCTGATGGGAAGGCGATG	17062
Db	87555	ACCACAAATCCGCGAGGTTGACGCTCTGTTTACGCGACGCGCCAGCAGAAACAGCT	87496	Qy	86415	TATCTGGGATTTATGATGATGATGATTTATTTAAATTTCAATCGTGGAAAGGATG	86356
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Qy	15989	GTGCGTATGGGGGGGAGCAGCAGCGAAAGCTATCGGTATGATGCGGCGAGTACGCT	16048	Db	17123	GAGTCTGATCTTCCAGACCCCTTGGATATACAGCGATGAATGTTATTCGCCATGGA	17182
Db	87435	GTACGGACCGGACAGCAGTATGACGGAAGTCTACCGTTATGACGGAACAGCCAGCG	87376	Qy	86295	GAGTCTGATCTTCCCGCGGCTTGGATATACAGCGATGAATGTTATTCGCCATGGA	86236
Qy	16049	ATTATCAAAACCGCACCGGCAAACTGGCAAACTGGCAAACTGACACAGCGGCTGAT	16108	Db	17183	CAGGTGAACCTTTGTTCCCTATATGTTGGGAACATGAGCAAGTAAAGTAAATGATA	17242
Db	87375	ATCTGAGGTGACGTCGAGAAACGAGAGGAGCAGCAGCAGCGCGGTTATGTTAC	87316	Qy	86235	CAGGTAAACCTTTGTTCTTTACATGTTGGGAATATGAACGATAAAGTAAAGTAA	86176
Qy	16109	CTCCGGGCTGAGTTACGTTATGATGGCAAAATGGGTGACGGAAGAAAGGCTGCGAG	16168	Db	17243	GGTATCTGGGGTGTAGTAGCCCGCGGCTTCCCGTAGCGATGTTACATCAGGG	17302
Db	87315	CTCCGAGGCTGGAACTGCTGACAGCAGCGCGGTGACAGAAACGGAAGGCTGCGAG	87256	Qy	86175	GGTATCTGGGGTGTAGTTGGCGTCCAGGTCCATTCGCGATGCAATGTTACATCAG	86116
Qy	16169	GTTATACGTTGGCGAGGCTGGCGGCG-----ACAATGGCGGTATTTGCACTGGAG	16222	Db	17303	GAAAGTAACTTTTTCACAAACAGTGAAGAACTGTTAAATTTCTATAAATCTACAATA	17362
Db	87255	ATTATCACTCTCGTGAAGGCGGCGCGCGCAGGTGACGAGTGCAGGTGCTGCTATGG	87196	Qy	86115	CAATGAGTCTTTTTCGACAGCAGTAAAGAGCTGTTTAACTTTTACAAATCGAGTA	86056
Qy	16223	ATCGGAAGCGGATGCTCGATGAGGACTCGGTGCTTACAGTTACGATTAACCTGTTG	16282	Db	17363	CTCTTTCTGAAACACTGGTCCCAAGATTTTATGGACAGAGGAAAGAAATAGTCGA	17422
Db	87195	AAGGCAAGCGGACGCTATCGATATGACCAATGACCACTGCGCTACAGCTATGATC	87136	Qy	86055	CGCTACCAGAACACTGGCAACAGAAATTTTATTTGCAAGAGGCGCTGGTATAGT	85996
Qy	16283	GGCAGCAGCGCTGGAGCTGGACAGAGAGGTTTACCTTATCAGTGAAGGAGGTTCTAC	16342	Db	17423	CCTCGCATGCTGAACTTCTTGTATAACGAGGATCATGTACTAATCGTAAACGATTC	17482
Db	87135	GGCAGCAGTACGCTTGAGGTGGATGGGATGGCAATGTTATCAGCATGAGGAATACTAC	87076	Qy	85995	CGCGCATGCTGACGCTTCTTGTATAAACGAGCAATCATGCAATTAATCGTAACG	85936
Qy	16343	CGGTATGGCGAAGCGGCTGTTGACGCGCGGAGTGGAGGTGAGGCTGATCAAAACT	16402	Db	17483	GCCTTA 17488	
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Thu Jan 27 14:55:28 2005

AJ414152/2
LOCUS AJ414152 313050 bp DNA linear BCT 21-NOV-2002
DEFINITION Yersinia pestis strain C092 complete genome; segment 12/20.
ACCESSION AJ414152 AL590842
VERSION AJ414152.1 GI:15980308
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SOURCE Yersinia pestis C092
ORGANISM Yersinia pestis C092
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.
REFERENCE
1 (bases 1 to 313050)
Parkhill, J., Wren, B.W., Thomson, N.R., Titball, R.W., Holden, M.T.G., Prentice, M.B., Sebahia, M., James, K.D., Churcher, C., Mungall, K.L., Baker, S., Basham, D., Bentley, S.D., Brooks, K., Cerdeno-Tarraga, A.M., Chillingworth, T., Cronin, A., Davies, R.M., Davis, P., Dougan, G., Fellwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Kariyeh, A.V., Moule, S., Oyston, P.C.F., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Genome sequence of Yersinia pestis, the causative agent of plague Nature 413 (6855), 523-527 (2001)
TITLE
JOURNAL
MEDLINE
PUBMED
21470413
11586360
REFERENCE
2 (bases 1 to 313050)
Parkhill, J.
Direct Submission
Submitted (04-OCT-2001) Submitted on behalf of the Yersinia sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
NOTES
Details of Y. pestis sequencing at the Sanger Centre are available on the World Wide Web
(URL, http://www.sanger.ac.uk/Projects/Y_pestis/).
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Microbiology, Horticulture Research International, Wellesbourne,
Warwick, CV35 9EF, UNITED KINGDOM

FEATURES

source

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VERSION A69711.1 GI:4774324
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 38258)
AUTHORS Morgan,J.A., Jarrett,P. and Ellis,D.J.
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VERSION	AF046867.1		
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REFERENCE	1 (bases 1 to 13162)		
AUTHORS	Bowen, D., Rocheleau, T.A., Blackburn, M., Andreev, O., Golubeva, E., Bhartia, R., and ffrench-Constant, R.H.		
TITLE	Insecticidal toxins from the bacterium Photorhabdus luminescens		
JOURNAL	Science 280 (5372), 2129-2132 (1998)		
MEDLINE	98306208		
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AUTHORS	Bowen, D.J., Rocheleau, T.A., Blackburn, M., Andreev, O., and ffrench-Constant, R.H.		
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 Db |||||
 QY 11822 CTGCTGCTACTGCGCAATTTCAATGATGATACCTGTGGCGTTCGGTGGTGCAGGATGAGA 11881
 Db |||||
 QY 9169 CGGCTTGTTATCTGCCCTTTCCAAATGATTTGCTATGCTATACCGAAATTCAGGATGAAA 9228
 Db |||||
 QY 11882 TCACCGGTAAACGCTGTCAGGACGCTGTTTATGCGCAACGCGTCTGGGACGGCGAGG 11941
 Db |||||
 QY 9229 TCAGCGGCAACCGGCTCACAGTGAAGTCACTACAGCCACGGGCTCTGGGATGTTAAAG 9288
 Db |||||
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 Db |||||
 QY 9289 AGCGGAAATCAGAGGATTTGGCTGCATCAACAGACAGATACCAACGTTTTC---TC 9345
 Db |||||
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 Db |||||
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 Db |||||
 QY 12062 TACCGGAGTACAGAGCGTCTGCGGAGACGTAATGGCAAAACGATGCGCGCGCTTTTG 12121
 Db |||||
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 Db |||||

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Db 10600 GGTTCCTGGGCGACAGAGCGAGGCAAGCCGAGGCTATTCCAACCCGCTTACACCCAC 10659
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Qy 13367 TGTATGTACGGACAGTTG----- 13385
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Qy 13409 -----TGCCCCCGCACGTTGGTGTGCTGGCTACCGATC 13441
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Qy 13682 CGTATTTCTGGACAGTTGGCAATATGTCAGTGATGACAGTGGCCGCGAGCCTGTATG 13741
Db 11200 CCTATTTCTAAATGACTGGCGTTACGTTAGTATGACGGCACGAGATGACCTGTTG 11259
Qy 13742 CCGACACGCACTTTTACGATCCGACGGCAATGGCAGGTTATTACGGCAAAAGGTG 13801
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Qy 13802 AACGGCGACAGGTGCTGTATACCCCGTGGTTTGTGCTCAGTGAAGACAGAAATGATACG 13861
Db 11320 ATTTGCGAGAAAGCTGTACACCCCGTGGTTTATTTGTGAGTGAAGATGAACGATACAG 11379

Search completed: January 27, 2005, 14:37:14
Job time : 83907 secs

Db 31369 CAATTCTGCCATGTGATGGCACAGTTATATGCTTTCGGTACAGACACTCGC 31310
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Db 31069 ATGGTTTCCGCGCGGTGAACACAGCTTCAGTGTGGCAGGATATCAACAACGCTTTCGAG 31010
Qy 5024 GTGACCAAGCTGACAGCTGGCTGGACATGATGAGCAGCCCTGTCCATTAGCCATCCGGT 5083
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Qy 5378 ATACGCTGTATATCAACCGGCGCTTAAACGGAATAGAACTCAGCGCCATGGCAGAGTG 5437
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Db 29944 GCGCATCAGGCTTTTCAAGGCGAGGACACTCTGCTGGTGTGTTCTACAAAAACCGGAAG 29885
Qy 6107 CTCTATTGCGGTTTTTACTCCGTCAACGCAAGCCGACTTTTGAATAACGCTCAGCTGATT 6166
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Qy 6686 AAAACTTCAGCGGAATTTTGTGATGATAAATGATAACCGCTTTTAAATAGCGGAGTACA 6745
Db 29284 TTGTTGAGTTTCCATTTTCTCAAAACAAATTTTAAACACCGTTTTTCACGTTGGTAGC 29225
Qy 6746 TCAAAAGTTAATACGTTGCTCTATTTGGCTCTCAAGATTTTTTGGAGTGTAAAGTCCGTC 6805
Db 29224 AATAAAACAGGATTTTAAAAAGTGCAGTTATGCTGTTGATGTTAATAATTTCTCAGGCG 29165

QY	6806	ATCCGGCATTTCAGATATATGAATTAATTCGATGATATCATACTGACATCCGGCGTAAT	6865	Db	28084	AACTCCGGCGCTGGAGAGACCACTCTCTGGAATGCAATCCCTGGATGCCATCGAT	28025
Db	29164	TTCCAGATATTTAGTTCTTATCAATCATCCGGCTGCTGGATATTGATACAGGCATTAAC	29105	QY	7538	CCCGATGCAATAGCCAGTAGACCCCATGATGATTAACAAGTTCGCCACCTTTATATGCTGAC	7597
QY	6866	GGGACTGAAATTAATCCTGGCCTCCGCTGAATGATATAATGATAGCTGAGTCTGCAA	6925	Db	28024	CCGGATCCGTCGCCCAAAATGACCAATGACATACAAAGATTGCCACCTTTATGCGCTG	27965
Db	29104	AATACCGATATCAAAATTTACGTTGATGGCTGGCAGTAACCAACCACTTTACGGCACT	29045	QY	7598	CTCGACCTGCTGATTTCCCGCGGTGATGGCGCTACCGGCTACCGGCTGCTCGAGGGACACCTT	7657
QY	6926	TCGGGAATAATCTTTTCAACACCAATCGCTGAGTTTACCGTTAATACCAAGTATAT	6985	Db	27964	TTGGATCAACTTATTTCTCGCGCGGATATGGCTTATCGAGAACTGACCGCGATCGTTG	27905
Db	29044	GACCATATGCTTCTTCCGGCAACACAGTTTTTGATGCTATGCGTACACCTTTAAGCCA	28985	QY	7658	RACGAGCCCGGATGCTGTGATGTCAGGCCCTGAAACCTTCTGGGCGACGAGCCCTATATT	7717
QY	6986	GTTGAAGATGAGTTTGACGTGACGTTTACGTTACCGCTGTGATGATGAGATACGTCGTG	7045	Db	27904	AATGAAGCCAAATGTGTGATGTCGTACTTTAGAAATGCTCGGTGATGAGCGCGAGAT	27845
Db	28984	CTGGAAATCGATCTTCATCGTTGGCTTTTACCAATAATTTGCTCTCTCGGATATCGTT	28925	QY	7718	TCCTTTGACCGCACTGTGCGGCTTGACCTGGGTGACGACGAGCGAGGTGACGGA	7777
QY	7046	CTGCGCGCGGACGGCCATATTAAACGTCATTTCGAAACATTAATGATGACATTCCTGTT	7105	Db	27844	TACGGTAGCCAAACAGTGGGCAGCACCGTCCCTTCCGGGCGGAGTCAAAACCGTGCAG	27785
Db	28924	TTTGAGACCAAGCAAGACGGGCGAGTCTGGGTAAAGTCAAGCAAAATATATCGGTG	28865	QY	7778	CCGGATTACAGAGGCCCTGCTGGCGGTGGCCGCTGGTGGTGGTCCCGCTCCCGAGACAGG	7837
QY	7106	ATCGCATTTAGTAAAAATACCGTGGCGCGCAGTATATTGTTTCAC-----	7152	Db	27784	GCGGCTTATCAGCAGGATCTTACGATGCTGGGCCGCTGGTGGGTTTCCAAGAAATCTCCGT	27725
Db	28864	AAACGGTAAATTAATTCGGAAGATATTCTGTTCTGCGTGAACCTCATTCGGGTGCC	28805	QY	7838	ACGGCGAATTCCTCAGCGCACTGTTCTCCGCGACGAGAACGAGGTGCTCAAAGCTAC	7897
QY	7153	-----TCCGGGTAAACGATGTGGCGCTTATTCGCTCAACACCTCTTTGGCCGCACTG	7207	Db	27724	ACCGTAACTCGTTGGTGGTGTGTTCTGCGCGAATAAACCCGGCGCTCACCGATTAC	27665
Db	28804	CAATATATGAGCTCGGGGTGATCGTATTTCGTTTAATACCCCTGCTGGCTTCTCAACTG	28745	QY	7898	TGGCAAACTTGGCAGACGGCTCCATAACCTGGCGCAACAACCTCTCCATGACGGCCAG	7957
QY	7208	GTACACGGCGGAATACCGGATGACACCATTTCTTCAATGAGACCCAGAGGCTTACC	7267	Db	27664	TGGCAAACTCGCTGGCTTGGCTTTAACTTCGCGCAATACTTTCCATTGACGGACAG	27605
Db	28744	GTATCAGAGCAACACGGGCATTTGATATCTCTGCAATGGAACCCAGCGGTACCG	28685	QY	7958	CGCTTTCCCTGTCGTCTACGCCAGCGCTCGAACCGCTCGCCGCTCGAGAGTCCGCTC	8017
QY	7268	GAAACCGCCCTGGAAGA-----	7284	Db	27604	CGGTTATCGCTGGCGATTTACCGCGAGCTACCGATCCGAAAGCGCTGCTCACAGTAGT	27545
Db	28684	GAACTCCGTTGGAGAGAGCTTCTTTGCCAACTTTGTCGCTAAATATGACCCCTGCT	28625	QY	8018	GTCAACAGCGCGCAGGGTCTGCAGCACTCCCGCGCGCGGTGATGCGCTTTACAGTTTC	8077
QY	7285	-----	7284	Db	27544	GTACAGGCTCTCAGGGCGGTAGTGCAGTGTCTCCCGCGCACATTGTGTTATACCGCTTC	27485
Db	28624	GAACATGGCGATGAGCGGTGTTTAAATATCCATATTGGGAATGTTGGCGGTAAACCGGA	28565	QY	8078	CCGGTATGCTGGAGAAACCCCGGGGATGTTGAGCTGCTGACCGGGTTTCGGCAACACA	8137
QY	7285	-----	7284	Db	27484	CCGGTATGCTGGAGCGGACCCGCAATCTGGTAGCGCAATTAACCCAGTTTCGGCACTCT	27425
Db	28564	AGGCGCTTTATACAGCGGAATGTTATCCGATACGTCGGAACCAAGTATGACACTGTTT	28505	QY	8138	CTGCTCGGTATTACCGAGCGTCAAGATGCGGAGGCGCTGGCCAACTGCTGCAGACCCAG	8197
QY	7285	-----	7284	Db	27424	CTGCTCAGTATGGCAGCATGATGATGCCATGAACTCACTCACCAGCTGCTACTACAGCAG	27365
Db	28504	GTCCCTTATGCGGAAGGTATTATCATGATGAAGGTGTGAGATTGGGGGTTGGATACCAG	28445	QY	8198	GGCAGTGAACTGATACGCCAGGGCTTTCGCCAGCAGGATTAACGTCCTCGAGGAATTCGAT	8257
QY	7285	-----	7284	Db	27364	GGTATGGAATCGCGACACAGAGCATCCGTATTTCAGCAACGAACCTGTCGATGAAGTGGAT	27305
Db	28444	AAATTTACCTATGACAACTTGGGAATCTGCTTTCTTTTATTGATGAGACAAACAG	28385	QY	8258	GGGGATATTGGCCCTTGAGAGAGCCCGCGGGCGCGCAGATGGGTTTGAACGTTAC	8317
QY	7285	-----	7284	Db	27304	GCTGATATTGCTGATTGGCAGAGCGCCGCGAGTGCACAAAATCGCTCGGAAAAATAC	27245
Db	28384	CAATTTGATTAATTAACGATGCTGATCATGATTCAGGAATGACGCAACAGGGGATCGTG	28325	QY	8318	AAAGTCTTCTACGAGCGGACGCTCAACACCGCGAAAAACAGCCCATGCACTTGTACCTC	8377
QY	7285	-----	7284	Db	27244	CAGCAGCTGATGACAGGATATCAACACGAGAAACAGCGGCAATGTCACTGCTTGAT	27185
Db	28324	AAAAATATCAAGAAATACAAAGGATTTTGAATGTTTCTATCGCAACGGGCTATTCCGCC	28265	QY	8378	AGTTCTCGCTGCTGCTGGCATCAACCGCGCGCTCTTTTGGCCGAGCGCGCGCGAT	8437
QY	7298	TTTTATGACTTCTCCGAGCAATGCCCTCTATTCTGGGAGCTGTTCTATTACAGCCG	7357	Db	27184	GCAGCGCAGGTGAGTCTCTGGCCGGCAGGTGCTTTCAATAGCGGAAGGGTGGCCGAT	27125
Db	28264	CCGATGATTTCAATAGTGCAGCGCTCTATTACTTGGGAATTTGTTTATTACACCCCG	28205	QY	8438	ATGCTGCCAATATTATTCAGGGCTGGCGTGGGGCTCCGGCTATGCGGCACCTATTATAA	8497
QY	7358	ATGATGTTTCCAGCGGTTGTTGACGAGACAGCACTTCCCGGAAGCCACCGCTGGCTG	7417	Db	27124	TTAGTCCAAACGTTGTTGCTTTAGCTTGTGGCGCAGTCTGTTGGGGGGCAGCACTGCGT	27065
Db	28204	ATGATGCTTCCAGCGGTTGTTGACGAGAAAAACAAATTCAGCAAGCCACACAATGGATA	28145	QY	8498	GCCACCGCATCGGCATCCAGGTGCTCTCCGATGCCACCGCATATACGCGGACAAAAATC	8557
QY	7418	CAGTATGTGGAACCGCGCGGACGCTGGTAAACGGGTGCTGCAGAAATTACACCTGG	7477	Db	27064	GCTTCCGCTTCCGTGATGCTGCTTCTGCAACAGCTTCCCAATATTCCGAGACAAAAATC	27005
Db	28144	AACTACGCTACAAATCCCGCGGCTATATCGTTAAACGAGAAATTCGCCCCCTGGATCTGG	28085	QY	8558	AGCCAGTCGGAAGTGTACCGCGCTCCCGGGAGGATGGGAATTCAGCGGTGATGTGCG	8617
QY	7478	AATGTCGCTCGCTGGAGGAGACACCGGCTGGAAACGACTCGCGCTGGACTCCATTGAC	7537				

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Db 26944 GACGGTGAAGTCAACAATAATGATGCCAGTTGGAAAGCCTGAAATCCGCGCGAAGCA 26885
Qy 8678 GCTGAGCTGAGAAAACTTACCTTGGAGACCCAGCAGACCCAGGCAAGGCGCAGTTGGCA 8737
Db 26884 GCACAGATGCAAGTGGGAATATCAGAGAGACCCAGCAGGCCCATCTCAGGCTCAGTTAGAG 26825
Qy 8738 TTCCTGCAGAGTAACTCAACAATACGCTCTGTACAGCTGGCTGCGCGGCGAGTTGTCC 8797
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Db 26704 CTGCGCGCGAGCTGACCGACAACGGGTGTTACCTTTATCCGGGTGGGGCTGGAACGGT 26645
Qy 8915 GCAATCCCGTCTGCTGGCGGGAAACCTGTGATGCTGATCTGGCGCAGATGGAGCAG 8974
Db 26644 ACGACTCGGGTTTGATGGCGGGTGAACGTTGCTGTGATCTGCGGCAATTCGAGAAATGGAATA 26585
Qy 8975 GCCTGGCTGACGGGGATGACGGGCAATAGAGGTGACCGCGACGGCTCTGCTCTCGGAG 9034
Db 26584 GTCTGGCTGGAGCTGATGACGGGCACTGGAAGTGAACCGTACCGTCTGTTGGACAG 26525
Qy 9035 GTCATATACAGCTCGGGAGGATGCGGCAATTCCTCTGCGCGCAACAGGTGGTGGAACTG 9094
Db 26524 TTCTATCAGGCTTATCATCAGA---CAACTTTAATCTGACCGGAAATTCACGCAATTC 26468
Qy 9095 GTCAGTAACTGCTGGCGGAGTGGCGGTACGAAAGCAACGATTAAGATGGATCAACAG 9154
Db 26467 CTGCTGAAGGGAAGGCAACGTAAGAGCTTCGCGCAATGAATTTAATACTCAGTAACCGT 26408
Qy 9155 CAACCTCAGGCGCACCTGAACTGGCTGACCTCGGTATCGGCAACGATTAACCGGTCTCC 9214
Db 26407 CAGATAGAGCTCAGTGGCATTTGCTGATTTGAAATTTTCAGCGACTACCCGCAAGC 26348
Qy 9215 CTTGGCAACATAGGCGCATCAAAACAATAAGCGTCAAGCTCCCGGCGCTGGTGGCGCC 9274
Db 26347 CTTGGCAATACCGTCAAGTGAACAGGTGAGTGTCACTTCGCGCGCTGGTTGGCGCG 26288
Qy 9275 TATCAGGACGTCGCTGGTCTCAGCTACGGCGGAGTATGTCATGCCCCGGGGTTCG 9334
Db 26287 TATGAAGATATTCGGGCGGTGCTGAATTTACGGGGGCGAGCATCGTCAATGCCACGCGTTC 26228
Qy 9335 AGCGCTGCGGCTCTCACACGGAATGAACGACAGCGGCAATTCACAACTGGATTTCAT 9394
Db 26227 AGTGTATTGCTCTCTCCACGGGTGAATGACAGTGGTCAATTTATGCTGGATTCAAC 26168
Qy 9395 GACCGCGTTACCTGCGGTTTGAAGGACTTCCAGTTGATGACACAGGAGACCCCTGACACTG 9454
Db 26167 GATTCCCGTTATCTGCGGTTTGAAGGTATTTCCGTTGAATGACAGCGGCGCTCAAGCTTG 26108
Qy 9455 AGCTTCGGGATGTCAGCGCAACCAACAGCGGATGCTCTCAGTCTGAGGCAATCATC 9514
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Qy 9515 CTGCATATCCGTTACACATTATCAGCTGATGAGTATCAACATAGCGCAGCCCCCGAAC 9574
Db 26047 CTGCATATCCGTTATACATTCGTTCTTAATTTAAACAATTGTGATAGCGGCTCTGA - 25989
Qy 9575 GAGGCGCTGAGGAGACTGAGCATGCAAAATCATCAAGACATGGCCATTACTGCCCCCA 9634
Db 25988 GGGAGCCGTTTAAAGGAGTTTTATGCAAGGTTTCAACACCTTTGAAACTTGAATACCGT 25929
Qy 9635 CGTTGCTTCGGGGGCGTGGCTGACCGGGCTCAAGGGTGATATCGCGCGCGCAGGGC 9694
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Qy 9695 CGGATGTCGGCGACCCCTGAGTATTCCTTGGCGGTTAGCCCGGTCGGGTTACGCC 9754
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Qy 9755 CCACTGGGGCACTTAATATCAACAGCGGTCGGGAAACGCGCCCTTTGGCATTCGGCTGG 9814
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Qy 9815 GTATCGGCGTGTCTGCTCAGCGTCTGACGCGCAACGAGGACCACTTACCTACCATGATA 9874
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Qy 9875 CTGATGAATTCACCGGTCGGGAGCGTGGGTGCTGTGTCGCGCACTCACGCTCTCTGCA 9934
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Qy 9935 CCCAAGAGCAACGCGAGGCGCACTCACTACTGCGGGAATAAACCCAGGCGGAAGCTTCAACG 9994
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Qy 9995 TTCAGGTTTACGTTCACTGACGAGGAGTCTCAGCGCGCTTGAGCGGTTGCTGCGCGC 10054
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Qy 10055 CCGA-----CGAGACAGAAACGGAATTTGGGTGTTATATACCCCTGACGACAGGTGG 10108
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Db 25148 GTGAGCGCTCATCTTCGCTGAACCTGTACCCGAACTCAATGTGTGAGAAACAATGTGT 25089
Qy 10457 -----GTGGGAGTGGCTGTGCTCAGGATGTTTTCGAGGATGTTTTCGCGGATGAGT 10501
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Qy 10622 TGGAATAAGGAAAGTCTTCTCACTAGTCTGCTGAGAAACGTCGACACAGGTGGCTTATG 10681
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Qy 10682 AGTCGAGCGGAGAGTCTTGTGCTTCCGCGCACTGGCATTTGGGGTGGCAAACTTTACCC 10741
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 QY 11156 ACATGGTGTATTCGGGCGCGAGTGTTCGCTCTATTCCGGCAAAACAGATGGTTGA 11215
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 QY 11336 TGGCGTCAATGGAGTACGTTACTTGGCCAACTTGGGGCAACGGTCTGTTTCGGTCAGCCGG 11395
 DB 24188 TAACGGCAGATAGCTGCGTACTTGGCCGAACCTGGGCAATGAAATTTGGTGAACCTC 24129
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 QY 12701 TGAACGTTGAACACCTGTTGGCGCCGAAAGCCTGCTCGGATAGTACAGTTCGGTACCG 12760
 DB 22811 TTTCCCTGATGTTTCTGCGACAGGTCGAGGACATTTGTTTGGCTGATGCGCGCAG 22752
 QY 12761 TGGCGGGTCAGCAGCAAGTCTGATCTGATTTCAACAGCCTTGCACCGCTCGCTGCTC 12820
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Qy 12933 GCAATCGGATACCTTTTCCCTCCAGGAGGAGAGACAGGCAATTTGGACCCAGTG 12992
Db 22580 GGAATACGGCAAAAGTCCGTTCACTGAAAGA--CAGATTTCAATGCTGCTGGTGGGACA 22523
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Qy 13233 GGTGACCACTGCGATTTCTGGGACGAGGATGATTTGCCACCGTTACAGTATGC 13292
Db 22282 GGTAAACAGCTTCCGTTTCTGGGGAGCTGAAACCGGTGAAACCAAGGATATACCCCTGC 22223
Qy 13293 CACGTTGTCCGTTCCGAGCGCGCAGCAGCGCTCTGGCGTTGACGGCGCCCTACCACT 13352
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Qy 13353 AGCACAGTGTGCTGTATGTCAGGACAGTGGGGAGATGACACAAATGAGAAATGCC 13412
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Qy 13413 CCGCCAGTGTGCTGTGCTACCGTACCGATCGTATGACAGTATACCGGACAGAGTCCG 13472
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Qy 13473 CCAACAGTGACATTTCACTGACGCTTTTGGGCGTGAGTTGCAATCGGCAACCCGGCAGGC 13532
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Qy 13533 CGAGGCAACGCTTGGCAACAGGACGCGAGGCAAACTGCTGAGCGCCAGTGCAGGATT 13592
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Qy 13593 CGCGGTCACTGTAGCAAGAAATTTCCGTGGGCGGTCAACGGGAGGCGGAGATGACAA 13652
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Qy 13713 TGATGACAGTGCCTGCGGACGCTGTTATGCGGACAGCAGCTTTTACGATCCGACGGCAGC 13772
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Qy 13773 GGAATGCGAGGTTATTAACGCAAAAGGTGAACGGCGGACAGTGTCTGATACCCGCTGGTT 13832
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Qy 13833 TGTGGTCACTGACAGCAGATGATACGTTGGCTAAACGACGATCTGACCTGAGGAG 13892
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Qy 13893 GAGGGGGGACGCTGATGAGTCCGCTCGCCCTGACAGCGGCTGCCCTGATGGAGACAAAG 13952
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Qy 14073 GCCGAACAGAAAGGCGGATGCTTTGGCCCTCTCTGGCAGCAGAAACCCGGGAAAGAAAG 14132
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Qy 14313 GCTATCGGTACAGACGACCTCGGAGGCAACCCGCGCTTTTGTTCGCCGAACCTGTTCCGC 14372
Db 21507 ----- 21508
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Qy	15066	AGACGAGACAGCATCGCCCTGAGGGGGTGCCTCGCGTACGCGGCGAGTTGCTGC	CGCG	15126
Db	20895	AAACCAACAGCATATCGTTAAACAGCATACCCCTTGTCCATCACACAGCAATTA	CTGAAAG	20836
Qy	15126	ACGCGCGGGGCAACTCGATGGGTGAGATGCCTCGCCTGGAAAGACCTGCTGATG	15185	
Db	20835	ATGACAGCGAAGCCGATTGGCAGGTATGGATGAATCTGGCTGGAAAAACCGCTGGCG	20776	
Qy	15186	GGGAGAGTTCATCCACAGACCCACGCTGATGCGAACCGGCGCGTCTGTAGCATCACCG	15245	
Db	20775	CGAAAAAGCTTCATTCTGTGACGACAAACGGAATGCTACCGGACGGTATTAACAGGATACAG	20716	
Qy	15246	ATCCAAAGGTAACTGCGAGCGTGGCATATGATGTGGCTGGGCTGCTATCGCGCAGTT	15305	
Db	20715	ATCTCGCGGAAACAAGAACAGTATCGCTATGATGTGCGCGGTCTGCTTTCAAGGCGAGTT	20656	
Qy	15306	GGTTGACGCTGAAGGACGGCACGGAGCAGGTCACTGCTGGCCTCCCTGACGTACTCGCGCG	15365	
Db	20655	GGTTGGCGCTGAAGGGGAAACAAGAACAGTTATCTGTGAATCCCTGACCTATTTCGCGTG	20596	
Qy	15366	CCGGGAAAAAGTTGCTTGAAGAACACGGCAACCGCGGTGGTAACTCTGTATTTACGAGC	15425	
Db	20595	CCAGCCAGAGCTTACCGGAGGAAACATGTGTAAACGGGATAGTGACTACATATACCTATGAAC	20536	
Qy	15426	CGAAAAACACAGCGCCTGACGGGGATTAAAAACGAAACGTCCTGCTGGGCACGCTGCCGAG	15485	
Db	20535	CCGAGACGCAACGAGTTATTGGCATAAAAACAGAACGTCCTTCCGGTCATCGCCGTGGG	20476	
Qy	15486	CAAAAGTGTGACGACCTGCGCTATACGTATGACCCGGTAGGCAACGTATCTACGCGTCA	15545	
Db	20475	AGAAAAATTTTACAAAAACCTGCGTTATGAATATGATCTCTGTCGGAAATGTGCTGAAATCAA	20416	
Qy	15546	ATAACGATCGGAAGAGACCCGCTCTGCGTAAACAGAAAGTGTGACCGGAGAAATACGT	15605	
Db	20415	CTAATGAATGCTGAATTAACCGCTTTTGGCGCAACAGAAATTTGTACCGGAAATACTT	20356	
Qy	15606	ACATCTACGACGCTGTACGAGCTGGTCAGGCCACAGGGCGTGAGATGGCCAATGCCG	15665	
Db	20355	ACACCTATGACAGCGTGTACGAGCTGGTTCTTCCGTCACTGGGCGTGAATGCGGAATATTG	20296	
Qy	15666	GCCAGCAGGCGCAAGCTTACCATCGCTACAGCCCCCTTCTTCTACAGACAGCTCTGCCT	15725	
Db	20295	GCCGACAAAAAACCAAGTTACCAAT-----CCCCGCTCTGATTGATTAACAATACTT	20245	
Qy	15726	ACACCAATTACACGCGCACTACCGTTATGACCGTGTGGCAACCTGACGAGATGGGCC	15785	
Db	20244	ATACGAATTACTCTCGCACTTACGACTATGATCGTGGGGGAAATCTGACAGCAATTCGCC	20185	
Qy	15786	ACAGTCCCTGCGACGAACAATAATATACGACAGACATCACGTTTAGTGACCGCAGCA	15845	
Db	20184	ATAAATTACCCGATCACCGGTAATACTATAAACGAAATGACCCGTTTTCAGATCACAGCA	20125	
Qy	15846	ATAGGCGGTPACTGACACGTTTGGCGGAAGTCGCGTCAGATGTTGATATGTTGTTCA	15905	
Db	20124	ACGGGCTGTACTGGAAGAGCTGGCGCAAGATCCCACTCAGGTGATATGTTTTCACCC	20065	
Qy	15906	CAGGAGTCAACAGAACACCTGCAACCGGGCAAGCACTGGTGTGGACCGCACCTGGAG	15965	
Db	20064	CCGGCGGGCATCAGACCCCGCTTGTTCGCGTCAAGATCTTTCTGGGACCCCGGTGACG	20005	
Qy	15966	AACGTCAAAAGGTGACACCGGTGGTGCGTGATGGGGGCGGACACGACGCAAGCTATC	16025	
Db	20004	AATTGCACAAAGTGATTTGGTCAATAGGGAATAACAGACTCATATTAGAAAGACAGTAACAGTG	19945	
Qy	16026	GGTATGATCGGGCAGTCAGCGTATTATCAAAACCGGCACCGCGCAAACTGGCAACAACG	16085	
Db	19944	GTTATGATGACGACAGTCAGCGGTGTCATTAAAGACTCATATTAGAAAGACAGTAACAGTG	19885	
Qy	16086	TTCAGACACAGCGGTAGTGTAACCTCGCGGCTGGATTACGTATCATGGCAATGGCG	16145	
Db	19884	AGCAAAATACAGCGAAACATTATATTTGCCAGAGCTGGAATGGCGCACGATATAGCGGCA	19825	
Qy	16146	TGACGGAAAAAGAACGCTGACAGTTATTACGGTGGGGGAGGCTGGGCGGCGCAAGTG	16205	

Db	19824	ATACATTA	AAAAAGAGTTTTT	TGCAGGTCAT	CATCTGTCGGTGAAT	TCGGTCAGGCACAAGTGC	19765	
Qy	16206	GCCTATTGCACT	TGGGAGATCGC	CAACCGGATGAC	TCTCGATGAG	ACTCGGTGGTTACA	16265	
Db	19764	GGGTGCTGAT	TGGGAAACAGG	CAAAACCGCGGATAT	CAGCAATGAT	CAGCTGGCGTACA	19705	
Qy	16266	GTTCAGTAAT	CACTGTGTGGC	CAGCAGCTG	GAGCTGGACAGAGAGG	TTACCTTATCA	16325	
Db	19704	GTATTGGCAAC	CTGATTGGCAGT	TAGGGCTTGG	AATTGGAAGT	CGGCGAGATCA	19645	
Qy	16326	GTGAGGAGAG	TTCTACCGTAT	TGGCGAAACGGCTGT	CTGACGGCGGAAGTAGG	TTG	16385	
Db	19644	GTCAAGAAAT	TATTACCCCTAT	TGGGGAACCGCGTGT	TGGCGCAGCCCGAAGT	CAGTCAG	19585	
Qy	16386	AGGCTCACTAC	AAAACTATCC	AGTATGCGGAAACGGCTGT	CTGACGGCGGAAGTAGG	TTG	16445	
Db	19584	AAGCTGATTAC	AAAAACCGTGC	GTGTTATTCTGGCAAG	AGCGGATGCAACAGGG	TTGTATT	19525	
Qy	16446	ATTACGGTTAT	CGGTATTAC	CAGCATGCGCAGGCGCT	TGGCTCTCCACGAC	CCGGCAG	16505	
Db	19524	ACTACGGTTAT	CGTTATTATCAAT	GTGGACAGGCGGAT	TGTTGAGTGAAT	CCTGCGG	19465	
Qy	16506	GCAACGGTGA	ACGGCTGAAACCT	TGTTCCGATG	TGTCGGGAATAAT	CCCGTCA	CGCTGTTG	16565
Db	19464	GTGAGT	TCGATGGTCT	CAATTTGTTCCGAA	TGTGCGAGGAATAA	CCCCATCG	TTTTTCTG	19405
Qy	16566	ACAGCAAC	CGGGCGATC					16582
Db	19404	ATTCTGAT	GTGCTGTTTC					19388

RESULT 2

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US-10-754-115-6/c
: Sequence 6, Application US/10754115
: Publication No. US20040208907A1
: GENERAL INFORMATION:
: APPLICANT: Hey, Timothy
: APPLICANT: Schleper, Amanda
: APPLICANT: Bevan, Scott
: APPLICANT: Bintrim, Scott
: APPLICANT: Mitchell, Jon
: APPLICANT: Li, Ze Sheng
: APPLICANT: Ni, Weiting
: APPLICANT: Zhu, Baolong
: APPLICANT: Merlo, Don
: APPLICANT: Apel-Birkhold, Patricia
: APPLICANT: Madeo, Thomas
: TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
: FILE REFERENCE: DAS-104XC1
: CURRENT APPLICATION NUMBER: US/10/754,115
: CURRENT FILING DATE: 2004-01-07
: PRIOR APPLICATION NUMBER: US 60/441,723
: PRIOR FILING DATE: 2003-01-21
: NUMBER OF SEQ ID NOS: 64
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 6
: LENGTH: 39005
: TYPE: DNA
: ORGANISM: Xenorhabdus nematophilus
US-10-754-115-6

```

	Query Match	10.1%	Score 1921;	DB 18;	Length 39005;
	Best Local Similarity	49.6%;	Pred. No. 0;		
	Matches 7299;	Conservative	0;	Mismatches 6275;	Indels 1143; Gaps 47;
Qy	2493	ACGATACAGCGGTGACGTGACGGATTTATTTCTCGGTTTCGTTTCCCGAGTCAAAAAA	2552		
Db	33588	ACGGTCAGACGATGACTCTTCGGATCTGCAATATTTATCTCTTCAGTGAACCTGAGAAAAA	33529		
Qy	2553	TCACTGGCAGACCCCTGTTCATGGGAGAGGTCGTATCTGTACAGTCAGCGGCAGCAGC	2612		
Db	33528	TCCTTTGATGACACAGCTCAGTCTGGGAGAGGCTCGGCATCTCTATCATGAACCTATAGAGC	33469		

Db	31309	CTCAGTGAACGGGAGCTATCCGTGCTGGTCACTCTCCGATTCCCGGTGCTGGGGCAAAA	31250
Qy	4790	CACCATCTGCC-----CATGACCTGCCGGCGTTTCGACATTAACGGCTTTTCATGCC	4843
Db	31249	AATCAACCTCCGGACAGACAATAATATGATACGCTATTCTCACTACCGATTCCACCAG	31190
Qy	4844	GTGGTTAACCGACGCGCAGCCATGCCGGGAGGTCTTGACCCGCACTTGAGACCGGAGAA	4903
Db	31189	TGAATTAATGGGTGGGCAATCCCGCTCTGACACGCTGATATGTGCGCCACGACACA	31130
Qy	4904	CTGTCTGCTCAGCCCTGCTGGCCGGGCCCTGTACAGAAATGAGCAGGATGTGACCGGCC	4963
Db	31129	CTCAGGCCACAGACTGGCTCCGTGATGGGCTGGACATCATGATGTGTAACGCGAGCC	31070
Qy	4964	TTGGCGAGGTGAGGGGGCCGTGAAACAGGACAACAGCGTGTTCACCTCTCGGGAAGAG	5023
Db	31069	ATGGTTTCCCGCGGTGAACACAGCTTCAGTGTGGCAGGATATCAACACCGTGTTCGAG	31010
Qy	5024	GTGACCCAGCTGAGCAGTGGCTGGACATCAGTACAGCCCTGTCCATTAGCCCATCCGTT	5083
Db	31009	TGGATAGATGGGCATCAGCACCTGACACGATGCCGTGCTTATCCGTACGCTGGTGAAT	30950
Qy	5084	CTGGCTAGCCTGATTGCCCTGAAAGTACATCAATGTGTCCGATGACAGTGCACCGTTGTAC	5143
Db	30949	ATCCGTTACGTGACTGATTAAACAAG-----CCGAGTCCGATCTGCCCTCTCTGG	30899
Qy	5144	AGCCAGTGGCAGTGTGATCCGTCTGCTGCAGCGCGGGCTGAAAAGACGCCAGAGCTCG	5203
Db	30898	GATGAGTGGCAGACACTGGCAGAAAATATGGAAGCCGACTCAGTACACAACAGGCTCAG	30839
Qy	5204	GCCTGCACCATTTCTGGAGGAGGGACACAGACGCCCTTTGTGCGTATTATCTCGGT	5263
Db	30838	ACGCTGGCGATTATACCGCGAGCGCTGAGTAGCGTGTGTGCAATTGGTTCTTGGCG	30779
Qy	5264	AATCTGGCACCGAACATGTGTATC-----CGGCGCGATGACCTCTTCGGGTATCTGCTG	5317
Db	30778	AATATCCAGCCAGAGGGGTGTCCCTGCACAGCGCGGATGACCTGTACAGCTATTTCCTG	30719
Qy	5318	CTCGATTAATCAGGTGTGACCAAGGTAAACACACCGGCATTTGGGAGGCCATTCGCGGC	5377
Db	30718	ATTGATAATCAGTCTCTTCTGCCATAAAACACACCGACTGCGCAGAGGCCATTGCGGT	30659
Qy	5378	ATACGGGTGATATCAACCGSGCCCTTAACGGAATAGAACTACAGCCCATGGCAGAGTGG	5437
Db	30658	ATTACAGCTCTACATCAACCGGGCGCTGAATCGGATAGAGCTTAATGCCGTGCCGATGTG	30599
Qy	5438	AGGGGGCGTCAGTTTTTCACTGACTGGGATACGTTCAACAAACGTTTACAGCACTTGGCG	5497
Db	30598	TCAACCGCCAGTTTTTACCGACTGG---ACGGTGAATTAACCGTTACAGCACTTGGGC	30542
Qy	5498	GGCGTCTCAGAGCTGGTTACTATCCGGAAAACTACTCGACCCGCGGTTCGCTATCGGG	5557
Db	30541	GGGGTGTGCGGCTGGTTTATTATCCGGAAAAATTACATTTGACCCAAACCCAGCGTATCGG	30482
Qy	5558	CACACGGCATGATGACACCCCTGCTGCTGCTGTGAGCCAGAGCATCAACCCGAT	5617
Db	30481	CACACCGGATGATGATGAATCTGTGGAAAAATCAGCCAGATGAATTCGCCGGGAC	30422
Qy	5618	ACCGTGGAGGATGCCCTTTAAACCTATCTGACCACCGTTTGGCAGAGATTGCCAATCTGAAC	5677
Db	30421	ACAGTGGAGGATGCCCTTTAAACCTTACCTGACCCGCTTTGAACCGTGGCGGATCTGAA	30362
Qy	5678	ACTGTACCGGATATCAAGTAACGCCAGCATCAGCAGGGGACTACATGTTATGGGT	5737
Db	30361	GTGTGTACGCCCTTATCACGACAAACGTCACAGCAACACCGGACTGACCTGGTTGTGCGC	30302
Qy	5738	CGCAGCATCACAGATCAGACTTAATGTTACTGCTGGCAGGCCCAACACACGAAAAATCCAA	5797
Db	30301	CAAAACGGGAGAACCTGCCGGAATACTCTGGGTAAACGTGGATATATCACGGATGCGAG	30242
Qy	5798	GACTCAATGATGCCCGGAATGCTCGACCGGATGGACAAAAATTAATCTCGCGAATGAAT	5857
Db			
Db	30241	GCGGTGNACTGGCCCCCAATGCTTGGAAAGAGTGGACGAAGATTGATACAGCGTCAAC	30182
Qy	5858	CGGTGTCAAGATTGTGTGCTCGGTGTTTTTCAACAGTCCGCTTTTATGTCTCGGTTC	5917
Db	30181	CCCTACAGGATGCAATAGCTCCGTCAATATTACAGGAAACGTTTGACACCTTATCTGGTA	30122
Qy	5918	GAGAGAAATCAGTCTGCTGATACGAGGACAGAGACACACACACCGACGACAGACTAC	5977
Db	30121	GAAGAAAGAGGATGGCGAAAAAATGGTACTGATCCGGTGGAAACC---TATGACCGTTTT	30065
Qy	5978	ACGCTGAAACTGTGCTTCGGGGCTACGACGGTACATGAGTTCGCCGGTGTCTGTTCCGAC	6037
Db	30064	ACTCTGAACCTGGCGTTTCTGCGTCATGATGGCAGTTGGAGTGGCCCTCTGTCTTACGAT	30005
Qy	6038	ATTACCGGCAACATCG-----	6053
Db	30004	ATCAACAACGAGTGGAGCGGTCACTGACAAAAAACCTGACACTGAACGGCTGGCGCTG	29945
Qy	6054	-----CATTTCCGAAACGAGGGCATGTGACCTGTAATCCCTGACTGACGAG	6106
Db	29944	GCGCATCAGGCTTTCAGGGCAGGACACTCTGTGCTGTTGTCTACAAAAACCGGAAG	29885
Qy	6107	CTCTATTGGCGCTTTTACTCCGTCAACAGCAAGCCGGACTTTGATAACGCTCAGCTGATT	6166
Db	29884	AGTTACTCGATTTTGGCGGACGCAATAAATAATGTGGCAGGCATGACCATTTACGGGAT	29825
Qy	6167	TCGTGGATAATGATATGACGCTAAATGTCACTCAGATATAGGGATTTTTTAAAGAGGTC	6226
Db	29824	GGCTCTTCAAAAAGATGGAGAACACAGCACTCAGCCGTTACAGCCCACTGAAAAATACC	29765
Qy	6227	AGTCACGAATTTAATACGAGCACTGAGAAATTTATTAATAATGTTTTTTTCAGACCCCTTC	6286
Db	29764	TTTGATATCATCTACTCAAGGCAACGACTTGTAAGAAAGCCAGCTATCGTTTCGGC	29705
Qy	6287	GCTAATTTATTTGCTAGTGCAACGAGTTTAAATGTAGTATGTTATCCACAGCGATTCTCA	6346
Db	29704	CAGGATTTTGAAGTGCCTGCCTGTTGAATATGGGTTCTGCCATCGGTGATGATGCTG	29645
Qy	6347	CTCCTTAATCTTAAACTACAAGTACTGTTTTTACTTAATGAAGATTCC-----TCTCTT	6400
Db	29644	ACGGTATGGAGAACCGGAATATTCGCGAGATAACCAAGTAAATCTCCACGCGATAACCTT	29585
Qy	6401	TTGACGCCAGAGCTTCATATTACAGCAAAATGTTTCGTGTTTGTAGTACTGCTGCATC	6460
Db	29584	GCTATTACGCTACATAACCCCGCTTCTACTGTGATATGATGGCAGTGGCATGTCACTC	29525
Qy	6461	GCCACTCAATCTACCA-----TAGAAAAATTCGTTTCAGCAGGAGATGAGAAATTTGAGAAA	6515
Db	29524	AGAAACAAACAAATCAGCGCCATGAACTGACGGGGTGGATGGAAAGTCCCAAGTACGGC	29465
Qy	6516	TTAATTTTATGACGGCAGCGCGCGGAGTTTGAACGAGTTTGTGGAGTGGATGTTT	6575
Db	29464	AATGCAATTTTATCATCCAAATACCGTTAAACATTAATGGCGGTACTCTGATCTGGGGGG	29405
Qy	6576	CTAATTTCAAAAGTATACCAAGTTCGAAA-----AGAAAGCAGTTGCTGTCACTGTA	6625
Db	29404	CCGATCACCGTTTATTAATAAAGAAACTATATTGCACTAGTTCACGCCCACTTGATG	29345
Qy	6626	AAATCTTATTCGCTCACTGGCGTTAGTGGTCTCTGTTGAGTTATTTATGATTCATCAAAAT	6685
Db	29344	AACGCAATTAACACTAGGCGTTTGATTCTAACACCAAGTTGAAAAATAATATTATGCGAGA	29285
Qy	6686	AAATACTTCAGCGGAATTTGTGAGATAAATGATNACCGCTTTAATTAGCGGACATACA	6745
Db	29284	TTGTTGAGTGTTCATTTTCTCCAAACACANTTTTTAAACACCGTTTTTTCAGTGTGATG	29225
Qy	6746	TCAAAAGTTAATTAAGTGTGCTATTGGCTCTCAAGATTTTTGGAGTGTAAAGTCCGCTC	6805
Db	29224	AATAAACCAGTGATTTTAAAGATGCGATGTTATGTTGATGTTAATAATTTCTCAGGGC	29165
Qy	6806	ATGCCGCACTTCAGATATATGAATTAATCGATGATATCATCTGACATCCCGCGTAAAT	6865
Db	29164	TTCCAGATATTAGTTCTTATCAATCATCCGGCTGGATGATATTGATATACAGGCATTAAC	29105

Db	26944	GACGGTGAAGTCAAAACAATGGATGCCAGTTGGAAAAGCCTGAAATCCGCGCGAAGCA	26885	Db	25868	CGGAAGGGGAGCGTCATTTTCACTGCCCTTGCCGATCTCTGTGGGCGGTGGTCTGGTGC	25809
Qy	8678	GCTGAGTGCAGAAAACCTTACCTTGAGACCAGACAGCCAGCAGAGGGCGAGTTGGCA	8737	Qy	9755	CCACTGGGCGACCTTAATATACAGCCGCTCGGGNAACGGCCCTTTTGGCAATTTGGCTGG	9814
Db	26884	GCACAGTCAGGTGGAATATACAGGAGACCAGCAGGCCCATACTCAGGCTCAGTTAGAG	26825	Db	25808	CGGTGCTATCACTGAATTAACAGCAGTACTGCCGGCAATGGGTCAATTCGGGATGGGTGGC	25749
Qy	8738	TTCTCGCAGAGTAAGTTCAACAATACGGCTCTCTACAGCTGGCTGGCGGCGAGGTTGTCC	8797	Qy	9815	GTATCGCGCGTGTCTGTCTCAGCGTTCAGCGCAACGGAGCACCTACTCTACGATGATA	9874
Db	26824	CTGTTACAGGTAATTCACAAACAAGCGCTTTACAGTTGGATGGCGCAAGCTGAGT	26765	Db	25748	AATGTGGGTTGGTTTATACGCTTCCGTCAGCCAGGGCGTTCCGCATATACGGGAC	25689
Qy	8798	GCAATTTATPACAGTTCTATGACCTGGCAGTATCCGCTGCTGATGGCGCAACAGGCC	8857	Qy	9875	CTGATGAATTCACCGCTCCGGAAGTGTGTGTGCTGCCGCACCTCACGGCTGTGGCA	9934
Db	26764	GCTATCTATTACAGTTCTTTGACCTGACCCAGTCTCTCTGCTGATGGCACAGGAGCG	26705	Db	25688	AAGATGAGTATCTCGGCGGATGGGAAGTGTGAGTATTGTGCGGACAGCAAGGGC	25629
Qy	8858	TGCGAGTGGATAAATTCGAGA---CTAGTCTGTTTATCCAGCGGGGGCTGGATGGGG	8914	Qy	9935	CCCAAGAAGCACGGCAGGCCACTCACTACTGGGATATAAACCCAGCGGGAAGTTCAACG	9994
Db	26704	CTCGCGCGAGCTGACCGACAACGGTGTGTACCTTTATCCGGGTGGGGCTTGGAAACGGT	26645	Db	25628	AACCAAGACAACGCCCACTCTACTGTTGGGACGGTCTTGACACAGCCGCACTCTG	25569
Qy	8915	GCAATGCCGCTCTGTGGCGGGGAAACCTGATGCTGAATCTGGCGCAGATGGAGCAG	8974	Qy	9995	TTTCAAGTTTACCGTTTCACTGACGAGGTGTCTCAGCCGCTTGAGCGTTGGCTGCCCG	10054
Db	26644	ACGACTGCGGTTTGATGGCGGTGAAACGTTGCTGCTGAATCTGCAGAAATGGAAAA	26585	Db	25568	TTTACCGCTATCAGTCCCGCTGGCAGAAAAAATCGTTCTGTAGAACACTGGCAGCCAC	25509
Qy	8975	GCCTGGCTGACGGGGATGACGGGCAATAGAGGTGACCGGACGGTCTGCCCTGTCCGAG	9034	Qy	10055	CCGA-----CGAGACAGAAAACGGAATTTTGGGTGTATATACCCCTGACGACAGGTG	10108
Db	26584	GTCTGCTGGAGCTGATGACGGGCACTGGAAAGTGACCCGTACCGTCTCGTTGGCACAG	26525	Db	25508	AGCAGAGACGTGAGGAAGAGACGTCTTTTGGGTACTTTTACTGCGATGTTTAGTGC	25449
Qy	9035	GTCTATACAGCTCGCGGAGGATGCGGCAATTCCTCTCTGGCGCAAGGTGTGGAACTG	9094	Qy	10109	CTCTGCTGGGCCGAAATGGCAGGCTCGCATCAGCAACCCCAAGCCCCAACACAGACCG	10168
Db	26524	TTCTATCAGGCTTATCATCAGAA---CAACTTTAATCTGACCGGAAATCTCAGCAATTC	26468	Db	25448	ACCTATTTCGGTAAGCATCCATGACGTATTGCTGACCGCGGAGTGAACCAAGATTG	25389
Qy	9095	GTCAATAAGGTTTCGGCGAGTGGGTACGAAAGCAACGGATTACAGATGGATCAACAG	9154	Qy	10169	CGGTTTGGCTGATGAGTCTCTCGGTATCACTTACCGGCAACAGATGTATTACCAATACC	10228
Db	26467	CTCGGTGAAGGAAAGCAAGTAGGAGCTTCGGCAATGAATTTAAACTCAGTAACCGT	26408	Db	25388	CCGCTGGCTGATGAGGAAACCGTCAGCATACCGGGAAACATATTTACTATCACTATC	25329
Qy	9155	CAACTCGAGGCCACCTGAACTGGCTGACTCGGTATCGGCAACGATTACCCGGTCTCC	9214	Qy	10229	GTGCGAAGATGATGACGGTTGTGACGAGCGGAGCGGACCGCAACCGCGCGCGCGG	10288
Db	26407	CAGATAGAAGCCTCAGTGGGATTTCTGATTTGAAATTTTTCAGCGCACTACCCGAAAGC	26348	Db	25328	GGGCAAGACGATCTTGACTGTGATGACATGAACTTCTCAGCATTCAGGTGTACCG	25269
Qy	9215	CTTGGCACCATGAGGCGCATCAAAACAATAAGCGTCAACGCTCCCGGCGCTGTGCGCC	9274	Qy	10289	CCCAAGTTATCCGTGGCGGCTGTGATGTTAAACCGTCAGCGGCTCGGACGCTACCGG	10348
Db	26347	CTTGGCAATACCCGTCAGTTGAAACAGGTGAGTGTCACTTGCAGCGCTGTGGCGCG	26288	Db	25268	CCGACGGTTATCGCAAAAGTCAGCTATGGCAATCTCAGCGCGGAAACCGCTTTTTCG	25209
Qy	9275	TATCAGAGCTCGTGGGTTCTCAGCTACGGCGGAAGTATGTCATGCCCCGGGTGTC	9334	Qy	10349	CGCTGTGTGC---GACACCATCAATGAGTGTGCTGCTGTTTATCTGTGTTTGTGATG	10405
Db	26287	TATGAAGATATTCGGCGGTGCTGAATTCGGGGGACGATCGTCAATGCCACCGGTTGC	26228	Db	25208	CGGTAATAACAGGTATTCCTGCTGATATGACTGCTGTTTATCTGTTTATTTGATACG	25149
Qy	9335	AGCGGCTGGCGTCTCACACGGAATGAACGACAGCGGCCAATTCCAACTGGATTTCAAT	9394	Qy	10406	GTGAGCTAGCTCGGTGCTGTGAAGCGCCGCGCTGGCAACAACAGGAA-----	10456
Db	26227	AGTGCTATTGCTCTCTCCACGCGTGAATGACAGTGGTCAATTTATGCTGGATTTCAAC	26168	Db	25148	GTGAGCGCTCATCTTCGCTGAACTCTGTACCCGAAATTCATGTGTGAGAAAAAATGTGT	25089
Qy	9395	GACCGGTTTACCTGGGTTTGAAGACTTCAGTTGATGACACAGGACCTTGACACTG	9454	Qy	10457	-----GTGGGAGTGGCTGTGCTGCTCAGGATTTGTTTTCGGGTATGAGT	10501
Db	26167	GATTCGCGTTATCTGCGGTTTGAAGGTATTTCCGTGAATGACACGCGCGCTGACGTTG	26108	Db	25088	CTGAAAAAATGTGCTGAAAAATGGCGTTGTGTCGCGACAGTTTCTCCGCTATGAAT	25029
Qy	9455	AGCTTCCGAGTCTGACGCAAAACACAGGCGATGCTCTCAGTCTGACGCGACATCATC	9514	Qy	10502	TTGGTTTTAACTCGCGACTCCCGCTGTGCGCTCAGGTGTTGATGTTTCCATTAAGTAC	10561
Db	26107	AGTTTCCGAGTCCGACTGATCGGCAGAAAGCCCTCTGAGAGCCCTGAGCGGATATCAT	26048	Db	25028	ATGGGTTGAAATTCGAACCCCTGCTGTGTGTGTCGCAAGTTCTGATGTTTCACTAGTGA	24969
Qy	9515	CTGCATATCCGTTTACACCATTTATCAGCTGATAGGTATCAACATAGCGAGGCCCGCGAAC	9574	Qy	10562	GTGTTCTGCGGGAGTTTCGGAGCGAATGATGCGCCAGCATGATTTCTCGCTGTGTC	10621
Db	26047	CTGCATATCCGCTATACCATTCGTTCTTAATTAACAATGTTGATAGCGAGGCTCCTGA-	25989	Db	24968	AAGCGCTGGCAGGGGAAAAAGTTGCAGAAAGAAACACCGCGCTGGTTTCCCGCTTTATTC	24909
Qy	9575	GAGGCTCGGAGAGACTGAGCATGCAAAATCATCAAGACATGGCCATTTACTGCCCCCA	9634	Qy	10622	TGGACTACAGGAAAGTCTTCACTCAGTCTGCTCGAGAACGTGCACAGGTGGCTTATG	10681
Db	25988	GGGAGCTGTTTAAAGAGTTTATATGAGGTTTCAACCTTTGAAACTTGAATACCGT	25929	Db	24908	TGGAATATGACCTGAACAACAAAGGTTTCTTCTGCAACCGGCCCGCAGACTGGCCATG	24849
Qy	9635	CGTTGCTTCCGGGGCGGTGCGGTCAACGGGCTCAAGGTGATATCGCGGCGCAGGGC	9694	Qy	10682	AGTCGGAAGGAGCTCTTGTGCTTGGCGCACTGGCATTTGGGTGGCAAACTTTTACC	10741
Db	25928	CATTGCCCTCTGGGGCGGATCACTAAAGGAATGGAGAACGACTCAATGCCGTCEGAG	25869	Db	24848	AAACGGAAGGTACGACGATGATGTCGCCGCTGGAATGATATCAAGCTGTTAATC	24789
Qy	9695	CGGATGTCGGCGACCTCGAGTATTCCTTTCGCGGTAGCCCCGCTCGGGTTACGCC	9754	Qy	10742	CGCCGACATTTGTCGCGATGGCAGACGCGTGAAGATATGGCAAGTTGAGTTGCTTCAAC	10801
Db				Db	24788	ATGGGTGTAATCTGAACCTGGCAGTCCATGCCGCGAGTTAGAAAAAATGAACACAGTTGCAGC	24729

Db 22580 GGAATACGGCAAAAGTGCCTTCAGTGAAAGA--CAGATTTCCATGCTGGGTGGACA 22523
QY 12993 TCAGGAGATGTTACCTATGCGCGGCGAGAGCAATTTCTGGCTACCGCTATCCTTTTCGGGA 13052
Db 22522 AAAGGAATTTACAGAATATGCGGTGCGAGCGAATTTCTATCGGCCATTTGGTCAACGGGA 22463
QY 13053 CAGTATGTTGACCGGCCCGGATTCACGCTGACGCTGACGCTGACGCTGCTATCAGCA 13112
Db 22462 AACCAAGCTTACAGGTAAACAGCAGTCAGTGGGATAGCATTTACTGTGTTATCACCGC 22403
QY 13113 GTGGCAGGATGCGCGAGGATTTGCACACAGCCGACTATGATGGCGCTTCCTGACGCC 13172
Db 22402 AACAGAGATGCGCTGCGCTGCGTATGCAAGCGCATTAGCATTAAGATTTATGTTGC 22343
QY 13173 CGTCCGGGTACGGACCCCAATGATTAATCTGAGTCCGCTCACTCTGGATGCTCTGGCCG 13232
Db 22342 GGAATACACACAGATGTCATGATTAATCACTATCACACGTCAGCTTTGATGCACTGGGAG 22283
QY 13233 GGTGACCACTCGGATTTCTGGGGCACGGAGATGTTATGCCACGGTTACAGTATGC 13292
Db 22282 GGTAAACAGCTTCGCTTTCTGGGGGACTGAAACCGGTGAAACAGGATATACCCCTGC 22223
QY 13293 CAGCTTGTCCGTTCGGACCGCGCAGCGCTCTGGCGTTGACGGCGCCCTACCACT 13352
Db 22222 -----GGAAATGAACTGTCCCTTTTATGTCCTCCCAACAGGT 22184
QY 13353 AGCACAGTGTCTGGTATGTCACGACAGTTGGGAGATGACGAATAGAGAAATGCC 13412
Db 22183 GATGATGCTCTGGCATTTGAAACCCGCTATACCTGTTGAGGGCTGATGTTATGCCCC 22124
QY 13413 CCGCGCTGGTCTGCTGCTACCGATCGCTATGACATGATACCGACAGCAGTCCG 13472
Db 22123 TCTGAGCTGATGGTTACAGCCAGCTTTCTAATGATGGGAGCTTTATGGAGAGTGAA 22064
QY 13473 CCAACAGGTGACATTCAGTACCGGTTTGGGCGTGAGTTGCAATCGCAACCGCGAGGC 13532
Db 22063 ACCGGTGGATCATCACTGAAGAT----- 22039
QY 13533 CGAGGGCAACGCTGGCAACAGGACCGACGCAAACTGGTGACGCCAGTGACCGATT 13592
Db 22038 ----- 22039
QY 13593 GCGGCTCACTGTAGCAACGAATTTCCGCTGGCGGTCAACGGAGGCGGAGTATGACAA 13652
Db 22038 -----GGTTATCTCCTGTGCTGTCTTTTCGCGCGCTGGCAACAAA 21998
QY 13653 TAAAGGTCTGCTGTTTCGGGTTTATCAGCCGTATTTTCTGGACAGTTGGCAATATGTCAG 13712
Db 21997 TAACCTGCGCTGCCATGCCAAGCAAGTCAATTCACAGAACCCACCCCATGTACTGAG 21938
QY 13713 TGATGACAGTGCCTGGCAGGACCTGTATGTCGACACGCACTTTTACATCCGACGCAACG 13772
Db 21937 TGTGATCACCGACCGCTATGATCCGATCCGATCCGAAACAACT----- 21896
QY 13773 GGAATGGCAGTTTATACGCAAAAGGTGAAACGGGACAGGTGCTGTATACCCCGTGT 13832
Db 21895 -----ACGTCAAACGTTTACGTTTGTAGTATGTTT 21866
QY 13833 TGTGGTCAGTGAAGACGAGATGATACCGTTGGGTAAACACGCGCATCTGACTGGGAAG 13892
Db 21865 TG-----GGCGAACCTTACAAACAGCCGTACGCCATGAAGTGGTG 21825
QY 13893 GAGGGGGGACGGTGTAGTCCGTGCGCCCTGACAGGCGCTGCCCTGTATGGAGACAAAG 13952
Db 21824 AAGCTGGGTACGTGATGATGAGTATGGAGCC----- 21796
QY 13953 ATGAAATACATCATCAGTTGCGCGGTTGTGCTGACAGGTGTTATGTTTGGGGCTT 14012
Db 21795 ATTGTGGCTGAAATCATGGCGGCTGAAACGGCGATGACAGATTTCCGTTGGGCGATT 21736
QY 14013 TCCCATTTGGCGTTTACCCGTCGTTTACCAACCGCGGACAGATCACTCAATGGCAACACCCAG 14072

Db 21735 TCCGAGCTACAGATATGACGGAAGGCCAAGCCCTCGCTAAGTATCAAC----- 21684
QY 14073 GCGGAACAGAAAGGCCCGATGCTTGGCCCTCTCTGGCAGCAGAAACCCGGGAAAGAAAG 14132
Db 21683 -----CGTATTTCTGAATAGTTGGCAGTAC-GTCAGTGTATGACAGTGCCTCGCAGG 21633
QY 14133 TGGAGCAGCAACGACAGACTGACATGAACAAGGTGGCTATATCATCTCTGAAGAAGACTG 14192
Db 21632 ATATATATCCGANTACCCATTACTATGATCCGTTGGGCGGTGAATATCAGGTTATCACGG 21573
QY 14193 GTGTGTCGCGTACGCTCCGCTGATGCTCAAGCGCACTGGTCAGCGCCCTGACGACACAC 14252
Db 21572 CCAGAGCGGGTTTCTGTCATCTTATCTACTCCCTGGTTTGTGGTGAATGAAGATGAA 21513
QY 14253 GTTACCACTCTCAGCGGCAACTTGGCAGTCTGTGAACCCGCGCTTTTCGCGAGTACC 14312
Db 21512 ATGAC----- 21508
QY 14313 GCTATCGGTACAGACGACCTCGAGGCCAACCCGGGTTTTGTTGCCGAACTGTTCGCG 14372
Db 21507 ----- 21508
QY 14373 CGCGCTACAGAGCGGGAGAGCTGGCAGCGTATGCTGACAGGACAGAGTGAATGG 14432
Db 21507 -----ACTGCCGTTGAATGACAGCAT-----AAGCT 21480
QY 14433 CAGGCTTGGGGCGGCTTATCAGCGGCTACGCGAGCAGAAAGAAATAAGCGGATTTA 14492
Db 21479 CAGTATGCTGCTTCACTGAACAGACATCACTCCATTTAGGAATGAA----- 21433
QY 14493 GCGGTTAAGAAAGTGACGCTGTTTTCGCGATTAATATTAACAGGAGATCACTAGCA 14552
Db 21432 -----TCATGAAGA 21424
QY 14553 CATCTTTTTCAGTAGCACCCGCTCGGTCGCGGCTGCTGCAACACCGCGCTTGGTGC 14612
Db 21423 ATTTGTTTACAGCAATACGCCATCCGTCACCGTACTGCAACACCGTGTGACAGATAC 21364
QY 14613 GGGAGTGCAGTACTACGCCATTCGGATACACCGGAGAGAGCGGACGAGGTATCACCT 14672
Db 21363 GCGAAATAGCTTGGTATCGGCAACCGCATCACTCAGGTAACCGATGAACGATCACCG 21304
QY 14673 GCCATCAGACCATGAGCGCGCAGCTTGTCTCAAAAGCCCGACCGGCTTACGCGG 14732
Db 21303 GTTATCAATATGATGCTCAAGGATCTCTGACTCAGAGTATGATCCGCAATTTATGAAC 21244
QY 14733 CCGGCTGACAA-----AATTTACGTACTCTGAATAGCC 14765
Db 21243 GCCAGCAGACAGGAGTGACAAGACGCCATTTACACCCCAATCTTATCTTGTCTATCAC 21184
QY 14766 TGACCGGACAGTACTGACAGCGCTCAGCGCGATGCGCGTACGCTGCGTGAACCTGAGCG 14825
Db 21183 TCAGTAAGAAGGCAATTTGCGTACGCAAGTGTGGATGCCGAACCCGCTGCTGCGCTCATG 21124
QY 14826 ATGCGCGCGGGCGGTTTCTGCGCGCTCAGCGGCTGGGACGGAAGCGGCTCACCC 14885
Db 21123 ATGTTGCCGGGCGTCCGCTTTTAGCTGTGTCAGCGCAATGG-----CGTTAGCC 21076
QY 14886 GCACCTGGCAATATGAAGACGATACCTGCGCGGCGCGCGCTGAGCATCACCGAGCAGG 14945
Db 21075 GAACGTTTCAGTATGAAGTATACCTTCGCGGACGATGCTAACGATTAACGAGCAGG 21016
QY 14946 TTACCGGTGAAGCGGCCAAATTAAGGAACGCTTCTGTTGACGCTGGCAATACGATGCGCG 15005
Db 21015 TAAAAAGGAGAGAACGCTGTATCAAGGAGCATGATCTGGTTCAGGAATAACCGCGCAG 20956
QY 15006 AGAAGATTTCTCAATCTGCTGCGCGAGTGTGTCAGTCAATTTACCATACCGCGGACTGGTGC 15065
Db 20955 AAAAAGGCATTAATCTGGCCGCGCAGTGTGCTGATTCATTCATCCACCGAATGAATC 20896
QY 15066 AGACGACAGCATCGCCCTGAGCGGCTGCCCTGCTGCGCTCAGCGGCGAGTTGCTGCCCG 15125
Db 20895 AAACCAACAGCATATCGTTAAACAGCATACCTTGTTCATCACACAGCAATTTACTGAAG 20836

Db 10978 TACGCTATAATCCCGCGGCTATATCGTTAAACGAGAAATCGCCCTCGATCTGGAAC 11037
Qy 7481 GTCGCTCCGCTGAGAGGACACCGGCTGGAACGACTCGCGCTGACTCCATTGACCCC 7540
Db 11038 TGC CGCGCGCTGGAAG--ACACTCCTCGGAATGCCAATCCGTTGGATGCCATTGATCCG 11095
Qy 7541 GATGCAATAGCCCAAGTACGACCCCATCATTAACAAGTCCCACTTTATGTGCTACCTC 7600
Db 11096 GATGCGCTGCACATATGACCCGACACACTATAAGTTGCCACTTTATGCGCCCTGTTG 11155
Qy 7601 GACCTGCTGATGTCGCCGCTGATGCGCCTACCGCTGCTCGAGCGGACACCCCTTAAC 7660
Db 11156 GATCAACTTATCTGCGCGCGGATATGCGCTATCGCGAACTGACCCGCGATGCTTGAAT 11215
Qy 7661 GAGCCCGGATGTGTAAGTTCAGGCTGAACTCTTCTGCGGACAGAGCCCTATATTTCC 7720
Db 11216 GAAGCCAAAGATGTGTAATGTGCGGTGTTTGAATATGCTGGGTGATGAGCGGAGGATTAC 11275
Qy 7721 TTTGAGCCGACTGGTCCGCGTTGACCTCGGTGAGCGACGCGAGGTTGACGCGACGC 7780
Db 11276 GGCAGCCAAAGTGGCGCGCACCGTCTCTTTCGTGGCGGGAACACACTGTGCAAGCG 11335
Qy 7781 GATTACAGAGGCCCTGCTGGCGGTGCGCGGTGCTGTCGCCCTCCCGAGACACGGAAG 7840
Db 11336 GGCCTATCAACAGACCTTACGGCGCTAGACAAACGAGAGGTTGCACTCAACCCCGCAAC 11395
Qy 7841 GCGAATTCCTGAGCGCACTTTCCTCCCGCAGCAGAACGAGTGTCTAAAGGCTACTGG 7900
Db 11396 GCTAACTCGTTGGTG--TTTGGTTCCTGCGGAATATAAACCCGGAATCAACCGGATTACTGG 11454
Qy 7901 CAAACCTTGGCAGACGCGCTCCATACTTCGCGCACAACTCTCCATTGACGCGCAGCGG 7960
Db 11455 CAAACC--TGCGTTTGGCGCTGGTTAACTCGCGCATATCTCTTCCA--TGACGGGCAACCG 11512
Qy 7961 CTTTCCCTGTCGTTACGCCACCGCGTCCGAAACCGTCCGCTCGCAGAGTGCCTGCTG 8020
Db 11513 TTATCGCTGCGGAATTACGGGAGC--TACGATCCGAAAGCGTGTCTCACCATATGGTA 11570
Qy 8021 AACAGCGCAGAGTGTGACGACTGCGCGCGCGGTGATGCGCTTTTACAGTTTCCCG 8080
Db 11571 CAGCTTCTCAGGCGGTAGTGAGTGTCTGCCCGCACATTTGCTTTATACCGCTTCCCG 11630
Qy 8081 GTCATGCTGAGAAACCGCGGGGATGTGAGCGCTGTGACCGGGTTGGCAACACACTG 8140
Db 11631 GTGATGCTGAGCGGCGCCGCAATCTGGTAGCGCAATTAACCACTTGGCACTCTCTG 11690
Qy 8141 CTCGGTATACGAGCGTACGAGTGGAGCGCTGGCCAACTGTCTGACAGACCCAGGCG 8200
Db 11691 CTCAGTATGCAGAGCATGATGATGCGGATGAATCACTCAACAGTGTCTACTACAGCAGGT 11750
Qy 8201 AGTGAACTGATACCCAGGCTTCCGACGAGGATAACGTCCTCGAGGAAATCGATGCG 8260
Db 11751 ATGGAATGGCGACACAGAGCATCCGTTATTCAGCAACGAACTGCTCGATGAAGTGGATGT 11810
Qy 8261 GATATTGCCCGCTTGAGGAGAGCGCGCGCGCGCGAGATGCGTTTGAACGTTACAA 8320
Db 11811 GATATTGCTGATTGGCAGAGCGCGCGCAGTGCAAAATCGTCTGGAATAATACCAG 11870
Qy 8321 GTGTTGACAGCGCGACGTCAACACGCGGAAAAACAGCCATGACCTTTACCTCAGT 8380
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Qy 8441 CTGCCCAATATTTCAGGCTGCGCGTCCGCGGCTCCGCTATGCGGCACTATTATTAAGCC 8500
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Qy 8501 ACGCCATCGGCATCCAGGTGCTCTCGATGCGACCGCGCATATCAGCGGACAAAATCAGC 8560
Db 12051 TCCGCTCCGTGATGTCGCTTTCTGCCACAGCTTCCCAATATTCCGACAGAAATCAGC 12110

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Db 12111 CGTTCCGAAGCCTACCGCGCGCGCGTCAAGAGTGGGAAATTCAGCGTGATATGCTGAC 12170
Qy 8621 TCTGACGTGGCGCAGATTCATGCCAGCTGGCGGCATGCGCAGTGGCGGAAGGGCT 8680
Db 12171 GGTGAAGTCAAAACAATGATGCCAGCTGGAAAGCTGAAATACGCGCGAGAGCA 12230
Qy 8681 GAGCTGCAGAAAATTTACTTGAGACCCAGCAGACCCAGCGCAGTGTGGCAATTC 8740
Db 12231 CAGATCAGGTGGAATATCAGGAGACCCAGAGGCCACTACTCAGGCTCAGTTAGAGCTG 12290
Qy 8741 CTCGAGAGTAAAGTTCAACAATACGGCTCTGTACAGCTGCTGCGGGGAGGTTGTCCGCC 8800
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Qy 8801 ATTTATTACAGTTCTATGACCTGGCAGTATCCGCTGCTGATGCGCAACAGGCTCTG 8860
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Qy 8861 CAGTGGGATAAATTCGAGA--CTAGGTCTTTATCCAGCCGGGGCTTGGATGGGGCA 8917
Db 12411 CGCGCGAGCTGACCGACAACCGTGTACTCTTTATCCGGGGTGGGGCTTGGAAACGCTAG 12470
Qy 8918 AATGCGGTCTGCTGGCGGGGAAACCTGATGCTGTAATCTGGCGCAGATGGAGCAGCC 8977
Db 12471 ACTGCGGGTTTATGCGGGTGAACGTTTGTCTGCTGAAATCTGGCAGAAATGGAAGATC 12530
Qy 8978 TGGCTACGCGGGGATGAGCGGCAATAGAGGTGAGCGGACGCTCTGCCCTGTCGAGGTC 9037
Db 12531 TGGCTGGACGTGATGAGCGGCACTGGAAGTGACCGGTACCGTCTGTTGGCACAGTTC 12590
Qy 9038 TATACAGCCTCGCGAGGATCGGCAATCTCTGCGCCGACAAAGTGTGGAACCTGGTC 9097
Db 12591 TATCAGCGCTTATCATCAGACAAC--TTTAATCTGACCGGAAATCAACGAAATCTCTG 12647
Qy 9098 AGTAAGCTTCCGGGAGTCCGGTACGAAACGAAACGAAATACAGATGATCAACAGCAA 9157
Db 12648 CGTGAAGGAAAGGCAACGTAGAGCTTCCGGCAATGAATTAATACTCAGTACCGCCAG 12707
Qy 9158 CTCGAGGCCACCTCTGAACTGCTGACCTCGGTATCGGCAACGATTAACCGGCTCTCCCTT 9217
Db 12708 ATAGAAGCTCAGTGGATGTTGTTGAAATTTTTCAGCGATATCCCGGAAAGCTTT 12767
Qy 9218 GGCACCATGAGGCGATCAAAACAATAAGCGTCACTCCCGCGCTGTGTCGGCCCTAT 9277
Db 12768 GGCATAACCCGTCAGTTGAAACAAGTGTGTCACCTTCCCGCGCTGTTGTTGCTGCTAT 12827
Qy 9278 CAGGAGCTCCGTCCGTTCTCAGCTACGCGGAGTATGTTGTCATGCCCGGGTTGCAGC 9337
Db 12828 GAAGATATCCGGCGGTGCTGAATTACGCGCGAGCATCGTATGCCACGCGGTTGCACT 12887
Qy 9338 GCGCTGGCGGTCTCACAGGAATGAACGACGCGCAATTCACCTGATTTCAATGAC 9397
Db 12888 GCTATTGCTCTCTCCACGCGGTGATGACAGTGGTCAATTTATGCTGATTTCAAGAT 12947
Qy 9398 CCGCGTTTACCTCGGTTGAAGCACTTCCAGTTGATGACACAGGACCTCTGACCTGAGC 9457
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Qy 9458 TTCCCGGATGCTGAGCGCAACAAACAGCGGATGCTCTCAGTCTGAGCGACATCATCTCTG 9517
Db 13008 TTCCCGGATGCGACTGATCGACAGAAAGCGCTGCTGGAGAGCCTGAGCCATATCATCTG 13067
Qy 9518 CATATCCGTTACACCATTAACGCTGATAGGTATCAACATAGCGAGGCCCGCCGACAG 9577
Db 13068 CATATCCGCTATACCATTCGTTCTTAAATTAACAATGTTGATAGCGAGCTCCTGAGG-G 13126
Qy 9578 GGCCTGCGAGGAGATGAGCATGCAAAATCATCAAGACATGGCCATTACTGCCCCACCGT 9637
Db 13127 AGCCTGTTTAAGGAGTTTATATGCGGGTTCAACACCTTTTGAACCTTGAATAACCGTCAT 13186

Qy 9638 TGCCCTTCGGGGGGCGGTGCGGTCAACCGGCTCAAGGGGTGATATCGCGCGCGCAGGCGCG 9697
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Qy 9698 ATGGTGGGGGCAACCTGAGTATCCCTTGGCGGTAGCCCGGTGCGGGTTACGCCGCCA 9757
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Qy 9758 CTGGGGCACTTAATTTATCACAGCGGTGCGGGAACGCCCTTTGGGCATTTGGCTGGGGTA 9817
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Qy 9818 TCGCGGTGCTGTGTCAGCGTCTGTAACCGCAACGGGACCACTTACCTACGATGATAGT 9877
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Qy 9878 ATGAATTTACCGGTTCGGGACGGTGAGGTGCTGGTCCGGCACTCACCGGTGCTGGCACCC 9937
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Qy 9938 AAGAAGCAGCGCAGCCACCTCACTACTGGGGATAAACCCAGCGGGAAGCTTCAACGTTTC 9997
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Qy 9998 AGGTTTACCGTTTACGTAACGAGGGTGTCTCAGCGCTTGTAGCGTTGGCTGCCCGCG 10057
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Qy 10058 A-----CGAGACAGAAACGGAAATTTTGGGTATATACCCCTGACGGACAGTGGCTC 10111
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Qy 10232 CGGAAGATGATGACGGTTGTGAAGAGGGGAGCGGACCGGCAACCGGCGCGGCGCC 10291
Db 13786 CAGAAGACGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 13845
Qy 10292 AACGTTATCGGTGCGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 10351
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Qy 10352 TGGTGTCGACACCAATCAATGGATA-----GCTGGCTGTTTATCTCGGTGTTGATTTAGTG 10408
Db 13905 TAAATCAGGTATCCCTGTTGATATGATGATGATGATGATGATGATGATGATGATGATGATG 13964
Qy 10409 AGCTAGCTGCTGTC-----TGCTGAAGCGCGCGCTGGC 10444
Db 13965 AGCGCTTATCTTCGCTGAACTCCGTAACCGAATCAATGTGTGATGATGATGATGATGATGATG 14024
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Qy 10505 GTTTTAACTCGGACTCGCGCTGTCGCTGAGGTTTGTGATGTTCCATTAACCTAGGTG 10564
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Qy 10565 TTCTGGGGGAGTTCGGGAGCAATGATGCGCAGCAATGATTTCTGCTGCTGTTGCTG 10624
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Qy 10625 ACTACGGGAAGTCTTCACTAGTCTGCTGAGAACGTCACCAAGTGGCTTATGAGT 10684
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Qy 10685 CGGACGGACGCTCTGTGCTTGGCGCACTGGCATTTGGGTGSCAAACCTTTTACCCCGC 10744

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Db 14325 GCGTGAATCTGAATCGCAGTCCATCGCGAGTTAGAAAAAATGAACACGTTGCGAGCAT 14384
Qy 10805 ATCAGCTGTGAGACCTTAAACGGGAGAGGTGTTGGGTATC-CTGTATCAGGACA---GC 10860
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Qy 10861 GGTGCTCTGTGTGTTACCGTGAACCGGTACGCCA---GTCCGGGATGATCCGGATGCTGTG 10917
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Qy 10918 ACCTGGGGGCGCTGCGGCGCTGCGGCAATGCCCGCTTTTGGCATTAACAGCGGATCCTG 10977
Db 14505 ACCTATGAGGAGCGAAACCACTGCCACATATTTCCGGCACAACAGGAAAGCGGATGTTG 14564
Qy 10978 GCGGATCTTAATGGGATGTTGCGCTGGAGTGGTCTGTTACCGCCCCCGGTGTTGGCGGG 11037
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Qy 11038 ATGTATGATCGCACCCCGCGCGCTGTTGCTGATTTCAACCCCTGTCAGCTTCCCC 11097
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Qy 11158 ATGCTCTTATCGGCGCGCGCTGCTGCTCTATTTCCGGCAAAACGATGTTGGAAT 11217
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Qy 11278 CGTACCGCTCGTGGCTTCACTGATATGGTGGCAGTGGACAGCAGATTTTGAACGAGGT 11337
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Qy 11398 AATATTTCCCGGTTTATGACGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11457
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Qy 11458 GATACCGAGTTCGGGTACCA-CGGACCTGATTTATGCGATGAGTGAACGCTGTTAGTAT 11516
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Qy 11577 TGTGCGCTATGATCGCACCTCGCATGCTGCAAGTGGCGGATATCCAGGGGCTGGGGTGGC 11636
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Qy 11637 TAGCCTGTTACTGACCGGTCCCGCATGTGCGCTCATCTACTGCGGTGTGCGATTTATGCGC 11696
Db 15224 CAGCATTTATTTGACGATCCCCCATATGAAGGTGACGACTGGCGATTTGATATGACCAT 15283
Qy 11697 AGCAAAACCTGTTGTTGATGCGCATGAACAAATATGGGGCCCGGCGCATGCACTGCA 11756
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Qy 11757 CTATCCGAGTTCGTCAGTTCCTGGCTGGATGAGAAAGCGGAGGCACTTGGCGCAGCAG 11816

15344 Db TTATCGCAGCTCTGCCAGTTCTGGCTGGATGAGAAATACAGGCTTCTGAATCCGGAT 15403
11817 QY TTCCCTGCTGCTACTGTCATTTACATTTGATACCTGTGTGGCGTTTGGTGTGAGGA 11876
15404 Db GACGGTGTGAGTACTTACCGTTCCGGTGCATGTGTGTGGCGACGGAAGTGTGGA 15463
11877 QY TGAGATCACCGGTAAACCGTCTGTGTGACGACGTGCTTTATCGCCACGGGTCTGGACCG 11936
15464 Db TGAATTTCCGGTAAACCGATGACGACGCTTATCAATTAATGATTTGATTTACCGGC 15523
11937 QY GCAGGACCGAGTTTCCGGGGTTTGGTTTGTGTGATCAGGATACCGATACCTTGGC 11996
15524 Db TCTGGAACGGAGTTTCTGTGTTTGGGGGTGACGCAAACTGATATTGATTTACCGGC 15583
11997 QY AAG-----CCAGGTACGGCGAGGAACCTGAGTATGCTTCTGTGAGCGGGAACCTGTA 12050
15584 Db GAGTGGACACAGGGGACATCTGAACCCACCGCACCTTCCGCGACGCTTAATTTGTA 15643
12051 QY TGCCACCGGGTACCGGAGTACGAGCGTCTGCCGGAGACGTAATTTGGCAAAACGATGC 12110
15644 Db CGGACTGGGCTACGGGAGTCTGATTTCTTCTGCCACGGAATATTTGGCAGGGGATCA 15703
12111 QY CGCGCTTTTCCGATTTCCGACCGCTTTTAC-----TGTCGGTTTCAGGAGGATGA 12164
15704 Db ACAGGCAATTTCCCAATTTTACCCACGCTTTACCGGTTATGACGAAAAATCCGGTGTGA 15763
12165 QY GCAGACATATCTCCGGACGACGACGATCTGTGTCAGCGAGCCCTGAAAGGAT 12224
15764 Db TATGACGGTCAACCGGACGCAACGAGGAATATCTGTTTACATCGAGCCCTTAAAGGACA 15823
12225 QY CCGTCTGCGAGTGAATATACGGTCCGATGCGAGCGCGCGGATATCTCTTACAG 12284
15824 Db ACGTTTACGAGTGAAGTGTATGGGATGATGATCTATCTGCGCGGTACGCTTATTC 15883
12285 QY CGTCACTGAGTCTCGCCCGAGTACGGCTAGTTGAAGCGAATGGA---GACTACCCGGT 12341
15884 Db AGTGGATGAATCCGACACCAAGTACGTTTGTGTACCGGTGATGATCGGACGTGCTGC 15943
12342 QY GTGTGGCGATGGGCGGGAAGCGTACGTACGTTTATGACCGGTACCAATGA-TC 12400
15944 Db GGTACTGGTTTCCGTGGCGGAATCCCGCCAAATACCGATATGAAGGGGTGTTACCGATT 16003
12401 QY CTAATGCCAACAGCAGCGGTACTCTCAGTGAATGAATACGGTTTCCCACTCGCTCAGG 12460
16004 Db CAGAGTGCACCAAAAGATTGTCTTAAATATGATGCTGATGATTTCCGACGACAAATC 16063
12461 QY TCAGTGTCAATATFCCAAGCGCTCCGTGCGGACAAATCCATATCCGGGTCTTAC 12520
16064 Db TTGAGATTGCTTATTCGAGACGTCCAAGCTGAGTTCTCGCCTTATCCGATACCTGC 16123
12521 QY CGGAGCGCTGTTCCGCAACAGTTATGACGACGACGACGATATTAAGCTGGGGTTC 12580
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12581 QY AACAGACAGTGCACATCACTGTTTCACTGTCTGAGGGGCAATGTTGTTGGGGTTCG 12640
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12641 QY CGAGGCGTTCGCGGACGATGATATACGTTCTCTCGGACAAAGTCCCGGAAGGGGTC 12700
16241 Db TGGATACCTCAACGAGTACGAGTATTTATCAAGCCGATAAAGTCCCGGACGGTGGAT 16300
12701 QY TGAGCTGGAAACCTGTTGGCGCCGAAAGCTGTCTCGGATGATGAGTCCGTTACGC 12760
16301 Db TTTCCCTTGAATGGTTTCTGCT-----CACAGTGCAGGACGATTTGTTGCTGCTG 16351
12761 QY TGGCGGTGACGACGAGTCTGGTATCTGGATTCACAGACGTTGCGCCGCTCGCTGCTC 12820
16352 Db ATGCGGACGGATATCTGGACATCAGCGTGTAGCATATACCGGTCCAGAGACCAAC 16411
12821 QY CGGCACTCCCGCCCAAGTATGCTTTTATCGAAACCGCGCTGCTGATGAGGATGATGTA 12880
16412 Db CCGCTATTCTCGCTGGTGGCATACTTGAACCGGACGAGTTTGTATGACGATCGTTGG 16471

12881 QY GTTCACTGCTCTCTACATTTGTGA-----TGAAATCTCGACGAGCCGTTACCG 12932
16472 Db CGGCTTTTGGAGAGTGTGATGAGAGAGCTGACAAAAAGCTGATGATGCGGGT 16531
12933 QY GCAATCCGATACCTTTTCCCTCGAGGAGGAGGAGCAGAAAGGCAATTTGTGACCCAGTG 12992
16532 Db GGAATACGCAAAAGTGCCTTCAGTGAAAGA---CAGATTTCCATGCTTGGGTGGACA 16589
12993 QY TCAGGATATATGTTACTATGCGCGCGCAGAGCAATTTCTGGGTACCGCTATCTCTCGGA 13052
16590 Db AAAGAAATTTACAGAAATGCGCGTGCACAGCGAATTTCTATCGCCATTTGGTCAACGGGA 16649
13053 QY CAGTATGTTACCGCGCCAGTTTACCGTGCAGCGTACCGGTACGACTCGCTCATCAGCA 13112
16650 Db AACCAAGCTTTACAGGTCAAAACGACAGTACGTTGGGATAGCCATTACTGTGTTATCACCG 16709
13113 QY GTGGCAGGATGCGCAGGATTTGTCAACACAGCCGACTATGACTGGCGCTTCTCGACGCC 13172
16710 Db AACAGGATGCGGCTGCGCTCGGTATGCAAGCGCATACGATTATCGATTTATGTTGC 16769
13173 QY COTCCGGGTGACGGAACCCCAATGATTAATCTGAGTCCGTTCACTCTGGATGCTCTGGCCG 13232
16770 Db GGATAACACCAAGATATCAATGATAAATATCACACCGTGAAGTTGATGCTGCTGGGAC 16829
13233 QY GGTGACCACTCTCGGATTTCTGGGCGACGAGAAATGTTGTCACCGGTTACAGTGATGC 13292
16830 Db GGTAAACAGCTTCCGTTTCTGGGGACGTAACCGGTGAAACAGGATATACCCCTGC 16889
13293 QY CAGCTTGTCCGTTCCGGACGCGCAGCAGCCGCTCTGGGTTGACGGCGCCCTACCACT 13352
16890 Db G-----GAAATGAAACTGTCCCTTTATTGTCCCCACAACGCT 16928
13353 QY AGCAGATGCTGTGTATGTCACGGAAGTTGGGAGATGACGACAATGAGAAAATGCC 13412
16929 Db GGATGATGCTCTGGCATTTGAAAACCGGCATACCTGTTGAGGGCTGATGTTTATGCCCC 16988
13413 QY CCGCAGCGTGTGCTGCTGCTACCGTATGACAGTATGACAGTATGATACCGGACAGGTCG 13472
16989 Db TCTGAGTGTGATGTTTACGCGCAGCTTTCTTAATGATGGGAGCTTTATGGAGAGCTGAA 17048
13473 QY CCAACAGGTGACATTCAGTGACGTTTGGGCGTGAATGCAATCGGCAACCCGCGACGC 13532
17049 Db ACGGCTGGGATCATCACTGAAGAT----- 17073
13533 QY CGAGGCAACGCTGGCAACGAGGACGCAACGCGAATCTGTTGACGGCCAGTGACGGATT 13592
17074 Db ----- 17073
13593 QY GCGGCTCACTGTAGCAAGAAATTTCCGCTGGCGGTTCACCGGAGGGCGGAGTATGACAA 13652
17074 Db -----GGTTATCTCTGTGCTGCTTTTTCGCGCTGGCATCAAA 17114
13653 QY TAAAGTGTGCTGTTTGGGTTTATCAGCGTATTTTCTGGAGTGTGGCAATATGTCAG 13712
17115 Db TAACTGCGCTGCGCATGCCAAAGCAAGTCAATTCACAGAACCCACCCCATGTACTGAG 17174
13713 QY TGAATGAGTGCCTGCGGACGCTGTATGCGACAGCAGCTTTTACGATCCGACGCGACG 13772
17175 Db TGTGATCACCGACCGCTATGATGCGGATCCGGAACCAAC----- 17213
13773 QY GGAAATGGCAGGTTTATTCGGCAAAAGGTGAACGGCGACAGGTGCTGTATACCCCGTGT 13832
17214 Db -----ATTAAGTCAACGTTTA----- 17230
13833 QY TGTGTTGAGTGAAGCAGAAATGATACCGTTGGGTAAACGACGATCTCTGAGTGGGAAG 13892
17231 Db -----CGTTTGTGATGTTTGGGCGAAACCTTACAAACAGCC-----G 17270
13893 QY GAGGGGGGACGTTGATGAGTCCGTCGCCCTGACAGGCGCTGCCCTGATGAGGACAAAG 13952
17271 Db TAGCCATGAAAGTGGTGAAGCTCGGTACCTGATGAGTATGAGGCAATGTTGGCTGAAA 17330

QY	13953	ATGAAATACACTATCAGGTTGGCGGTTGTGCTGACAGGTTATGGTTTGGGGGCTT	14012	Db	18171	AAAAAGCAATAATTTTGGCGCCAGTGGCTCATTTATGATCCACCGGAATGAATC	18230
Db	17331	ATCAAGCGCC-----	17341	QY	15066	AGACGACAGCATCGCCCTGAGCGGTGCGCTCGCGTACGCGGCGAGTGTCTGCCCG	15125
QY	14013	TCCCATTTGGGTTACACCGTTCGTTACCACGCGSCAGATACAAATGGCAACACGCCAG	14072	Db	18231	AAACCAACAGCATATTTGTTAAACAGCATACCTTTGCTCCATCACACAGCAATATAGTGAAG	18290
Db	17342	-----CCTGAAACGGGGAATTAACAATTTCCGTTGGGCAATTTCCCGACG--T	17389	QY	15126	ACGCGCGGGGGCCAACTGGATGGGTGAGGATGCCTCGGCTCGGAATGACTCTGTGGATG	15185
QY	14073	GCCGAACAGAAAGGCGGATGCGTTGGCCCTCTCTGCGCAGCAAAACCCGGGAAAGAAAG	14132	Db	18291	ATGACAGCAAGCCGATTGGACCGGTATGGAATTTGGCTGGAATAACGCGCTGCGCG	18350
Db	17390	ACAGATATTAACGGGAAAGGCAAGCCCTCGCTTACGTTTCAA-----	17435	QY	15186	GGGAGAGTTTCTTACCCAGAACCCACGCTGATGCGACCGGCGCGTCTCTGAGCATACACG	15245
QY	14133	TGGGAGCAGCAACGACAGATGACATGAACAAGTGGCTATATATGCTGAAGAAAGACTG	14192	Db	18351	CGAAAGCTTCACTTCTGTGACGACACCGATGCTACCGGACCGTATTAAACGAGTACAG	18410
Db	17436	-----ACCGTATTCCTGAAATTAATTTGGGCAACTATGTCAAGTTGACCAAAAAAT	17485	QY	15246	ATGCAAAAGGTAATCTGACGCGTGTGGCATATGATGTGCGGTGCTATCGGCGAGTT	15305
QY	14193	GCTGCTGCGGTGACGCTGCGCTGATGCTCAGCGCACTGGTCAGCGCTTCGACACACC	14252	Db	18411	ATGCTCCGGAACAAGCAACGATATCGCTATGATGTGCGCGTCTGCTTCAAGCGAGTT	18470
Db	17486	GCCCGGAGGATATGTATGCGGATACCCATTAATCTATGATCCGTTGGGGCGTGAATATCAG	17545	QY	15306	GGTTGACGCTGAAGGACGCGCACGAGCAGGTATCGTGGGCTCCCTGACGTACTCGGCGG	15365
QY	14253	GTTACCAACCTCCAGCGGCAACTTGGCCAGTCTGTAACCGCGCGCTTTCCGCGACTACC	14312	Db	18471	GGTTGCGCTGAAGGGGAACAAGAACAGTTATCGTGAATCCCTGACCTATTCGGCTG	18530
Db	17546	GTTATCACCGCAAGCGGGTGGCTGATCCTTATCACTCCCTGCT-----	17594	QY	15366	CCGGGAAAAAGTTGCTGGAAGAACACGCGCAACGCGCTGTGTAACCTCGTATATTTACGAGC	15425
QY	14313	GCTATCGGTACAGAGACCTCGGAGGCCAACCGCGCGTTTTGTTGTCGCGAACTGTTCGCG	14372	Db	18531	CCAGCCAGAAGCTTACCGGAGGAACATGTTAAACGGGATAGTACTACATATACCTATGAAC	18590
Db	17595	-----	17594	QY	15426	CGGAACACAGCGCTGACGGGGATTAACACGGAAGTCCGCTCGGCGCAGTTGCCGGAG	15485
QY	14373	CGCGCTACAGAGAGCGGAGAGCTGGCAGCGTATGCTACAGGACCAGATGAATGG	14432	Db	18591	CCGAGACGCAACAGAGTTATTGGCATAAACAGAACGTCCTTCCGCTCATGCCGCTGGGG	18650
Db	17595	-----TGTGGTGAATGAAGTTGAATAATGACATCCCGG-----	17627	QY	15486	CAAAAGTGTGACGAGACCTGCGCTATACGTATGACCCGGTAGGCAACGTTACTCAGCGTCA	15545
QY	14433	CAGCGCTGCGGGCGCGCTATCAGCGGCTACGCAAGCAGAAATAAAGCGATTTA	14492	Db	18651	AGAAATTTTACAAACCTTGGCTTATGAATATGATCTCTGCGAAATGTCTGAAATCAA	18710
Db	17628	--TGAATGACAGATAAAGCTCAGTGATGCTGTTACTGAAACAGATCACTCCATTTA	17685	QY	15546	ATAACGATCGGAAGAGACCCGCTTCTGCGCTAACACAGAAAGTGGTACCGGAGAAATACGT	15605
QY	14493	GCGGTTAAGAAAGTGACGCGTGTTCGCGATTAATTAATTAACAGGAGATCAATGAGCA	14552	Db	18711	CTAATGATGCTGAATTAACCCGCTTTTGGCGCAACAGAAAAATTTGTACCGAAAAATCTT	18770
Db	17686	GGAATGAA-----TCATGAAGA	17702	QY	15606	ACATCTACGACAGCTGTACCAAGCTGGTCAGCGCCACAGGGCGTGAGATGGCAATGCCG	15665
QY	14553	CATCCTGTTTCAGTAGCACCCGCTCGGTGCGGTGCTCGAACACCGGCGCTGTGGTGC	14612	Db	18771	ACACCTATGACAGCTGTACCAAGCTGTTTCCGCTACTCGGCGTGAATGGCGAAATATTG	18830
Db	17703	ATTTCGTTTCAGCAATAACCCCATCCGTCACCGTACTGGACAAACCGTGTGCAACAGTAC	17762	QY	15666	GCCAGCAGGCAACGACTTACCATCCGCTACAGCCCGCTTCTCTACAGACAGCTCTGCGCT	15725
QY	14613	GGGAGCTGCAAGTACTACCGCCATCCGATACACCGGAGGAGACGCGAGCTATCACCT	14672	Db	18831	GGCGACAAAAAACAGTTAC-----CCATCCCGCTCTGATTTGATTAACAATCTT	18881
Db	17763	GCGAATAGCTGTTATCGGCAACCCCGATACACCTCAGGTAAACGATGAACGATCACCG	17822	QY	15726	ACACCAATTAACGCGCACCTACCGTTATGACCGTGTGGCGAACCTTGACGAGATCGGCC	15785
QY	14673	GCCATCAGCAGATGACGCGGAGCTTTGTCAAAAGCGCCGACCCGCGGTTACAGCGG	14732	Db	18882	ATACGAATTAATCTCGCACTTACGACTATGATCGTGGGGAATCTGACCAAGATCGCATA	18941
Db	17823	GTTATCAATATGATGCTCAAGGATCTCTGACTCAGAGTATTTGATCCGCGATTTTATGAAC	17882	QY	15786	ACAGTCCCTCGCCAGCAACATTAATTAACGACAGATACAGGTTAGTACCGGAGCA	15845
QY	14733	CCGCTCTGACA-----AATTCAGTACTCTGAATAGCC	14765	Db	18942	A-----TTCAGATACCGGTAATAACTATACAAACGAAACATGACCGTTTCAGATCAGACGA	18997
Db	17883	GCCAGCAGACAGCGGAGTGACAAGAACGCCATTAACCCCAATCTATTCTCTGTCTATCAC	17942	QY	15846	ATAGGCGGTACTGACACGTTGGCGGAAGTGCCTGACAGATGTTGATATGCTGTCTCAGTG	15905
QY	14766	TGACCGGACAGTACTGACAGCGTACAGCCGATGCGGTAGCTCGCTGGAATCAGCG	14825	Db	18998	ACGGGCTGTACTGGAAGAGCTGGCGCAAGATCCCACTCAGGTGGATATGTTGTTTACCCC	19057
Db	17943	TCAGTAAGAAGGCAATTCGTAAGCAAGTGTGATGCCGGAACCGGTGTCGCGCTGTGATG	18002	QY	15906	CAGGAGGTACCAAGACACCTGCGACCGGGGCAAGCACTGTGTGTGGAGCCCACTCGTGAG	15965
QY	14826	ATGCCGCGGGCGGGCTTTCTGGCGGTACACCGGGGCTGGGACGGAAGCGCGGTCAACC	14885	Db	19058	CCGGCGGCGCATCAGACCCCGCTTGTTCGCGGTGAGGATCTTTTCTGACACCCCGGTGACG	19117
Db	18003	ATGTTCCGCGGCTCCGTTTATGCTGTGACGCCAATGG-----CGTTAGCC	18050	QY	15966	AACTGAAAAAGGTGACACCGGTGCTGCTGATGGGGGGGCGGACGACAGCGGAAAGCTATC	16025
QY	14886	GCACTGGCAATATGAAGAGATACCTTCCGGGCGCGCCGCTGAGCATCACCGAGAGG	14945	Db	19118	AAATGCAACAAGTGAATTTGGTCAATAGGGAATAACGACGCGCTGATCAGGAATTTCTACC	19177
Db	18051	GAACGTTTTCAGTATGAAGTGAATAACCTTCCGGGACGATTTGCTAAAGATTTACCGAGCAG	18110	QY	16026	GGTATGATCGGCGAGCTGAGCGTATTATCAAAACCGGCAACCGGCAAACTGGCAACACG	16085
QY	14946	TTACCGGTGAAGCGCCCAATTAATACGAAACGCTTCGTGACGTTGCGCAATACGATGCCG	15005	Db	19178	GTTATGATCGACAGCTGACGCGTCAATTAAGACTCATATTTCAGAAAGACGAGTAAACAGTG	19237
Db	18111	TAAAGAGAGAACCGCTGTATCAGCGAGGATTTGATTTGGTCAGGAATTAACCGCGCAG	18170	QY	16086	TTACAGACAGCGGGGTAGTGTACTTCCCGGGGCTGGAGTTTACGTATCATGCGCAAAATGGCG	16145
QY	15006	AGAAGATTCCTCAATCTGGCTGGCGAGTGTGTGCTCAGTCAATTAACGATACCGCGGACTGGTGC	15065				

Db 19238 AGCAATACAGCGAACAATTATATTTGCCAGAGCTGGATGCGCGCACGACATATAGCGGCA 19297
Qy 16146 TGACGGAAAAGAAAGCTGCAGGTTATTACGGTGGCGAGGCTGGCGGGGCAAGTGC 16205
Db 19298 ATACATTAAGAAGTATTTTGCAGGTCATCACTGTCGGTGAAGCGGTTCAGGCAAGAAGTGC 19357
Qy 16206 GCGTATTGCACTGGGAGATCGGCAAGCGGATGACCTCGATGAGGACTCGGTGCGTTACA 16265
Db 19358 GGGTGTGCAATTGGGAAACAGGCAACCGCGCGATATCAGCAATGATCAGTCTGCGTACA 19417
Qy 16266 GTTACGATAACCTGGTGGGAGCAGCGAGCTGGAGCT-GGACAGAGAGGGTTACCTTATC 16324
Db 19418 GTTATGGCAACCTGATTGGCAGTAGCGGGCTGGAAATTGGGACAGTGAAGCGGAGATCAT 19477
Qy 16325 AGTGAGGAGGTTCTACCGGTATGGGGAACGGCTGTTCTGACGGCGGGAAGTGAAGTT 16384
Db 19478 AGTCAGGAAGAATATTACCCCTATGGGGGAACCGCGG-TGTGGGCAACCGGAAATCAGTCA 19536
Qy 16385 GAGGCTGACTACAAAATCTATCCGATATCTCAGGCAAGGAGCGTCAAGCGGAGCGGGCTGGAT 16444
Db 19537 GAAGCTGATTACACAGCGCGGCTTATTCTGGCAAGAGCGGGATGCAACAGGGTTGTAT 19596
Qy 16445 TATTACGGTTATCCGTTATTACACCGCATGGCAGGCGCTGGCTCTCCACGGACCGGCA 16504
Db 19597 TACTACGGCTATCGTTATTATCAATCGTGACAGGCGGATGGTTGAGTGTAGATCCTGCC 19656
Qy 16505 GGCACGGTGGACGGGCTGAACCTGTTCCGATGTCGGGAATATCCCGTCAGCGTGT 16564
Db 19657 GGTGAGCGCGATGGTCTCAATTTGTTCCGAATGTGCGGAATTAACCCCATCGTTTTTCT 19716
Qy 16565 GACAGCAACGGGGGATC 16582
Db 19717 GATCTGATGGTCTTTC 19734

RESULT 4

US-10-753-901-6
; Sequence 6, Application US/10753901
; Publication No. US20040194164A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Schafer, Barry
; APPLICANT: Bevan, Scott
; APPLICANT: Young, Scott
; APPLICANT: Guo, Lining
; TITLE OF INVENTION: Xenorhabdus TC Proteins and Genes for Pest Control
; FILE REFERENCE: DAS-105X
; CURRENT APPLICATION NUMBER: US/10/753,901
; PRIOR FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,717
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 39005
; TYPE: DNA
; ORGANISM: Xenorhabdus nematophilus
US-10-753-901-6

Query Match 7.2%; Score 1365; DB 18; Length 39005;
Best Local Similarity 52.4%; Pred. No. 0;
Matches 3947; Conservative 0; Mismatches 3070; Indels 510; Gaps 23;
Qy 2511 TGACGGATTATTCTCGCGTTCGTTTCCGAGGTCAAAAATCACTGGCGCAGCGCTGT 2570
Db 10773 TGACAAACATTCGTTTATGTCCTTCAGCGAATTCGTATAGGACAAGTGGNACTCTGA 10832
Qy 2571 CATGGGAGAGGTCGTATCTGTACAGTCAGCGCAGCAGCAAGAAAGAAACCGGC 2630
Db 10833 CGTGGCGAAGAACAGACTTTTATATCAACAGGCTCATCAGGAATCAAAACAGAAATAAAC 10892

Qy 2631 TCACGAATCCCGTATTCTGGCGCGGCGAATCCCTACTAGTGTGAATGCGGTCGCTCG 2690
Db 10893 TTGAAGAACTGGCGATTTTGTCCCGTGTAAATCCCACTGGCTAATACCACTAACTTA 10952
Qy 2691 GAATACGGCAGCAGCGGCTGCGCAGCTATGATGACTGGTGTGGCTCCCGCGCAGAC 2750
Db 10953 ATATTACCGCTCAACCTTAACAATAGTTACAACAGTTGGTTTATGGCGGTGCCACC 11012
Qy 2751 GTTTCGCCCGCCCGCTCGGTGGCTCCATGTTCTACCGCGGCGTATCTGACGAGC 2810
Db 11013 GTTGTGTAACACCGGATCAATGCTCTCCATATTTTACCAGCGGCTATTTTAAACAGAA 11072
Qy 2811 TCTACCGTCAGGCGAAGACCTGCGATCCGACACCTCGCTGTTCCGCTGGACATCCGC 2870
Db 11073 TATATCGGGAAGCGAAGATTTTCATCTGCAATTTCTCAATATCACCTGAATAAACGAC 11132
Qy 2871 GTCCGACCTCGCGCGCTGGCGCTTAGCCAGAATAATGACGACAGAGCTCTCCACCG 2930
Db 11133 GCGCGGACATTCCTTCACTGGCAGCTGACACAGAAATAATGATGAGAGAAATTTCCACAT 11192
Qy 2931 TGAGCTGTCCAAATGAGCTACTGTATCGCGGTATCGGGGACGCGAAGGGCTTGACGAG 2990
Db 11193 TATCCTTATCTAATGAATTTACTGCTGCATAATATTTCAGACGTTAGAGAAAACCTGACTATA 11252
Qy 2991 ACAGCGTCAGGAGCTGCTCGCGGGTATCGCTGACCGCGCTGACCCCTATCACTGG 3050
Db 11253 ACGGTGTATGAATAATGTTGTCCATTACCGGCAACCGGCAATGACACCTATCATCTCG 11312
Qy 3051 CGTAGAGCGCGCGCCCAAGCAATTTCTGGTCAGGACCGGACGCTGATGGGGTTTCAGCC 3110
Db 11313 CGTATGAGTCAGCGCTCAGGCAATTTTATGCAAGATAAAACCTCACCAGATTAGCC 11372
Qy 3111 GTAAATCCGGATGTGGCGAGCTTATGAGCCCTGCTCCATGCTGGCAATTTGAAGCGATA 3170
Db 11373 GTAAATACAGACGTAGCGGAATTAATGGACCCCAACATCGCTACTGGCTATTAAGACTGATA 11432
Qy 3171 TTTTACCGGAGCTGTATCAGTACTGCGCGAAGAAATACGACAGACAGTACGAGAC 3230
Db 11433 TATCGCTCAATGTATCAATCCTTTGTAGAAGAAATACACCGGAAAATCAACAGAAAC 11492
Qy 3231 TCTGGAGTAAGAAATTTGGTGATATGCCCTCCCTCACTGTATCTTATGATGCACTTG 3290
Db 11493 TGATGAAGAAAATTTTCGTCAGATGATGATCTGATTTTAAAGAGTTATGCTCTTTGG 11552
Qy 3291 CAACATTTTATGATCTTGATTAAGATGAGCTAACTCGTTGTTATGTCATTAAGCGTGGACT 3350
Db 11553 CTGCTACTACGATTTGCTTATGATGAACCTCAGTTTATTTGTCAATCTCTCTCGGTA 11612
Qy 3351 TTTTCAAAATCCAAACATGAATCACTACATTAATAGTCAATTAAGTGTGTAACCTCTGAATG 3410
Db 11613 AGAAAAATACAAATCAACAGTATAAGATGAGCAACTGATAACATTTGGTCAATGACGGA 11672
Qy 3411 AAAGCAGCTGTTTAAATACTATACATCAATTTTAAAGAACGCTAGCGGAGACTCACAGC 3470
Db 11673 ATGATAGCGCAACGCGCAAGATTGATTAGCGAACCCGCAAGATTTCTACGATTACATT 11732
Qy 3471 AGATTAAACCTGAGCTTATACCTTATGGGATGGAACATATCTTTATAATTTTCAGCGTG 3530
Db 11733 TAAACTATGCAAGACTTAATTCCAATCAAGAAAATGAATACAAATATATATTTTCAGTGTAA 11792
Qy 3531 TGTCAACGATATCAGAGGATAGTTTCAAACTAGGTCGTTAGGTTCTTCAACAGTAGCAATC 3590
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Qy 3591 TTTTACTCGGGATTATCAGCTTCAAAAAGGGGTTTCGCTATAGCATTTCTGTGAAATAG 3650
Db 11853 ACCAAGATAAAAATTTGCTCCCAATTTGCTAATACCACTTACAGTATTCCTCAATTAATGA 11912
Qy 3651 ATGAAGGAAGTAAATGATGGATCACAATAGGATTTGATAGGAA-----AG 3698
Db 11913 CGACAGAGCAATCAACCAACGGTATAACATCCGCTTATGGCGAGTTAAACCAATCCGT 11972

Qy	3699	GGGGGGGATATTACTCAACAGTAAACTTCTACTCTGATTTGAATGATCTTCGCGATATCA	3758	Db	13053	AGAAATTCGAATCAGAAACCCACAGCACTGCAACATGATCTCCCACTTTTCAAGCGCTGA	13112
Db	11973	CGGATGCTATCAATGCCAATGATCACTTTAAATGATGAGATTCCCGGTGATATATTC	12032	Qy	4830	CGGTTTTCATGCGCTGTTAAACCGCAGCGCAGCCATGCGGGGAGGTCTTGACCCGAC	4889
Qy	3759	TTCTTAAATTAATAAGTTATCGCTATACAGGCGCAGCGGATGACCAACGCGAAA	3818	Db	13113	CCGCTTCCATGCTGTGATCATGCTGTGTAAGCTACGCGACAGAAATCTTAAACAGAT	13172
Db	12033	TGTTAAAGCTGAATTAAGCGATTCTGTTGTATAAAGCCACAGGATATCTCCAGAGATA	12092	Qy	4890	TTGAGACCGGAGAACTGTCTGAGCCCTGCTGCGCCGGGCTGTCA CAGAATGAGCAGG	4949
Qy	3819	TATATCAATCAACCAATATTCTTAATAACCGTCTCACCATTTGACATGCGGTCTCTGAGTA	3878	Db	13173	TGAACTAGGAGCGCTGACTGCCGAACTTGGCGGTGGCTTAAATTTGATGCTCAGG	13232
Db	12093	TCGCGAAGTAATAGAAAGTATTTATGATGACTTAACTTGCAGCAATGTTGGGTA	12152	Qy	4950	ATGTGACCGCGCTTGGCCGAGGTGAGGGGGCGCGGTGAACAGGACAA CAGCGTGTTC	5009
Qy	3879	AAATCTTCCTGCTGCTGCTGATGAGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGT	3938	Db	13233	TTGTGACACAAGCAATTTGCAACAGCGGTTTGGGAGTGAATACC-----TTTA	13280
Db	12153	AGCTGTTTATGTTCAATATATATGAGCACTATAATATTTAGCGTCAGCGATGCGCTGG	12212	Qy	5010	CTCTCTGGGAAGAGGTGGACCGCTGAGCAGTGGCTGGACATGAGTGAGAGCCCTGTCCA	5069
Qy	3939	TATGTGCAAGCAACCATCAGTACAGCGGTTTCAGCGGCAACCGGCTGTTCACCA	3998	Db	13281	CCAACTGGAGAACTATAGATGTCTCACTGCAATGGCTGGATGTGCTGTCTACATTTGGGTA	13340
Db	12213	TATGTGTCTTCAAGATATGAGCAATATTTCCACTAAACAAACCCAGTCAATTTTACAA	12272	Qy	5070	TTACGCCATCCGCTTGGCTAGCTGATTTGCCCTCTGAAGTACATCAATGTGTCCGATGACA	5129
Qy	3999	CGCTGTTCAACACCCCGCTGAACCGCCAGCTGTTTCTGCAAGATGATACCCCTCG	4058	Db	13341	TTACCCCGGATGTTGCTGCACTCATAAATTTAAATATATCGGTGAACAGAAACCC	13400
Db	12273	TACTGTTCAATACACCGCTATAATATGCGCAAGATTTTCTGCTGATATACCAACTGG	12332	Qy	5130	GTGCAACGTTGTACAGCAGTGGCAGGTGTATCCGCTCTGCTGACGGCCGGCTGAAAA	5189
Qy	4059	ACTTACGCTCTGAAGCACCGGAGGATGCTTTCCGCTCTAGCGTACTGAAACGGCATTTA	4118	Db	13401	CGATGCCAACTTTTGTATGATTTGCAAGCCCGCAGTACTTTTGTGACGGGACTGAACA	13460
Db	12333	ATTTAAACCCCGGTGAATCAAAAACCAATTTTATTTGGGAATAATGAACGGCTTTCA	12392	Qy	5190	GCAGCCAGAGCTCGGCGCTGACAGTATCTGAGGAGGGGACGAGCGCCCTTTGTG	5249
Qy	4119	ACATCAGGCTCGGGCTTTCACGCTCTGGCAGTTGGCAGCGGTGACAGCGCTG	4178	Db	13461	GTCAACAATCCGACCGCTTCAGGCATGGCTGATGAAGCCACGACAGCGGCGCAGTG	13520
Db	12393	GAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	12452	Qy	5250	CGTATTATCTGCGTAACTCTGCGACCGCAACATGATGATCCGCGCGCATGACTCTTCCGGT	5309
Qy	4179	GGTTAGTCTGCTGCTGACAAATATCGCGCACTTACCGAGTGAAACTCTCTGCTGACA	4238	Db	13521	CTTACTACATAAAATAGTGCACTCAACAGATTAAAGACCGGATGATGTTGTACAGCT	13580
Db	12453	AAATTATGTTCCATCGAAGACCTGCTCTGCTTTATCGGTTGCTGCTGCGCAGACA	12512	Qy	5310	ATCTGCTGTGGAATAATCAGGTGTGACCAAGTGAAGTAAAAACCCCGCATTTGCGGAGCCA	5369
Qy	4239	TCCACGACTTCCGCTGCTGAGTGTCAATGTTGCTGCTCGCTCTCCCTTTTCAGCGGG	4298	Db	13581	ATCTGCTGATTGATACCAAGTTTCTGCCCAAGTGAAGTAAAAACCCCGGTGTGCAAGCCA	13640
Db	12513	TTCAATCTGACAGTGAATGAATTAATCCATGTTGTTGCGGTTTCTCCCTATGTGAACA	12572	Qy	5370	TCCCGGCGCATACGCTGTATATCAACCGGCGCTTAAACGGAATGAGTACTCAGCGCCATGG	5429
Qy	4299	TGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4349	Db	13641	TTCCAGCAGCTTCACTGTTTATGTTCAACCGGCGCTGTAATGTTGAAGGAAAGTATCAA	13700
Db	12573	CGAAATTTGGCTTTTCTGATACAGCATTAACGCAATTAACAGCTTTCTGTTCCAAAT	12632	Qy	5430	CAGAGGTGAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5489
Qy	4350	CCACCACTGCTCAGCGAGCGGCTGAGCGTTCAGCGATGCTGCTGCTGCTGCTGCTGCTGCT	4409	Db	13701	AGCAGTGAATAAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	13760
Db	12633	GCACCGAGTGGCTGACAAACAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	12692	Qy	5490	CCTGGGCGGCTGCTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5549
Qy	4410	CGCAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4469	Db	13761	CCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	13820
Db	12693	ATATTACAGCAGCTGCTTACGCGGATATTGAAACCTTATCAACGACACTAAGTAATG	12752	Qy	5550	GTATCGGCGAGACCGGCGATGAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5609
Qy	4470	GACTGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4529	Db	13821	GTATTGGTCAGACAGGTATGATGAACCACTGTTTACAGCAACTTTCCAAAGTCAGTTAA	13880
Db	12753	GATTATCAACACTTCTCAGCGTATGACCAACTGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCT	12812	Qy	5610	ACCGGATACCGGTGAGGATGCTTTTAAACCTTATCTGACCACTGTTTGAAGCAGATTGCCA	5669
Qy	4530	CCGCGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4589	Db	13881	ATATCGATACCGTGAAGATGAGCTTTTAAATTTATCTGACCGCATTTTGAAGATGCTGCTA	13940
Db	12813	CTGCGAGATTTCAATGATTTACGCAAGACAGCAGAACTATTTTCTGCTGCTGCTGCTGCTGCT	12872	Qy	5670	ATCTGAACACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5729
Qy	4590	AGTTGAAGCCAGAGGGGCTGACGCTGACGGAATTTTCTTTTGGTGATGAATGATCCCGCC	4649	Db	13941	ACTTGCAGGTGATTAGCGGATATCATGACAGTATCAATGTCATGAGGAGTCACTTATT	14000
Db	12873	AGATAAACCAAGGACTGACATTCGATGATTTTATGATTTTATGCGGCTAAACCGTATC	12932	Qy	5730	ATGTGGGTCCGAGATCAGATCAGACTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5789
Qy	4650	CAATGACGAGCAGCGGGCGAGATGAGCGGTTTCTGCCAAGCCCTGTGCACTGCGAC	4709	Db	14001	TAATTGGTTTATAGCCAGACAGAACCCAGAAATATATTATTTGGCGCAATGTGCTATCACC	14060
Db	12933	GCTCAGAGAAATGAACACAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	12992	Qy	5790	AAATCCAAGACTCAATGATGCTCCGCAATCTGCGACCGGATGAGCAAAAAATTAACCTGCG	5849
Qy	4710	TGATCATCCGAGCAGCGGCTTACAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4769	Db	14061	AGTGCCAGCAGCGTCAATTTGCTGCCAATGCTGCGGAGGAGTGGAAAAAATTTGAATATC	14120
Db	12993	TGATTTGCGCAATATTGGACTCAGCGAAACGAACTGACCTGTTGGTGACAAAAACCGG	13052	Qy	5850	GAATGAATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5909
Qy	4770	GACGCTTCCGACAGGATGGCAACATCTGCCCCATGACCTGCGCGGCTTCCGCGACATTA	4829				

Db 14121 CCATCAATGATGCGCAGGAAAATATCAGACCTCTATTATTACAAAGTCTCGTTTGTATTATAC 14180
Qy 5910 TCTGGGTGGAAGAGAAATCAGTCTGCTGATACGAGGCGCAGAGACGACGAAACACCCAGC 5969
Db 14181 TGTGGCTGGAAACAAAAGAGCTGAAAATGAAAGTGAAGATGGCAAGATAGATATCAGT 14240
Qy 5970 AGAGCTACAGCTGAAATCTGCTCGGCGCTACGACGGTACATCGAGTTCGCCGGTGT 6029
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Qy 6030 CGTTCGACATACCGGCAACATCGCATTTCCGG-----AAACGAGGCGCATGCAATG 6082
Db 14298 ATTTTAATGACTGATATAAATAGAAAACCTGATCAATRAAAAAGCCAGCATTTGATGT 14357
Qy 6083 ACCTGTAATCCCTGACTGAGAGCTCTATTGCGCGTTTACTCCGTACACGACGACCC- 6141
Db 14358 ATTTGTTCTTCTGATTAAGAAAAGACGTCATTTATGTTTATTTTCCATGAGAAAAAGACA 14417
Qy 6142 -----GGACTTTGATAACGCTCAGCTGATTTCTGTGGATAATGATATGACGC 6188
Db 14418 ATTAATCTTTAATAGTCTTCCTGCAAGAGAGGATGACCATTAACCTGATATGACAT 14477
Qy 6189 TAAATGTCATCTCAGATA-----TAGGGATTTTAAAGCGCTCAGTCACGAATTTA 6239
Db 14478 TATCCCATCTCACAAGAAAATGATTTAGAGCCCATTTGTTAAGAGCACATATCAGAACTTG 14537
Qy 6240 ATACGAGCACTG---AGAAATTTAATAAATGTTTTTCAGACCCCTTCGCTAATATT 6296
Db 14538 ATACGAGGACAGAAATCAAGTCAACAATCAATTTGCTACAGATTAATTTGGCGGAATATA 14597
Qy 6297 TTGTCAGTCAACAGCTTAATTTGA---TGATGTTATCACACAGCGATTTCTCACTCCTTA 6353
Db 14598 AGGAATCTATACCAACAATAAATAGCCAGTTTACCGGAATATTTTGATCTCT 14657
Qy 6354 ATTTCTAAAACACTCAAGTACTGTTTTTACTAAAGAGATTCCTCTCTTTTGAOCCAGAGC 6413
Db 14658 CGTATATATCACCAGGAAATGGTCATATTAATTAAGTTCATCTCCTTCAATGGAATTA 14717
Qy 6414 TTCCATATTACAGCAATGTTTCGTGTTTGTAGTA-----CTG 6452
Db 14718 ATTTTTCAAAAGGCAATATATATAAATGATGAGGTAAATACCTGTTATCGATGGTAGAAG 14777
Qy 6453 CTGGCATCGCACTCAATCTACCATAGAAAAATTCGTTTCAGGCGGAGATAGAAATTTGAGG 6512
Db 14778 ATGAAACGGTTATTTTATTTGATTATGATAGACATGATGAATGCTTTGGAAGAAGAAG 14837
Qy 6513 AAATTAAT-----TTTTATGAGCGCCAGGCGCGCGCGGATTTGACCG 6555
Db 14838 AAGTTTTTCATTTATGAAACTTTTGGATTTTATTTATTTCCATCGATCTTAAAAATGCCGAAT 14897
Qy 6556 ATTTGTTGGAGTGGATGTTCTTAATTCAAAAGTATACAGGTC-GGAAAAGAGCAGTTG 6614
Db 14898 ATTTTAGAGTGTAAATGTCATTAAGAACCAAGGAAAAAATTCCTAGAAAAATCAGAAATTG 14957
Qy 6615 GTCTCACTGTAAATCTTAATTCGCTCACTGGCGCTTAGTGGTT-----CTGTTGAGTTAT 6669
Db 14958 GAGTTCGTATAATTTATGATATGAAATCAAAATGATCTGAATTCAACTTGATCTAA 15017
Qy 6670 TATTGATTCATCAAAATAAATACTTCAGCGGAATTTTGTGAGATA-----AAATGATAACCGC 6726
Db 15018 TAGTATTAGATTGGAAAGATAACACAGGATATGGCATACTATATGTGAATCATTTACTA 15077
Qy 6727 TTTTAATTTAGCGGAGTACATCAAAAGTTAATTAAGTGTGCTGTTATGGCTCTCAAGATT 6786
Db 15078 ATGATGTTTCAATCAATTAATAACATGGGAATATTCGGGCAGCTGTTCTTCGGAGGATC 15137
Qy 6787 TTGGAGTGTAAAGTTCGCTCATGCGGCACCTTCAGATATATGAATTAATCGATGATCAT 6846
Db 15138 CATGTGTGATTATTTTCAATAGCACAGATATAAAATTTGCTTCATCTATGATCGAAC 15197
Qy 6847 ACTGACATCCGGGTAAATGGGACTGAAATTAATTAATCCTGGCCCTT----- 6890
Db 15198 AGATCCAAGATAAAAAATAGTTTATTTTATTAATAAATAGTCTGATATTTCTAGTGGAGT 15257

Qy 6891 -----CCGCTGAATGGTATAATGATAAGCTGAGTCTGCAATCCGGAATAAT 6937
Db 15258 TAAATGCTGAAGACCATGTTGGCATCTAAACCTTTCACAGAACTGACCCCTATGTTATATG 15317
Qy 6938 CTTTTTCAACACCAAAATCGCTGAGTTTTTA----- 6965
Db 15318 ATTTTAATCAAGTAAAGTTGATATTGAAGGCTATCATATTCTCTGGTGAGCGAGTTTA 15377
Qy 6966 -----CCGTTAATACCAAGTGAATTTGTTGAA----- 6991
Db 15378 TTATTAAAGCAACCCGACGCGGTATTAACGATATTGTTATTGAATCGCAATTCATATAA 15437
Qy 6992 ----- 6991
Db 15438 AACTAAATCCAAAGATACAAAGTATATCATCTGATATAAATGCCATCAGGCACAC 15497
Qy 6992 ----- 6991
Db 15498 AATATATGCAGATTGGCCCTTACAGAACCCGGTTAAATACTTTATTTTCCAGAAAATTAG 15557
Qy 6992 ----- 6991
Db 15558 CTGAAAAGAGCAATATTGGTATTGTAATGTTTAAAGTATGAAAACGCAAAATTTACCAG 15617
Qy 6992 -----GATGAGTTTTCAGTCGACGTTTACGTTTCACCGCTGTCGATCA----- 7032
Db 15618 AGCCGCAATTAGGTGAAGGTTTTTATGCGACATTTTAAGTTTGCCCTTCAATTAAGAGG 15677
Qy 7033 -----GAATAAAGCTGCTGCTGCGCCCGCGACGCGCATATTAACCGTCAATTC----- 7079
Db 15678 AGCATGTTGATCAACGTTGTTTAAAGATCCATATTGGGAATATTGATGCAATTTCTGCCA 15737
Qy 7080 -----GAAACATTAATAATGACACTTC 7101
Db 15738 GAAACACTTTATTACGAAGGAATGTTATCTGATATTGAAACACAGTAAACGCTTTTGTTC 15797
Qy 7102 CGTTATCGCATTTACGTPAAAATAACGTCGCGCGCAGTATATTCTGTTTCACTGCGGGTAA 7161
Db 15798 CTTATGCTAAAGGATATTAACATACGTTGAAGGTGTAGATTAGGGTTGGGTACAAAAA 15857
Qy 7162 CGATGTGGCGCTTATTTCGCTCAACACACCTCTTTGCGCCCAACTGTCGA----- 7212
Db 15858 TTATCTATGACAAATCCTGGGAATCTGCTTTCTTTTATTTTATGATGAGAGAAAAATCAAT 15917
Qy 7213 -----CCGCGGGAATACCGGGATTGACACCATTC----- 7241
Db 15918 TTATATTCAATTAATGATGCCGATCATGATTCGGGAATGACAAACAGGGGATAGTAAAAA 15977
Qy 7242 TTTTCCATGAGACCCAGAGGCTTTACCGAACCCCGCTGGAAGAGGGGAGTGTGTTT 7301
Db 15978 ATATCAAAAAATATAAGGGTTTTTATCATGCTGTTGTCATGAAAATAACACTGAACCCA 16037
Qy 7302 TGGACTTCTCCGAGAGCAATGCCCTCTATTCTTGGAGCTGTTCTATTATACAGCCGATGA 7361
Db 16038 TGGATTTCACCGCGCAATGCAATCTATTCTTGGGAATGTTCTATTATACAGCCCATGA 16097
Qy 7362 TGGTGTTCAGCGGTTTGTGAGGAACAGACACTTCCCGAAGCCACCCCTGGCTGCAGT 7421
Db 16098 TGGTATTCCAGCGCTTATTGCAAGAGCAGAAATTTTACCGAATCGACACACGCTGGCTGC 16157
Qy 7422 ATGTCTGGAACCCCGCGGACGCTGTTAAACGGGTGCTGCAGAAATTAACCTGGAATG 7481
Db 16158 ATATCTGGAACCCCGCGCGGATATTTCGTTACAGGTGAATGAGGATTTATTACTGGAACG 16217
Qy 7482 TCCGTCCGTGAGGAGGACACCGGTGGAACACTTCGCCCTGGAGTCCATTTGACCCCG 7541
Db 16218 TCGGCCAATTTGAGGAGAGATACGTCCTGGAATGCCAATCCGCTGGATTCCGTCGATCTG 16277
Qy 7542 ATGCATAGCCAGTACGACCCCATGCAATTACAAGTCCGCCACTTTATGTCGTACTCG 7601
Db 16278 ACGCCGTTCCCGACGATGATCCGACTATATAAGTGGCTACCTTTTATGAAAAATGCTGG 16337

Qy	7602	ACCTGCTGATTTGCCCGCGGTGATGCGCTACTACCGCTCTCTGAGCGGAGACACCTTTAACG	7661
Db	16338	ATTTTGTTGATTAACCGCGGAGATAGCGCTATTCGCCAGCTTGAAACGCTGATACCTTTAAACG	16399
Qy	7662	AGCCCGGATGTGGTACGTCTCAGGCGCTCGAACTTTCTGGGGCGACGAGCCCTATATTTTCCT	7721
Db	16398	AACTAAATGTGGTATGTACAGGGCGCTCACTTTATTTGGGTGATGAGCCTTATTTTTTCAT	16457
Qy	7722	TTGACCGCGACTGGTTCGGCGTTTGAACCTTGGGTGACGACAGCCAGAGGTGACGCGACGCG	7781
Db	16458	TGGATTAACGATTGGTCAGAGCCACCGCTGGAAGAAGCTGCCAGCCAAACAATGCGGCATC	16517
Qy	7782	ATTACCAGGAGGCCCTGCTGSCCGTTCGCCCGGTTCGTCGCCGCTCCGAGACACGAGCGG	7841
Db	16518	ATTATCAACATAAATGCTGCAACTCGCTCAGCGCGCTGCATTAACCCACGAAACGTACGG	16577
Qy	7842	CGAATTTCCCTGACGGCACTGTTTCTCTCCCGCAGCAGAAAGAGGTGCTCAAAAGCTACTTGGC	7901
Db	16578	CAAAATTCGTTAAACCGGATTTGTTCTCTCCCTCAAAATTAATAAAATCTGCAAGTTACTTGGC	16637
Qy	7902	AAACCTTTGGACAGCGGCTCCATAAATCTGCGCCAACAACCTCTCCANTTGAACGCCAGCCGC	7961
Db	16638	AGACATTGACGCAACGCCCTTATAACTTACGCGCAATAACTGACAATCGACGCTCAGCCAC	16697
Qy	7962	TTTTCCCTGTCGCTACGACCAAGCGCTCGAAACCGTTCGCCCTCGAGAGTGCCTGTCTCA	8021
Db	16698	TGTCATTATCTCTATGTCACCGCCCGCAGATTCGCTCCATGTATTCTCAGTCTCTGCCATCA	16757
Qy	8022	ACAGCGCGAGGTGTCTCAGCACTGCGCGCGCGGTGATGCGCTTTTACAGTTTCCCGG	8081
Db	16758	CTGCTTTCACAGCGCGCGCGGATTTACCTCATGCAAGTATGCCGATGTACCGTTTTCGG	16817
Qy	8082	TCATGCTGGAGAACCGCCGGGGGATGGTGAGCTCTGCAACCGGGTTCCGCAACACACTGC	8141
Db	16818	TGATTTCTGAAATATCCAAAGTGGGGGTAAAGCAGTTGATACAAATTTGCGCAATACCTTGC	16877
Qy	8142	TCGGTATTACGAGCGCTCAGATTCGCGAGCGCTCGGCCAAACTGTGTCAGACCCAGGCGCA	8201
Db	16878	TCAGCATTAATGTAACCGCAGGATGCAAGAGCCTTGGCTGAAATACTGCAAACTCAAGGCA	16937
Qy	8202	GTGAACTGATACGCCAGGCGCTTCGCCACAGGATAAGCTCTCGAGGAATTCGATGCGG	8261
Db	16938	GTGAGTTAGCCCTTGCAAAAGTATTAAATTCAGAGTATAGGTATGCTGAAATTTGATGCTG	16997
Qy	8262	ATATTCCCGCCCTTGGAGGAGAGCCGCGCGCGCGCAGATGCTTTTGAAAGTTTACAAAG	8321
Db	16998	ATAAATTTGGCGCTTCAAGAAAGCGTGCATGGTGCACTGCTCGTTTTCAGCAGTTTCAATA	17057
Qy	8322	TGTTGTACAGGCGGACGTCAACACGCGGAAAAACAGGCCATGACCTTGTACTCTAGTT	8381
Db	17058	CGCTGTACGACGAAAGATGTTAACCGTGGTGAATAAACAAGACGATGATCTTTACCTCTCTT	17117
Qy	8382	CGTCCGTGTCTCGGCATCAACGCGCGCGCTCTTTTGGCGGAGCGCGCGCGCGCATATGC	8441
Db	17118	CATCGGTCTTGAGCACACGCGGCAGACCCCTGCATATGCGCGCGCGCGCGCGCATCTCG	17177
Qy	8442	TGCCCAATATTTACGGGCTTGGCGCTCGGGGCTTCCCGCTATGCGGCGACTATTTTAAAGCCA	8501
Db	17178	TCCCAATATTTACGGTTTTGCTGTGGAGGTTTCCCGTTTTGGGGCGCTTTTCAATGCCA	17237
Qy	8502	CGGCCATCGGCATTCACAGTGTCTCCGATGCCACCCCGCATATCAGCGGCAAAATCAGCC	8561
Db	17238	GTGCGATTGGTATCGAAATTTCTGCTGACAGCAACACGTATTGCGCGCAGCAAAATCAGCC	17297
Qy	8562	AGTTCGGAAGTGTACCGCGCTCGCGGGAGGAGTGGGAAATCCAGCGGTGATAGTTCGCAGT	8621
Db	17298	AATTCAGAAATATACCGCTCGCGCTGCGCAAGAGTGGGAAATTCAGCGCAATTAATCGGAAG	17357
Qy	8622	CTCAGCTGGCGCAGATTGATGCCAGCTTGGCGGCCATGSCAGTGTGCGCGGAAGGGGCTG	8681
Db	17358	CTGAGATTAACAATTTGATGTCTCAATTAGCGACCGCTGCTGTGATGCTGTGAGCGGCAG	17417
Qy	8682	AGCTGCAGAAAACTTACCTTTGAGACCCAGCAGACCCAGGCGCAGGCGGAGTTGGCATTCC	8741

Db	17418	TATTACAAAAAACTATCTGGAAACTCAGCAGGCAAAACTCAGCGCAGTTAGCTTTC	17477
Qy	8742	TGCAGAGTAAGTTCAACAATACGGCTCTGTACAGCTGGCTCGGGGCGCAGTTGTCCGCCA	8801
Db	17478	TGCAAAAGTAATTCAGTAATCAGCGCTATACAACTGGCTCGTGGAGGTTGTCCGCTA	17537
Qy	8802	TTTATTACAGTTCTATGACCTGGCGAGTATCCCGCTGCCTGTATGGCGCAACAGGCTGGC	8861
Db	17538	TTTTATTATCAGTTTTATGATTTGGGGGTCTCACTCTGTTTAAATGCGAGCAAACTTATC	17597
Qy	8862	AGTGGCA--TAAATTTCGAGACTAGTCTGTTTTATCCAGCGGGGCGCTGGATGGGGCAA	8918
Db	17598	AGTATGAATTTGAATTAATCGGCAGCACACTTTATTAAACAGGTGCTTGGCATTGGGACTT	17657
Qy	8919	ATCCCGGTCTGCTGGCGGGGAAACCCCTGATCTGAACTCTGGCGCAGATGAGCAGGGCT	8978
Db	17658	ATCGGGGTTTATTAGCGGGTGAAACCCCTGATGCTGAATTTAGCAGATGAAAAAAGCT	17717
Qy	8979	GGCTGACGGGGGATGAGCGGGCAATAGAGGTGACCGGACGGTCTGCTGTCCGAGGTC	9038
Db	17718	ATTGGAAAAAGATGAACGGGCACCTGGAGGTCAACAGAAACCGTTTCTCTGGCTGAAGTG	17777
Qy	9039	ATACCAAGCTCGCGGAGGATCGGCATTCTCTCTGCCCGACAAGTGTGGAACTGGTCA	9098
Db	17778	ATGCTGCTCGACAGAAAT---AGTTTCATTTTAAAGATAAAGTGAATGAGTTAGTCA	17834
Qy	9099	GTAACGGTTTCGGGCAGTCGGGTACGAAAGCAACCGGATTACAGATGGATCAACAGCAAC	9158
Db	17835	ATCGAGTGAAGGCAGTCAGGCACAAACGCTTTAACGGTTTGAACGTGCAAGGACACAAAC	17894
Qy	9159	TCGAGGCGACCTTGAAACTGGGCTGACCTCGGTATCGGCAACGATTACCGGTTCCCTTG	9218
Db	17895	TGCAAGCCAGCCTCAAAATTATCGGATCTGAAATTTGCTACCGATTATCTGACGGTTTTAG	17954
Qy	9219	GCACCATGAGGCGCATCAAAACAAATAAGCGTCCACGCTCCCGCGCTGTCGCGCCCTATC	9278
Db	17955	GTAAATACCGCGTATCAAAACAAATCAGTGTGACATTTACTGCCCTTTTAGGGCCTTATC	18014
Qy	9279	AGGACGTCGCTGCGGTTCTCAGCTACGGCGGAAGTATGGTCAATGCCCGGGGTTGCAGCG	9338
Db	18015	AGGATGTCGGGCAATPACTAAGTTATTGGCGGCAGCACAATGATGCCGTGCTCAAG	18074
Qy	9339	CGCTGGCGGTCTCACACGGAAATGAACGACAGCGGGCAATTCCAACTGATTTCAATGACC	9398
Db	18075	CGATTGCGATCTCACATGGCATGAATGACAGTGGTCAATTCAGATGGATTTCAATGATG	18134
Qy	9399	CGCGTTACCTGCGGTTTGAAGACATTCAGATTTGATGACACAGGGACCTGACACTGAGCT	9458
Db	18135	CCAAGTACCTTGCCATTTGAAGGGCTTCCTGTGGCGGATACAGGCACATTAACCTTCAGTT	18194
Qy	9459	TCCCGGATGTCAGCGCAACCAACAGGCGATCTCCTCAGTCTGAGCGACATCATCTCTGC	9518
Db	18195	TTCCCGGTATCATGTGTAACAGAAAAAGCTTATTGCTCAGCCTGAGCGATATCATCTCTGC	18254
Qy	9519	ATATCGTTACACCATTTATCAGCTGAT	9545
Db	18255	ATATCGGTTACACCAATTCGTTCTTGAT	18281

RESULT 5
US-10-754-115-6
; Sequence 6, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Zhu, Weiing
; APPLICANT: Zhu, Baolong

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; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 39005
; TYPE: DNA
; ORGANISM: Xenorhabdus nematophilus
; US-10-754-115-6

Query Match          7.2%; Score 1365; DB 18; Length 39005;
Best Local Similarity 52.4%; Pred. No. 0;
Matches 3947; Conservative 0; Mismatches 3070; Indels 510; Gaps 23;

QY 2511 TGACGGATTATTCGCGTTCGTTCCGAGGTCAAAAATAATCACTGGCGACAGCTGT 2570
DB 10773 TGACAAACATTCGTTTATGCTTCAGCGAATTCGTCATAGGACAAGTGGAACTCTGA 10832

QY 2571 CATGGGAGAGGTCTGCTATCTGTACAGTCAGGCGCAGCAGCAGCAGCAGCAGCAGC 2630
DB 10833 CGTGGCGAGAAACAGACTTTTATATCAACAGGCTCATCAGGAATCAAAACAGAAATAAC 10892

QY 2631 TCACCGAATCCGTTATTCGCGCGCGGGAATCCCTACTGTGTGAATGCCGTTCCGCTCG 2690
DB 10893 TTGAAGAACCTGGCATTTTGTCTCGGTGCTAATCAACATGCTGCTAATACCACTAACCTTA 10952

QY 2691 GAATACGGCAGGCGCGCAGTCGCGAGTCATGATGATGATGATGATGATGATGATGATG 2750
DB 10953 ATATTACACCGTCAACCCCTAAACAATAGTTTACAACAGTGTGTTTATGGCGGTGCCACC 11012

QY 2751 GTTTTCGCGCGCGCGCTCGGTGCGCTCCATGTTCTCACGGCGCGGTACTCTGACCGAGC 2810
DB 11013 GTTTTGAACCCGGGATCAATGCTTCCATAATTTTACCAGCGGCTTATTTTAAACAGAAAT 11072

QY 2811 TGTAACCGTGAGCGGAAGGACTGTCATCCGAGACCTCGCTGTTCGCGCTGGACATCCGGC 2870
DB 11073 TATATCGGGAAGCGAAGATTTTCACTCTGACAAATCTCAATATCACTGAAATAAGGAC 11132

QY 2871 GTCCGACCTGGCGGCGCTGCGCTTAGCAGAAATAATATGAGCAGGAGCTCTCCACCC 2930
DB 11133 GCCCGACATTTGCTTCACTGGCACTGACACAGAAATAATATGAGTGAAGAAATTTCCACAT 11192

QY 2931 TGAGCCTGTCCAAATGAGCTACTGTATCGCGGTATCGGCGCAGCGGAGGCTTGAAGCAGC 2990
DB 11193 TATCCTTATCTAATGAATTAATGCTGCTAATATTTAGAGCTTAGAAGAACTGACTATA 11252

QY 2991 ACAGCGTCAGGAGCTGCTGCGCGGTATGCGCTGACCGGCGCTGACCCCTATCACTGGG 3050
DB 11253 ACGGTGAATGAATAATGTTGCTCACTTACCGGCAACCGGCGATGACACCTATCATCTGC 11312

QY 3051 CGTACGAGGCGCGCGCGCAGACCAATTTCTGTCAGGACCGCAGCTGATGGGTTTACGCC 3110
DB 11313 CGTATGAGTCAGCCCGCTCAGCGCAATTTTATTTGAAGATAAATAAACCCTCACCGCAATTTAGCC 11372

QY 3111 GTAATCCGGATGTGGCGCAGCTTATGACCTGCTCCATGCTGGCCATTTGAAGCCGATA 3170
DB 11373 GTAATACAGCTGAGCGGAATTAATGACCCCAACATCGTACTGCTGCTTTAAGACTGATA 11432

QY 3171 TTTTCCCGGAGCTGATCAGATACCTGCGGAAGAAATTAACAGACAGATTAACGAAGCAC 3230
DB 11433 TATCGCTGAATTTGATCAAAATCCTTGTAGAAGAAATTAACACCGGAAATTTCAACAGAAC 11492

QY 3231 TCTGGATGAATTTTGGTGATGCTCTCCCTCCTCAGTGTATCTTATGATGACACTTG 3290
DB 11493 TGATGAAGAAATTTTCGGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 11552

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QY 3291 CAACATTTTATGATCTTGTGATTACGATGAGCTAACTTCGTTATTGTCTTAAAGGCTGGAAT 3350
DB 11553 CTGCGTACTACGATTTGTCTTATGATGAACTCAGTTTATTGTCAATCTCTCTCTCGGTA 11612

QY 3351 TTTCAAAATCCAAAACAATGAATACATTAATAGTCAATTAAGTGTCTGTAATCTGTAATG 3410
DB 11613 AGMAAATAACAAATCAACAGTATAAGATGAGCAACTGATAAATGCTCAATGACGGGA 11672

QY 3411 AAAGCAGCTGTTTAAATAACTATACATCATTTATTTAAGAACCTGAGGCGGAGCTCACAGC 3470
DB 11673 ATGATACGGCAACCGCAAGATTGATTAAAGCGAACCCGCAAGATTTCTTACGATTACAT 11732

QY 3471 AGATTAACCCCTGAGCTTATACCTTATGGGATGGAACATATCTTTATATTTTACGCGTGG 3530
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QY 3531 TGTCAACGATATCAGAGGATAGTTTCAAACTAGGTCGTTAGGTTCTTAACTAGTAGCAATC 3590
DB 11793 AAAAAACAGAACCTGACCACTTGGATTTCGTCTCCAGATGGAGATAAAGAAATATATAT 11852

QY 3591 TTTTACTCTGGGATTTATCAGCTTCAAAAAGGGTTGCTATAGCATTCCTGTTGAAATAG 3650
DB 11853 ACCAAGATAAAATTTCTGTCGCCATTTGCTAATACCATTAAGTATTTCCCATTAATTTGA 11912

QY 3651 ATGAAGGAAAGTTAAATGATGGATCAAAATAGGATTGAGTAGGAA-----AG 3698
DB 11913 CGACAGAGCAATCAACACGGTATAACATCCGCTTATGGCGAGTTAAACCAAAATCCGT 11972

QY 3699 GGGGGGGATATTAATCAACAGTAACTTCACTCTGATTGAATATATGATCCTGGGATTAATCA 3758
DB 11973 CGGATGCTATCAATCCCAATGCATCTTTAAATGATGGAGTTCCTCCGCTGATATATTTCC 12032

QY 3759 TTTCTAAATTAATAAGTTATCCGCTTACAGGCCACGGGATGACCGGGGAAA 3818
DB 12033 TGTAAAGCTGAATAAAGCGATTCTGTTGTATAAAGCCACAGGATATCTCCAGAGATA 12092

QY 3819 TATATCAATCAACCAATATTTTAATAACGGTCTCAACATTCACCATTCGGTCTCTGAGTA 3878
DB 12093 TCTGCGAAGTAAAGAGTATTTATGATGACTTAAACCATTTGACAGCAATGTGTTGGGTA 12152

QY 3879 AAATCTTCTGCTGCTGCTACCTGATGCTGCTATCACTGATGCTGATGCTGCTGCTGCTG 3938
DB 12153 AGCTGTTTATGTTCAATATTTATGAGCAGCTATAATATTTAGCTGCTGAGCTGCTGCTG 12212

QY 3939 TATGTCGACACGAAACCTACGTGACACGAGGCTTCAAGCGGGAACCGGCTGTTTCAACA 3998
DB 12213 TATGTTGCTATTCAGATATCAGCAATATTTCACTAAACACACAGCTGCTGCTGCTGCTG 12272

QY 3999 CGCTGTTCAACCCCGCTGAAACGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4058
DB 12273 TACTGTTCAATACACCGCTTATTAATGGCCAGAGTCTTCTGCTGATAATACCAAACTGG 12332

QY 4059 ACTTACGCTCTGAAGCACCGGAGGATGCTTCCGCTCAGCGTACTGAAACCGGCTTTA 4118
DB 12333 ATTTAAACCCCGGTGAATCAAAAAACCAATTTTATTTGGGAATAATGAACACGCTGCTTCA 12392

QY 4119 ACATCAGCGCTCTGGGCTTTCCACGCTCTGCGAGTTGGCCAGCGGTGACACAGCGCTG 4178
DB 12393 GAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 12452

QY 4179 GGTGTTAGCTGCTCTGCTGCAATATCGGCGACTCTAOCGAGTGAATCTCTGCTGCTGCA 4238
DB 12453 AATTTATGTTTCCATCGAAGAACCTGCTCTGCTGTTTATCGCGTCTGCTGCTGCTGCTG 12512

QY 4239 TCCACGACCTATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4298
DB 12513 TTTATCATCTGACAGTGAATGAAATTCATGCTGTTGTTGCTGCTGCTGCTGCTGCTGCTG 12572

QY 4299 TGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4349
DB 12573 CGMAAATGCGCTTTTCTGATACAGCATTAACGCAATTAATCAGCTTCTGCTGCTGCTGCT 12632

QY 4350 CCACCACTTGGCTCAGCGGACAGGGCTGGAACGGTCAGCGATGTGTTCTGCTGCTGCTGCTG 4409

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Db	12633	GCACCCAGTGGCTGACAAACACAGAAATGGTCTGTCAAGTATGTGTTTCTGATGACCAACGG	12692
Qy	4410	CGCAGTACGGTACCTCTGCTGACCCCGACATTTAGAACCTGCTCGCTTCCCTCGCGCAACG	4469
Db	12693	ATAATTACAGCACTGCTTCTTACGCCGATATTTGAAAACCTTATCAGCACATAAGTAAATG	12752
Qy	4470	GACTGTGGGGCGTGAAGCTGTGTTCCCGGAAAACGCTCCCGGGGATGGCGCTCCCTTTATTTG	4529
Db	12753	GATTATCAACACATTTCTCACTCGGTGATGACGAACTGATCCGTGCAGCTGCCCGCTGATTTG	12812
Qy	4530	CCGCGCCATGACGTGGAGCGCACCGGATACGGCGAAGCGGATGCTGACTGTGGCGGAC	4589
Db	12813	CTGCCAGCATTTCAATTTGGATTTGAGCCAGACAGCAGAACTATTTTGTCTGSGATTAAATC	12872
Qy	4590	AGTTGAAGCCAGAGGGCGCTGAGCGTGCAGGAAATTTATTTCTTTGGTGATGAATGCCGCC	4649
Db	12873	AGATAAAAACCAAGGACTGACATTCGATGATTTTCTGATTTATTTGGCGCTAACCGTGATC	12932
Qy	4650	CAAAATGACGAGCAGGCGGGCGACATGGCACAGGGTTCTGCCAAGCCCTGTGGCAACTGGCAC	4709
Db	12933	GCTCAGAGAATGAAACACAGCAACATGGTGGCTTTTGTTCAGTACTGGGGCAACTTTCTC	12992
Qy	4710	TGATCATCCGACGACCGGCGCTCAGCACCGGCGAGCTGACGCTGCTGTGTGACGACGCGG	4769
Db	12993	TGATTTGGCGCAATATTGGACTCAGCGAAACGAACTGACCCGTGTGGTGTGCAAAACCGG	13052
Qy	4770	GAGCTTTCCGACAGAGTGGCACCATCTGCCCATGACTCTGCCGCGCTCTCGCGACATTA	4829
Db	13053	AGAAATCCNATCAGAAACCAACGACNCTGCAACATGATCTCCCNCTTTGCAAGCGCTGA	13112
Qy	4830	CGCGTTTTCATGCGCTGTTAAACCGCAGCGGAGCCATCGCGGGAGGTCTCTACCGCAC	4889
Db	13113	CCCGCTTCCATGCTGTGATCATGCGTTGTGGAAGCTACGCGACAGAAATCTTAACAGCAT	13172
Qy	4890	TTGAGACCGGAGAACTGTGCTCAGCCCTGCTGCGCGGGGCCCTGTCAAGAAATGAGCAGG	4949
Db	13173	TGGAATCTAGAGCGCTGACTGCGCAACAAATTGGCGGTGGCGGTTAAATTTTGATGCTCAGG	13232
Qy	4950	ATGTGACCGGCGCTTTGGCGCAGGTGAGGGGGCGGTGAAACAGGACAAAGCGGTGTCA	5009
Db	13233	TTGTGACAAAGCATTTGCAACAGACCGGTTTGGAGTGAATACC-----TTTA	13280
Qy	5010	CCTCCTGGGAAGGTGGACACAGGCTGAGCAGTGGCTGCACTAGTGTGAGACCCCTGTCCA	5069
Db	13281	CCAACTGGAGAACTATAGATGTCACTCTGCAATGGCTGGAATGCTGCTACATTTGGTA	13340
Qy	5070	TTAGCGCATCCGCTGTGGCTAGCTGATTTGCCCTGAAGTACATCAATGTGTCCGATGACA	5129
Db	13341	TTACCCCGGATGGTGTGTGCTGCACTCATAAAAATTAAAAATATATCGGTGAAACGAAACCC	13400
Qy	5130	GTGCACCGTTGTACGCCAGTGGCAGGTGGTATCCGGTCTGCTGTCAGACCGGGCTGAAA	5189
Db	13401	CGATGCCAACATTTGATGATTTGGCAAGCCCGCAGTACTTTGTTCAGCGGGGACTGAACA	13460
Qy	5190	GCAGCCAGAGCTCGGCGCTGCACGATTATCTGGAGAGGGGACACAGACGCCCTTTGTG	5249
Db	13461	GTCAACAAATCCGACAGCTTCAGGCATGGCTGGATGAAGCCACGACGACGCGCCAGTG	13520
Qy	5250	CGTATTATCTGCGTAAATCTGGCACCGAAACATGGTATCCGGGCGGATGACCTCTTCGGGT	5309
Db	13521	CTTACTACATCAAAAAATAGTGCACTTCAACAGATTAAGAGCGCGGATGAGTTGTACAGCT	13580
Qy	5310	ATCTGCTGCTGATTAATCAGGTGTGACGCAAGGTAAACCAACCCGATTCGGGAGCCA	5369
Db	13581	ATCTGCTGATTTGATTAACCAAGTTTCTGCCAAGTGAACCAACCCGCTGTGCAGAGCCA	13640
Qy	5370	TCGCGGCGATACGGCTGTATATCAACCGGGGCCCTTAAACGGAATGAACCTCAGCGCCATGG	5429
Db	13641	TTGCCAGCATTCAGTTATATGTCNACCGGGCGTTGATTAATGTTGAAGGAAAAGTATCAA	13700
Qy	5430	CAGAGGTGAGGGGCGTCAATTTTCACTGCTGGGATACGTTTCAACAAACGTTTACAGCA	5489

13701	AGCCAGTGAACCCCGTCAGTTCCTCTGCGA CTGGGAAACCTTACAATCGACGGTATAGCA	13766
5490	CCTGGCGGGCGTCTCAGAGCTGGTTTACTATCCGGAAAACTACCTCGACCCCGACGGTCC	5549
13761	CCTGGCGGGCGTATCTGAACTGGCTATTATCCGGAAAACTATATCGACCCCGACGATTC	13820
5550	GTATCGGGCAGACCGGCATGATGGACA CCGCTGCTGCAGTCTGTGACGCCAGAGCATATCA	5609
13821	GTATTGGTCAGACAGGTATGATGAACAACCTGTTACAGCAACTTTTCCCAAAGTCAGTTAA	13880
5610	ACCGCGATACCGTGAGGAGTGCCTTTTAAACCTATCTGACCAAGTCTTTGAGCAGATTGCCA	5669
13881	ATATCGATACCGTGAAGATAGCTTTTAAAAATTTATCTGACCGCATTTGAAGATGTCGCTA	13940
5670	ATCTGAACACTGTCTAGCGGATATCACGATAACGCCAGCATGACGACGGGACTACATGGT	5729
13941	ACTTGCAGGTGATTAGCGGATATCATGACAGTATCAATGCTCAATGAGGACTCACTTATT	14000
5730	ATGTGGGTGCGAGCATACAGATCAGACTAACTGTGTTACTGTGGCGCAGCGCCAAACACAGCA	5789
14001	TAAATTGGTTATAGCCAGACAGAACCCAGAAATATATTATTGGCGCAATGTGATCACCAAA	14060
5790	AAATCCAGAGATCAATGATCCCGGAAATGCTCGGACCGGATGGACAAAAAATTAACATGCG	5849
14061	AGTCCACAGCGGTCAATTGTGTCGAATGCTCTGGGAGAAATGGAAAAAAATTTGAAATAC	14120
5850	GAATGAATCCCGTGGTCAGATCTTGTGTGCTCGGTGTTTTTCAACAGTCGCTTTATGTGCG	5909
14121	CCATCAATGTATGGCAGAAATATACAGACTGTTATTTTACAAGTCTGGTTGTTTAC	14180
5910	TCTGGGTGGAAGAGAAATCAGTCTGTGTGATA CGGAGGCAGAGACGACAAACCACGACGC	5969
14181	TGTGGCTGGAACAAAAAGAGCTGAAAAATGAAAGTGAAGATGGCAAGATAGATATCACTG	14240
5970	AGAGCTACACGCTGAAACTGTGTTCCGGCGCTACGACGGTACATCGGAGTTCCTCCGGTGT	6029
14241	AT---TATATATTAATAACTGTACACATATTCGTTATGATGGCAGCTGGAGCTCACCGTTTA	14297
6030	CGTTGCAATTAACCGGCAACATCGCATTTCCGG-----AAACGACGGGCATGCATGTG	6082
14298	ATTTTAATGTGACTGATTAATAGAAACCTGATCAATAAAAANGCCAGCATTTGGTATGT	14357
6083	ACCTGTAATCCCTGACTGAGCAGCTCTATTCGGCGTTTTTACTCCGTACACGCAAGCC--	6141
14358	ATTGTTCTCTGATTATGAAAAAGAGCTCATTTATTGTTTATTTCCATGAGAAAAAGACA	14417
6142	-----GGACTTTGATAAGCTCAGCTGATTTCTGTGGATATGATATGACGC	6188
14418	ATTATTTCTTTTAATAGTCTTCTCGAAGAGAAGGGATGCCATTAACCTCGATATGACAT	14477
6189	TAAATGTCTATCTCAGATA-----TAGGGATTTTAAAGAGCGTCAGTCAGCAATTTA	6239
14478	TATCCATTTCTACAGAAATGATTTTAGCGCCATTTGTTAAGACCATTTATCAGAACTTG	14537
6240	ATACGAGCACTG---AGAAATTTATTAATAATGTTTTTTTTCAGACCCCTTCGGCTAAATTTT	6296
14538	ATACCAGACAGAAATACAAAGTCAACAATTTGTTCTACAGATTTTGGCCGCAATATA	14597
6297	TGTGAGTGCACAGGTTTAATTGA---TGATGTTATCCACAGCGAATTTCTCACTCCTTA	6353
14598	AGGAATCTATACCAACAAAAATAAATTAGCCAGTTTACCGGAAATATTTTTTGATCTCT	14657
6354	ATTTCTAAACTACAAGTACTGTTTTTACTTAATGAAGATTCCTCTCTTTTTCAGCCGACGC	6413
14658	CGTATATATCACCGAANAATGTCATTTAATTTTAACGTTCAATCTTCAATGGAAATTA	14717
6414	TTCATATTACAGCAATGTTTCGTGTTTGTGTAGTA-----CTG	6452
14718	ATTTTTCAAAAGGCAATATATATATGATGAGGTTAAATACCTGTTTATCGATGTAAG	14777
6453	CTGGCATCCGCNCTCAATCTACATAGAAAAAATTCGTTCCAGCGAGGATAGAAATTTGAGG	6512
14778	ATGAAACGGTTATTTTTTATTGATATGATAGACATGATGAATGCTTGGAAAAAGAGAG	14837

QY	6513	AAATTAAT-----TTTTATGAGCGCGCGCGCGGATTTGACGG	6555
Db	14838	AGATTTTCAATATGAACTTTGATTTTATTTCCATCGATCTAAAAATGCCGAAT	14897
QY	6556	ATTGTGGGAGTGGATGTTTCTAATTCAAAGATATACAGGTC- GGAAAGAGACGAGTTG	6614
Db	14898	ATTTTAGAGTGTAAATGTCATCTAAGAACCAAGGAAATTTCTAGAAATCAGAAATTG	14957
QY	6615	GTGTACTGTAAATCTTATTCGCTCACTGGCGTTAGTGGTT-----CTGTTGAGTTATT	6669
Db	14958	GAGTTGGTATAAATATGATTATCAATCAATGATGCTGAATTCAAACTTGATCTAAACA	15017
QY	6670	TATTTGATTCATCAATAAATACTTTCAGCGAAATTTTGTACAGATA---AAATGATACCCG	6726
Db	15018	TAGTATTAGATTGGAAAGATAACACAGGATATGGCATACTATATGTGAATCAATTACTA	15077
QY	6727	TTTTAATTTAGCGGAGTACATCAAAAGTTAATTACGTGCTGTCTATTGGCTCTCAAGATTT	6786
Db	15078	ATGATGTTTCAATCAATTAATAACATGGAAATATTGCGGCACGTTCCTTCGCGAGATC	15137
QY	6787	TTGGAGTGTAAAGTCTGATGCGGCACTTCAGATATATGAATTAATTCAGATATCAT	6846
Db	15138	CATGTGTGTATTATGTTCAATAGCACACAGATATAAAATTTGCTTCATCTATGATCGAAC	15197
QY	6847	ACTGACATCCGCGTAAATGGGACTGAATTAATCCTCGCCTT-----	6890
Db	15198	AGATCCAGATAAAACATTAGTTT-----TATTAATAAATGGCTCTGATATTTCTAGTGGAGT	15257
QY	6891	-----CCGCTGAATGGTATATATGATTAAGCTGAGTCTGCAATCCGCGGAATAAT	6937
Db	15258	TAAATGCTGAAGACCATGTGCATCTAAACCTTTCACAGBATCTGACCCCTATGTTATG	15317
QY	6938	CTTTTCAACACCAATCGTGAATTTA-----	6965
Db	15318	ATTTTAATCAAGTAAAGTTGATATTGAAGGCTATGATATTCCTCTGCTGAGCGAGTTTA	15377
QY	6966	-----CCGTTAATACAGTATGATTTGTTGAA-----	6991
Db	15378	TTATTAAAGNACCGGAGCGGTTATAACGATATTGTTATTGAATCGCCAAATTCATATA	15437
QY	6992	-----	6991
Db	15438	AACTAAAAATCCAAAGATACAAGTAACGTTATATCACTGATATAAATGCCATCAGGCAC	15497
QY	6992	-----	6991
Db	15498	AAATATGACAGATTGCGCTTACAGAACCGGTTAAATACTTTATTTCCAGAAAAATTAG	15557
QY	6992	-----	6991
Db	15558	CTGAAAGAGCCAATATTGTTATGTAAATGTTTAAAGTATGGAACGCAAAATTTACCAAG	15617
QY	6992	-----GATGAGTTTGAGTGAAGTTTACGTTTACCGCTGTCGATCA-----	7032
Db	15618	AGCGGCAATTGAGTGAAGGTTTTATGCGACATTTAAGTTGCCCTTACCAATAAGAGG	15677
QY	7033	-----GAATAAGCTGTGCTGGCGCGCGGAGCGGCATATAACCGTCAATC-----	7079
Db	15678	AGCATGGTATGAACGTTGGTTTTAAGATCCATATTGGGAATATTGATGGCAATTTGCGCA	15737
QY	7080	-----GAAACATTAATAATGACACTTC	7101
Db	15738	GACAACTTATTACGAAGGAATGTTATCTGATATTGAAACCAACAGTAACGCTTTTGTTC	15797
QY	7102	CGTTATCGCATTAACGTAATAATACGGTGGCGCGCAGTATATTCTGTTCACTCGCGGTAA	7161
Db	15798	CCTATGCTAAAGGATATTACATACGTGAAGGTGTAGATTAGGGTTGGGTACAAAAA	15857
QY	7162	CGATGTGGCGCTTATTGCGCTCAACACCTCTTTTCCGCGCAACTGCTGGA-----	7212
Db	15858	TTATCTATGACAAATCCTGGGAATCTGCTTTCTTTTATTATTGATGAGACGAAAAATCAAT	15917
QY	7213	-----CCGGCGGAATACCGGATTGACACATTC-----	7241
Db	15918	TTATATTCAATTAATGATCGCGATCATGATTCGGGAATGACAAACAGGGGATAGTAAAAA	15977
QY	7242	TTTCCATGAGAGCCAGAGGCTTACCGAACCCGCCCTTGAAGAGGGGAGTGTGTGTTTA	7301
Db	15978	ATATCAAAAAATATAAAGGTTTATTTCATGTGTTGTCATGAAAAATAACACTGAACCCA	16037
QY	7302	TGGACTTCTCCGAGGCAATGCCCTCTATTCTTGGAGAGTGTCTATTATCACGCCGATGA	7361
Db	16038	TGGATTTCAACGCGCCCAATGCAATCTATTCTTGGGAATTTGTTATTATCACGCCCATGA	16097
QY	7362	TGTTGTTCCAGCGGTTGTTGAGGAAACAGCACTTCCCGGAAGCACCCGCTGGCTGCACT	7421
Db	16098	TGGTATTCGAGCGCTTATTGCAAGAGCAGAAATTTTACCGAATCGACACGCTGGCTCGCT	16157
QY	7422	ATGCTGTGHAACCCGCGCGGACGTGTGTAACCGGGTGTCTGAGAAATTAACCTTGGAATG	7481
Db	16158	ATATCTGGAACCCGCGCGGATATTTCGGTTTCAGGGTGAATGCGAGATTATTACTGGAACG	16217
QY	7482	TCGCTCGCTGGAGGAGGACCGGCTGGAACAGCTCGCGCTGAGCTGCATTTGACCCCG	7541
Db	16218	TCGCGCCATTGGAGGAAGATACGCTCTGGAATGCCAATCCGCTGGATTCCGTCGATCCTG	16277
QY	7542	ATGCAATAGCCAGTACGACCCATGCTATTACAAGTGCACCTTTTATGTCTGCTACTCG	7601
Db	16278	ACGCGTTGCCAGCATGATCCGATGCACTATAAGTGGCTACCTTTTATGAAATGCTGCG	16337
QY	7602	ACCTGTGATTCCCGCGGTGATGCGCTTACCGCTGTCTGAGCGGGACACCTTTAAACG	7661
Db	16338	ATTTGTTGATTACCCGCGGAGATAGCGCTATCGCAGCTTGAACGTGATACCTTAAACG	16397
QY	7662	AGCGCGGATGTGTTACGTCCAGGCGCTGAACTTCTTGGGCAACGAGCCCTATTATTCCT	7721
Db	16398	AAAGCTAAAAATGTGTTATGACAGGCGCTCACTTTATTTGGTGATGAGCCCTTTATTTTCAT	16457
QY	7722	TTGAGCGGACTGTGCGGTTGAGCCTGGGTGAGCGCAGCAGCAGGTTGAGCGGACGCG	7781
Db	16458	TGGATAACGATTGGTCAGAGCCACCGCTGGAAGAGCTGCCAGCCAAACAAATGCGGCATC	16517
QY	7782	ATTACAGAGAGCCCTGTGCGCGTTCGCGCGGTTGGTGGTCCCTCCCGAGACGAGACGG	7841
Db	16518	ATTATCAACATAAAATGCTGCAACTGCGTCAGCGGCTGCTATTACCCAGCAACGTAACG	16577
QY	7842	CGAATTCCTGACGCACTGTTCTCCCGCAGCAGAACAGGTTGCTCAAGGCTACTGCG	7901
Db	16578	CAAAATTCGTTAAACCGCATTTCTCCCTCAAATTAATAAAAACTGCAAGGTTACTGCG	16637
QY	7902	AAACCTTTGCAAGCGGCTCCATAACCTGCGCCACAACTCTCCATTGACGCGCAGCCGCG	7961
Db	16638	AGACATTGACGCAACGCTCTATTAATTAAGCCCTAACCTGACATTCGACGCTCAGCCAC	16697
QY	7962	TTTCCCTGTCTGCTACGCAACGCGCTCCGAAACCGTCCGCCCTGCGAGAGTGCCTGCTCA	8021
Db	16698	TGTCATTATCTCTATGCAACGCGCAGATCCGCTCCATGTTACTCAGTGTGCTGCTATCA	16757
QY	8022	ACAGCGCGGAGGTTGCTGAGCACTGCGCGCGCGGTTGATGCGCTTTACAGTTTCCCGG	8081
Db	16758	CTGCTTCAACAGCGCGCGGATTTTACCTCATGCAAGTATGCGGATGATCCGCTTTCCCG	16817
QY	8082	TCATGCTGAGAACCGCGCGGATGTTGAGCTGCTGACCGGTTTCGGCAACACACTGCG	8141
Db	16818	TGATTTCTGGAATAATGCCAAGTGGGGGTAAGCAGTTGATACAAATTTGGCAATACCTGCG	16877
QY	8142	TCGGTATTACCGAGGCTCAGGATGCGGAGCGCTGGCCAAACTGCTGCGAGACCCAGGCA	8201
Db	16878	TCAGCATTAATGAAACGCGAGGATGCAAGACCTTGGCTGAAATACTGCAAACTCAAGGCA	16937
QY	8202	GTGAAGTATGACCCAGGCGCTTCCGACAGGATACGCTCCGAGGAAATCGATGCGG	8261
Db	16938	GTGAGTTAGCCCTGCAAAAGTATTAAAAATGCAAGTATGCGTGAATTTGATGCTG	16997
QY	8262	ATAATTGCCCGCTGGAGGAGAGCCGCGCGCGCAGATGCGTTTTTGAACGTTTACAAAG	8321

Db 16998 ATAAATTGGCGCTTCAAGAAAGCGTCAATGGTGACAGTCTCGTTTTCAGACATTTCAATA 17057
 Qy 8322 TGTGTACGAGCGGAGTCAACACCGCGGAAACAGGCGATGCTTGTCTCACTGAGT 8381
 Db 17058 CGCTGTACGAGGAGATGTTAACGCTGGTGAAGAAACAGGAGATGATCTTTTACCTCTCTT 17117
 Qy 8382 CGTCGCTGCTGTGCGGATCAACCGCGCTCTTTTGGCGAGCGCGCGCGATATGC 8441
 Db 17118 CATCGGCTTGAGCACGAGCGCACGCCCTGCATATGGCGCGCGCGCGAGATCTCG 17177
 Qy 8442 TGCCCAATATTACGGGCTGCGCTGCGGGGCTCCCGCTATAGGGGCTATTTAAAGCCA 8501
 Db 17178 TCCCAATATTACGGTGTGCTGTGGAGGTTCCCGTTTGGGGCGCTTTTCAATGCCA 17237
 Qy 8502 CCGCATCGCATCCAGGTGCTCCGATGCCACCGCATATCAGCGGACAAATCAGCC 8561
 Db 17238 GTGGATTTGGTATCGAAATTTCTCGGTGACGACACGCTATGCGCGAGACAAATCAGCC 17297
 Qy 8562 AGTCGGAAGTGTACCGCGCTGCGCGGAGAGTGGAAATCCAGCGTGATGTCGCGAGT 8621
 Db 17298 AATCAGAAATATACCGTCCGCTGCGCAAGAGTGGAAATTCAGCGCAATATGCGGAAG 17357
 Qy 8622 CTGACGTGGCGCAGATTTAGTCCAGCTGGCGGCGCATGCGAGTGGCGCGGGAAGGGCTG 8681
 Db 17358 CTGAGATAAAACAAATTTGATCTCAATTTAGCGAGCTGGCTGTACGTGCTGAAGCGGCG 17417
 Qy 8682 AGCTGCAGAAACCTTACCTTGAGACCCAGCAGACCCAGGACAGCGCGAGTGGCATTC 8741
 Db 17418 TATTACAAAACAACTATCTGGAATCTCAGCAGGACAACTCAGCGCGCATGTAGCCCTTC 17477
 Qy 8742 TGCAGAGTAAAGTTCACAAATACGCTCTGTACAGCTGGCTGCGGGGAGGTTGTCGCCCA 8801
 Db 17478 TGCAAGTAAATTCAGTAATGCAGCGCTATACACTGGCTCCGTGGAGGTTGTCGCTA 17537
 Qy 8802 TTTATTAACGATTTCTAGCTGCGAGTATCCCGCTGCTGATGCGGCAACAGCGCTGGC 8861
 Db 17538 TTTATTAACGATTTCTAGCTGCGAGTATCCCGCTGCTGATGCGGCAACAGCGCTGGC 8861
 Qy 8862 AGTGGG- --TAATTCAGACTAGTGTGTTTATCCAGCGCGGGGCTGGTGGGCGCA 8918
 Db 17598 AGTATGAATTAATTAATGCGGAGCAGACACTTTTATTAACAGGCTGCTGGCATGGGACTT 17657
 Qy 8919 ATGCGGCTGCTGCGCGGGAACCTGATGCTGAATCTGGCGAGATGGAGCAGGCT 8978
 Db 17658 ATGCGGCTTATAGCGGTTGAACCTGATGCTGAATTTAGCAGATGGAAAGCT 17717
 Qy 8979 GGTGACGCGGGATGAGCGGCAATAGAGTGAAGCGGAGTCTGCTGTCCGAGGCT 9038
 Db 17718 ATTTGGAAGAGATGAACGGGCACTGGAGGTCAACAGAACCGTTTCTGCTGGAAGT 17777
 Qy 9039 ATACGAGCTCGGAGGATCGGCAATCTCTGCGCGACAGGTTGGTGGACTGTGCA 9098
 Db 17778 ATGCTGTGTGACAGAAAT- --AGTTTCATTTTAAAGATAAAGTGAAGTGAAGTATGCA 17834
 Qy 9099 GTAACGCTGCGGAGTGGGATACGAAAGCAACAGGATTAACAGATGATCAACAGCAAC 9158
 Db 17835 ATGAGGTGAAGGAGTGGAGGACACAGCTTAACGTTTGAAGTGAAGTGAAGGACACAC 17894
 Qy 9159 TCGAGGCAACCTGAACTGCTGACCTCGGATATGCGCAACGATTAACCGGCTTCCCTTG 9218
 Db 17895 TGCAAGCGAGCCTCAATATTACGATCTGAATATTGCTACCGATTAATCTGAGCGTTTGA 17954
 Qy 9219 GCACATGAGGCGATCAACAAATAGCTCAGCTCCGCGGCTGGTCCGCCCTATC 9278
 Db 17955 GTAATACGCGGCTATCAACAAATCAGTGTGACATTAACCTGCGCTTTTAGGGGCTTATC 18014
 Qy 9279 AGGAGCTCGGCTGCTCAGCTACGCGGAGTATGGTATCATGCCCGGGTTGACAGC 9338
 Db 18015 AGGATGTTGCGGCAATAGTATGTTATGGCGGACACAAATGACGACGCTGCTGCAAG 18074
 Qy 9339 CGCTGGCGGCTCTACAGGGAATGAACAGCAGCGGCAATTTCCAACTGGATTTCAATGACC 9398

Db 18075 CGATTGCGATCTCACATGCGCATGAATGACAGTGGTCAATTTCCAGATGGATTTCAATGATG 18134
 Qy 9399 CGGTTACCTGCGGTTTGAAGGACTTCCAGTTGATGACACAGGACCTGACACTGAGCT 9458
 Db 18135 CCAAGTACCTGCGCATTTGAAGGGCTTCTGTGCGGATACAGGACATTAACCCCTCAGTT 18194
 Qy 9459 TCCCGATGCTGACGCGCAACCAACAGGCGATGCTCTCAGTCTGAGCGACATCATCTGC 9518
 Db 18195 TCCCGATGCTGAGTGAACACAGAAAGCTTATTTGCTCAGCTGAGGATATCATCTGC 18254
 Qy 9519 ATATCCGTTACACCATATATCAGCTGAT 9545
 Db 18255 ATATCCGTTACACCATTTGTTCTTGAT 18281

RESULT 6

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 ; Sequence 13, Application US/10753901
 ; Publication No. US20040194164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bintrim, Scott
 ; APPLICANT: Mitchell, Jon
 ; APPLICANT: Larrinua, Ignacio
 ; APPLICANT: Apel-Birkhold, Patricia
 ; APPLICANT: Schafer, Barry
 ; APPLICANT: Bevan, Scott
 ; APPLICANT: Young, Scott
 ; APPLICANT: Guo, Lining
 ; TITLE OF INVENTION: Xenorhabdus TC Proteins and Genes for Pest Control
 ; FILE REFERENCE: DAS-105X
 ; CURRENT APPLICATION NUMBER: US/10753,901
 ; PRIOR FILING DATE: 2004-01-07
 ; PRIOR APPLICATION NUMBER: US 60/441,717
 ; PRIOR FILING DATE: 2003-01-21
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 13
 ; LENGTH: 7569
 ; TYPE: DNA
 ; ORGANISM: Xenorhabdus nematophilus
 US-10-753-901-13

Query Match 7.2%; Score 1364.6; DB 18; Length 7569;
 Best Local Similarity 52.5%; Pred. No. 0;
 Matches 3943; Conservative 0; Mismatches 3064; Indels 510; Gaps 23;
 Qy 2511 TGACGGAATTTATTTCTCGCGTTCTGTTCCCGAGGTCAAAAATACATGCGGACAGCTGT 2570
 Db 65 TGACAAACATTTCTGTTTATGTTCTTTCAGCGAATTTCTGCTATAGGACAAAGTGGAACTCTGA 124
 Qy 2571 CATGGGAGAGGTCTGCTATCTGTACAGTCAGGCGGAGCAGAACAGAAAGAAACCGGC 2630
 Db 125 CGTGGCGAGAAACAGACTTTTATATCAACAGGCTCATCAGGAATCAAAACAGAAATAAC 184
 Qy 2631 TCACCGAATCCCTATTTCTGGCGCGGCAATCCCTACTGTTGTAATCGGCTTCCGCTGG 2690
 Db 185 TTGAAGAACTGCGCATTTTGTCCGTTCTAATCCACAATCGGCTAATACCACTAACCTTA 244
 Qy 2691 GAATAGCGGAGGAGCGGCGAGTCGAGCTATGATGATCTGTTGGCTCCGCGGACAGC 2750
 Db 245 ATATTACCGCTCAACCCCTAAACAATAGTTTACACAGTTGTTTATGCGCGTCCGCGCACC 304
 Qy 2751 GTTTCCCGCGCGCTGGTGGCTCCATGTTCTCACCGGCGGCTATCTGACCCAGC 2810
 Db 305 GTTTGTGTAACCGGAGTCAATTTCTTCCATATTTTCCAGCGGCTTATTTAACAGAA 364
 Qy 2811 TGTAACGCTGAGGAGGAGGACCTGATCCGAGCACTGCTGTTCCGCTCGACATCCGGC 2870
 Db 365 TATATCGGAGGAGGAGATTTTCTCCTGACAAATCTCAATATCACCTGAATAACGAC 424
 Qy 2871 GTCCGACCTGCGCGGCTGGCCCTTAGCAGAAATATATGAGCAGAGCTCTCCACC 2930
 Db 425 GCCCGGACATTTGCTTCACTGGCACTGACACAGAAATAATATGGATGAAGAAATTTCCACAT 484

QY	2931	TGAGCCTGTCCATGAGCTACTGTATCGCGGTATCGGGCAGCGAGGCGCTTGACGAGC	2990	QY	3999	CGCTGTTCAACACCCACCGCTGAAGCGCCAGCTGTTTCTGCAGATGATACCCCCCTCG	4058
Db	485	TATCCTTATCTAATGAATTAATCTCTGCTGATTAATTAATGCGCAAGAGTTTCTGCTGATTAATACAAACTGG	1624	Db	1565	TACTGTTCAATACACCGCTTAATTAATGCGCAAGAGTTTCTGCTGATTAATACAAACTGG	1624
QY	2991	ACAGCGTCAGGGAGCTGCTCGCGGGTATCGCTGACCGGCTGACCCCTATCACTGGG	3050	QY	4059	ACTTAGCTCTGAAGCACCGGAGGATGTTCCGTCTCAGCGTACTGAACCGCATTTA	4118
Db	545	ACGGTGAATGAATAATGTTGTCACCTTACCGGCAACCGGCATGACACCTATCATCTGC	604	Db	1625	ATTTAAACCCCGGTGAATCAAAAACCAATTTTATTTGGGATTAATGAACGCTGCTTCA	1684
QY	3051	CGTACGAGCGGCCGCCAAGCCATTTCTGGTGAGAACCGGACGCTGATGGGTTGAGCC	3110	QY	4119	ACATCAGCGCCCTCGGGGCTTTCCAGCTCTGGAGTGGCCAGCGGTGACAGAGCGCTG	4178
Db	605	CGTATGAGTCAGCCCGTCAGGCAATTTTATGCAAGATAAAACCTCACCGCATTTAGCC	664	Db	1685	GAGTGAATGATACGTAACCTGTATACATATATGAAGCTGGCTAATGSCGGAACAAATCCAG	1744
QY	3111	GTAACTCGGATGTCGCGCAGCTTATGACCCCTGCTCCATGCTGGCCATGAAGCCGATA	3170	QY	4179	GGTTAGCTGCTCTGCTGACATATCGCGCACTCTACCGAGTGAACCTCTCGGCTGACA	4238
Db	665	GTAAACAGACGTCAGCGGAATTAATGGACCAACATCGCTCTGGCTATTAAGACTGATA	724	Db	1745	AAITTTATGTTCCATTCGAGAACTGTCTCTCTTTATCGCTTCTGCTGCTGGCAGACA	1804
QY	3171	TTTTCACCGGAGCTGATCAGATACTGCGCGAAGAAATTAACAGACAGCTTACGAAGCAC	3230	QY	4239	TCACGACCTATCCGCTGGTGAGCTGTCAATGTGTGCTGCTCCCTCTTTCAGCGGG	4298
Db	725	TATCGCTGNAITGTATCAATCTTGTAGAGAAATTAACCGGAAATTCACAGAAC	784	Db	1805	TTTCATCATCTGACAGTGAATGAATTAATCAATGTTGTTGCTGCTCTCCCTATGTGAACA	1864
QY	3231	TCGTGAGTAAGAAATTTGTTGATATGCTTCCCTCTCACTGTTATCTTATGATGCACTTG	3290	QY	4299	TGGCGCGCGGCTCGCTGCTCCGATTAATGAGCTGACGCA-----GTTTCTGTACGACA	4349
Db	785	TGATGAAGAAAAATTTCCGGTACAGATGATGTAATTTTAAAGATGATGCTTCTTTGG	844	Db	1865	CGAAAAATTTGCCCCCTTTTCTGATACAGCAATTAACGCAATTAATCAGCTTTCTGTCCAAT	1924
QY	3291	CAACATTTTATGATCTTGTATTACGATGAGCTAATCTGTTATTTGCTAATTAAGCTGGACT	3350	QY	4350	CCACACCTGGCTCAGCGAGCAGGCTGACGCTCAGCGATGTTTCTGATGCTGACCA	4409
Db	845	CTCGCTACTACGATTTGCTTATGATGAATCAGTTTATTTGTCATCTCTCTCTCGGTA	904	Db	1925	GCACCCAGTGGCTGACACACAGAAATGCTGTGATGATGTTTCTGATGACCAACCG	1984
QY	3351	TTTTCAAATCAAAATGAATACATCAATTAATAGTCAATTAAGTGTGCTAATCTGAAATG	3410	QY	4410	CGCAGTACGGTACCTGCTGACCCCGCAATTTGAGAACCTGCTGCTTCCCTGCGCAACG	4469
Db	905	AGAAATACAAATCAACAGTATAAGATCAGCACTGATTAACATTTGGTCAATGACGGGA	964	Db	1985	ATAATTTACAGCACTGTCTTACCGCGGATATTGAAACCTTATCAGCACACTAAGTAATG	2044
QY	3411	AAAGCACTGTTTAAATACATACATTAATTAAGAACGCTGAGCGGAGACTCAACG	3470	QY	4470	GACTGTGGGCGCGTGAAGTGTTCGCGGAAACGCTCCCGCGATGCGCTCCCTTTATTG	4529
Db	965	ATGATACGGCAACCGCAAGATTGATTAAGCGAACCCGCAAGATTTCTACGATTCACATT	1024	Db	2045	GATTATCAACACTTTCACTCGGTGATGACAACTGATCGTGCAGCTGCGCGCTGATTG	2104
QY	3471	AGATTAACCTGAGCTTATACCTTATGGGATGGAACATATCTTTATTAATTTACGCGTG	3530	QY	4530	CGCGCCCATGAGCTGGAACGACCGATACCGGCAAGCGATGCTGACTTGGCGGAGCC	4589
Db	1025	TAACTATGAGAACTAATTTCCAATCAAGAAATGAATACAAATATAATTTTCAGTGTA	1084	Db	2105	CTGCAGCAATCAATGGAATTCAGCAAGACAGCAAACTATTTGCTGTGATTAATC	2164
QY	3531	TGTCAACGATATCAGAGGATAGTTTCAAACTAGGTCGTTAGGTTCTTAACAGTAGCAATC	3590	QY	4590	AGTTGAAGCAGAGGGGCTGACGCTGACGGAATTTATTTCTTTTGTGATGAATGCGCCC	4649
Db	1085	AAAAAACAGAACTGACCACTTGGATTTTGTCTCCAGATGGAGATAAGAATATATAT	1144	Db	2165	AGATAAAACCAAGGACTGACATTCGATGATTTTCATGATTAATGCGGCTAACCGTGATC	2224
QY	3591	TTTACTCTGGGATTAAGCTTCAAAAAGGGGTTGCTTATAGCAATCTCTGTTGAATAG	3650	QY	4650	CAATATGACGAGCGGGGCGCAGATGGCAGGGTTCTGCCACCTGTGGCAACTGGCAC	4709
Db	1145	ACCAAGATAAAAATTTTCGTCGCCATTTGCTAATACCAATTAACGATTTCCCAATTAATGA	1204	Db	2225	GCTCAGAGAAATGAACCAAGCAATGGTGGCTTTTTTGTGATGATCTGGGGCAACTTCTC	2284
QY	3651	ATGAAGGAAGTTAAATGATGGGATCACAATAGGATTTGAGTAGGAAA-----G	3698	QY	4710	TGATCATCCGACGACCGGCTCAGCACGCGGAGCTGACGCTGCTGGTGCAGCAGCCGG	4769
Db	1205	CGACAGCAATCAACAACGGTATTAACACTCCGCTTATGGCGAGTTAAACCAATCCGT	1264	Db	2285	TGATTTGTGGCAATATTGGACTCAGGGAACGAACTGACCTGTGTTGTTGTCACAAACCGG	2344
QY	3699	GGGGGGGATTAATCAACAGATAAATTTCACTCTGATGAATATGATCTCTGGCATTTCA	3758	QY	4770	GACGCTTCGCGCAGGATGGCACCATCTGCCCATGACCTGCGGCGCTTCGCGACATTA	4829
Db	1265	CGGATGCTCAATGCAATGCATCTTTAAATGATGAGTTCGCCGGTGATATATCC	1324	Db	2345	AGAAATTTCAATCAGAAACCAAGCACATGCAACATGATCTCCCACTTTTGAAGCGCTGA	2404
QY	3759	TTCTTAAATTAATAAGTTATCCGCTTATACGGCCACGGGCATGACGCGGGA	3818	QY	4830	CGCGTTTCACTGCTGTTTAAACCGCGGACGCAATGCGGGGAGGTCTTGACGCGCAC	4889
Db	1325	TGTTAAAGCTGAATAAAGCGAATTCGTTTGTATTAAGCCACAGGCAATCTCCAGAGAATA	1384	Db	2405	CCCGCTTCCATCTGTGATCATGCGTTGTGGAAGCTACGCGACAGAAATCTTTAAACAGCAT	2464
QY	3819	TATATCAAAATCACAATATTTTAAACGGTCTCACCATTTGACCATGCGGCTCTCAGTA	3878	QY	4890	TTGAGACCGGAGAACTGTCTGACGCTGCTGCGCGGCGCTGTCAAGAAATGACGAG	4949
Db	1385	CTGGCAAGTATAGAAAGTATTTATGATGATTAACCTTGAACCAATGTTGGGTA	1444	Db	2465	TGGAACTAGGAGCGCTGACTGCGGAACAAATTTGGCGGTGGCGTTTAAATTTGATGCTCAGG	2524
QY	3879	AAATCTTCTGGTCCGTTACCTGATCGTCACTATCAGCTTGTGTTGGCCGCTCACTGA	3938	QY	4950	ATGTGACCGGCGCTTGGCGCAGGTGAGGGGCGCGGTGAACAGGACAAACAGCGTGTCA	5009
Db	1445	AGCTGTTTTATGTTCAATATTAATGACGCACTATAATATTAGCGTCAGCGATGCGCTG	1504	Db	2525	TTGTGACACAACCAATTTGCAACAGACCGGTTTGGGAGTGAATACC-----TTTA	2572
QY	3939	TATTTGCAACGAACTACAGTGACGCGGTTTACGCGCGAAACCGGCTGTTTACCA	3998	QY	5010	CCTCTCTGGGAAGGTGGACAGGCTGACAGTGGCTGGACATGAGTGAGAACCTGTCCA	5069
Db	1505	TATTTGTCTATCAGATATCAGCAATATTTCCACTAAACAACCAACCCGATCTTTTACAA	1564	Db	2573	CAAACTGGAGAACTATAGATGTCTCTGCAATGGCTGGATGTGCTGTCTATTGGGTA	2632
QY				QY	5070	TTACGCCCATCCGCTCTGGCTAGCTGATTTGCCCTGAAAGTACATCAATGTGTCGATGACA	5129

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Db 5130 GTGACCGTTGTACAGCAGTGGCAGGTGTATCCGGTCTGCTGCAGGCGGGCTGAAAA 5189
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Db 2693 CGATGCCAAACATTTGATTTGGCAAGCCGCCAGTACTTTTGTGACGGCGGACTGAACA 2752
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RESULT 7
 US-10-754-115-13
 ; Sequence 13, Application US/10754115
 ; Publication No. US20040208907A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hev, Timothy
 ; APPLICANT: Schleper, Amanda
 ; APPLICANT: Bevan, Scott
 ; APPLICANT: Bintrim, Scott
 ; APPLICANT: Mitchell, Jon
 ; APPLICANT: Li, Ze Sheng
 ; APPLICANT: Ni, Weiting
 ; APPLICANT: Zhu, Baolong
 ; APPLICANT: Merlo, Don
 ; APPLICANT: Apel-Birkhold, Patricia
 ; APPLICANT: Meade, Thomas
 ; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
 ; FILE REFERENCE: DAS-104Xc1
 ; CURRENT APPLICATION NUMBER: US/10754,115
 ; CURRENT FILING DATE: 2004-01-07
 ; PRIOR APPLICATION NUMBER: US 60/441,723
 ; PRIOR FILING DATE: 2003-01-21
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 13
 ; LENGTH: 7569
 ; TYPE: DNA
 ; ORGANISM: Xenorhabdus nematophilus
 US-10-754-115-13

Query Match 7.2%; Score 1364.6; DB 18; Length 7569;
 Best Local Similarity 52.5%; Pred. No. 0;
 Matches 3943; Conservative 0; Mismatches 3064; Indels 510; Gaps 23;

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 Db 665 GTAATACAGACGTAGCGGAATTAATGGACCAACATCGCTACTGGCTATTAAAGACTGATA 724
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 Db 725 TATCGCTGAATTTGTATCAAAATCTTTGTAGAGAAATTTACCGGAAATTTCAACAGAAC 784
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QY 4239 TCCACGACTATCGCTGGTGAAGCTCTCAATGTTGCTTCCGCTCTCCCTTTTTCAGCGGG 4298
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QY 4590 AGTTGAAGCCAGAGGGCTGACCTGACGGAATTTATCTTTTGTGATGAATGCGGCC 4649
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Db 22138 GGCTGAAATGATGCTGATAAATTTGGCGCTTCAAGAAAGCCGTCATGTCGACAGTCTCG 22079
QY 8305 TTTTGAACGTTACAAAGTGTGTACGAGCGGAGTCAACACCGGCGGAAAAACAGSCCAT 8364
Db 22078 TTTTGAAGTTTCAATACGCTGTACGACGAAAGTATTTAGCTGTGTGAAAAACAGAGCAT 22019
QY 8365 GGAATTTGATCTCAGTTCCGTCGCTGTGCGCATCAACCGCGCGCTCTTTTGGCCGA 8424
Db 22018 GGATCTTTACCTCTCTTCATCGGTCTTGAGCACCGGACAGCCCTGCATATGGCGC 21959
QY 8425 GCGCGCGCGGATATGCTGCGCAATATTTTACGGGCTGGCGGTGCGGGGCTCCCGCTATGG 8484
Db 21958 CGCGCGCGGAGATCTCGTCCCAATATTTACGGTCTTGTGTGGAGGTTTCCCGTTTGG 21899
QY 8485 GGCACATATTTAAAGCCACCGCATCGCATCCAGGTGTCTCCGATGCCACCGCATATC 8544
Db 21898 GCGGCTTTTCAATGCCAGTGGATTTGGTATCGAAATTTCTGCTGAGCAACAGTATTC 21839
QY 8545 AGCGGCAAAATCAGCAGTCCGAAGTGTACCGCGTCCGCGGAGAGTGGGAAATCCA 8604
Db 21838 CGCAGCAAAATCAGCCAAATCAGAAATATACCGTCCGCGTCCGCAAGAGTGGGAAATCCA 21779
QY 8605 GCGTGTAGTGGCAGTCTGACGTGGCGCAGATTTGATGCCAGCTCGCGGCCATGSCAGT 8664
Db 21778 GCGCAATAATTCGCGGAAGCTGAGATAAAACAAATTTGATGTCAATTAGCGACGCTGCTGT 21719
QY 8665 GCGCGGGAAGGGCTGAGCTGCAGAAACTTACCTTTGAGACCCAGCAGACCCAGGACCA 8724
Db 21718 ACCTGTGAAGCGCAGTATTAACAAAATACTATCTGAAACTCAGCAGGACCAACTCA 21659
QY 8725 GCGCGAGTTGGCAATCTCTGAGAGTAAAGTTCAACAATACGGCTCTGTATGAGCTGGCTGG 8784
Db 21658 GCGCGAGTTAGCCCTTTCTGCAAAAGTAAATTCAGTAATGACGCGCTATACAACTGGCTCG 21599
QY 8785 GCGCAGGTTGTCGCGCAATTTATACAGTTCTATGACCTGGCAGTATCCGCTGCTGAT 8844
Db 21598 TGAACGTTTCCGCTATTTATATCAGTTTATGATTTTGGCGGTCTCACTCTGTTAAT 21539
QY 8845 GCGCAACAGGCTGCGCAGTGGGA---TAAATTCGAGACTAGGTGCTGTTATCCAGCGGG 8901
Db 21538 GGCAGAGCAAACTTATCAGTATGAAATGAAATATGCGGACGACACTTTATTAACAGG 21479
QY 8902 GGCTGTGAATGGGGCAAAATCCGCTGTGCTGGCGGGGAAACCCCTGATGCTGAATCTGGC 8961
Db 21478 TGCTTGGCAGTGGCACTTATGCGGTTTATAGCGGGTGAACCCCTGATGCTGAATTTAGC 21419
QY 8962 GCAGATGACAGCGCTGCTGATCGGGGATGACGGGCAATAGAGTGAACGGGACGCT 9021
Db 21418 ACAGATGGAATAAAGCTATTTTGAATAAAGATGAACGGGCACTGGAGGTCAACGAAACCGT 21359
QY 9022 CTGCTCTCGAGGTCTATACCAACCTTCGCGGAGGATGCGGCATTTCTCTGCGCCGACAA 9081
Db 21358 TTCTCTGGCTGAAGTGTATGCTGCTGTGACAGAAAT---AGTTTCAATTTAAAGATAA 21302
QY 9082 GGTGTGGAACTGTGTCAATGAGTTCGGGAGTTCGGGAGTTCGGAAGCAACGGAATTAACA 9141
Db 21301 AGTGACTGAGTTAGTCAATGAGGTGAAGGACAGTGCAGGACACACGCTTAACGGTTTGA 21242
QY 9142 GATGATCAACAGCAACTCCAGGCGCCCTCGAACTGGCTGACCTCGGTATCGGCAACGA 9201
Db 21241 CGTGAAGGAGACAACTGCAGCCAGCTCAAAATTAATCGGATCTGAATTTGCTACCGA 21182
QY 9202 TTATCCCGGTCTCCCTTGGCAATATGAGCGCATCAAAACAAATTAAGCGTCAACGCTCCGGC 9261

Db 21181 TTATCTCAGCGTTTAGTAAATACACGCGGTATCAACAAATCAGTGTGACGTTACTGTC 21122
QY 9262 GCTGTGCGGCGCTTATCAGGAGCTCGGTGCGGTTCTCAGCTACGCGGAAGTATGCTCAT 9321
Db 21121 CTTTTAGGCGCTTATCAGGATGTCCGGCAATACTAGAGTTATGCGGCGAGTACAATGAT 21062
QY 9322 GCGCGCGGTTGACGCGCTGGCGTCTCAACGGAATGAACGACAGCGGCAATTTCCA 9381
Db 21061 GCCAGTGGCTGCAAAAGGATTTGATCTCAGATGCGATGAATGACAGTGGTCAATTTCCA 21002
QY 9382 ACTGATTTCAATGACCGCGTTACTGCGGTTTGAAGGACTTCAGTTGATGACACAGG 9441
Db 21001 GATGATTTCAATGATGCTAAGTACCTGCCATTTGAAGGGCTTCCTGTGGCGATACAGG 20942
QY 9442 GACCTGACATGAGCTTCCCGATGCTGACGGCAAAACAGGCGATGCTCCTCAGTCT 9501
Db 20941 CACATTAACCTCAGTTTTTCCCGGTATCAGTGGTAAACAGAAAGCTTATTGCTCAGCT 20882
QY 9502 GAGCGACATCATCTCGCATATCCGTTTACACCATTTATCAGCTGAT 9545
Db 20881 GAGCGATATCATTTTGCATATCCGTTACACCATTCGTTCTTGAT 20838

RESULT 9
US-09-817-514A-3
; Sequence 3, Application US/09817514A
; Patent No. US20020078478A1
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 4431
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4431)
US-09-817-514A-3

Query Match 5.9%; Score 1108.8; DB 9; Length 4431;
Best Local Similarity 56.0%; Pred. No. 2.4e-268;
Matches 2493; Conservative 0; Mismatches 1732; Indels 225; Gaps 12;
QY 9598 ATGCAAAATCATCAAGACATATGCGCAATTAATGCCCCCACTGTCCTTCGCGGGCGGTGG 9657
Db 1 ATGCGAATTCACAAACATTCAGTGTACCGAGTGTCTATTACCCAAAGCGCGCGCT 60
QY 9658 GTACCGGCTCAAGGTTGATATCGCGGCGGACAGGCGCGATGTCGCGGACCCCTGAGT 9717
Db 61 ATTACCGGTATGGTGAAGCATTAACACAGCGCGGCGGATGGTATGGCCGCTTATCC 120
QY 9718 ATTCCCTTCGCGGTAGCCCGGTAGCGCCCGCTTACGCCCGCCACTTGAATTTATCAC 9777
Db 121 CTGCCATTAACCATTTCCCGCGGCGGTGTTACGACACCTCTCGCTCACTCTGAATTACAAC 180
QY 9778 AGCGGTCGCGGAAACGCGCCCTTTTGGCATTTGGCTGGGGTATCGCGGGTGTCTGTGTCCAG 9837
Db 181 AGTGAACCCGTAACAGCCCAITTTGCTCTCGTTGGGACTGCGGCGCTCATGSCAATTCGT 240
QY 9838 CGTCTGTCGCGCAACGAGACCACTACCTACGATGATCTGATGAATTCACCGGTCGCGAC 9897
Db 241 CGTCGACCAAGTACCGGCGTACCGAATTACGATGAACCGCATCTTTCTGGGGCGGAA 300

Db 2452 ACCGGATTACCTCGCGTAGAATATCGTTATCGCGCGGTATTGGCGTGGCGAATAGCAA 2511
 Qy 12115 GCTTTTCCGATTTCGCGACCCGTTTCACTGTCTCGGTTTCAGGAGAGGATGAGCAGACATAT 12174
 Db 2512 GCTTTTCGCGGTTTACGCCACGCTTTTACTCTCTGGAAGAGGGCAAGATGTTCACTG 2571
 Qy 12175 ACTCCG---GACACAGCAGACATTTCTGTTGTCAGGAGCCCTGAAAGCATCTCTGCTG 12231
 Db 2572 ACACCGGAAGATGACCATATCTATCTATGTTAAACCGGCGCTAAAGGTGAGCCACTG 2631
 Qy 12232 CGCAGTGAGTTATACCGTCCGATGCGCAGCAGCGCCGATATCCCTTACAGCGTCACT 12291
 Db 2632 CGTAGTGAATCTACCGGCTGATGAGCGGACACAGACAGATCCCTTATACAGTACT 2691
 Qy 12292 GAGTCTCGCCCGCAGGTACGGCTAGTTGAAAGCAATG---GAGACTACCGGCTGTTGG 12348
 Db 2692 GAATCCCGTCCACAGGTGCGCAATTAACAGATGGCGCCACCGCTTTCCCGGCTGCTCG 2751
 Qy 12349 CCGATGGCGCGAAAGCGGTACGTCTAGTTTATGAACGGTACCAATATCTCAATGC 12408
 Db 2752 GCCTCAGTGTGAAAGCGGTAGTTATCACTACGAACGTTATATCAGTATCCCCAGTGC 2811
 Qy 12409 CAACAGCAGCGGTACTCTCTCAGTGATGAATACGGTTTCCCACTGGGTGAGTCACTGTC 12468
 Db 2812 AATCAGGATATCAGTTGTCCAGTACCTTATTCGGGCAACCACTGAAAAGGTTTCCGTA 2871
 Qy 12469 AATTATCCAGACGCCCTCGTTCGGCGGACAAATCCATATTCGGCGTCTTACCGGCGAGC 12528
 Db 2872 CAATATCCCGCGCGCAACAAACCAATCCGTATCCCGATACCCCTACCGGATACG 2931
 Qy 12529 CTGTTCGCCAAAGTTATGACGAGCAGCAGCATATAGCCCTGCGGTTGCAACAGAGC 12588
 Db 2932 CTGTTTCCAGCAGTTATGACAGTCAACACACTATTTGGGATTAACCTGCCGACAACTC 2991
 Qy 12589 AGTGCAATCACCTTGTTCACCTGTCTGAGGGCAATTTGTTTGGGTTTGGCGAGGCG 12648
 Db 2992 AGTTGGCACCATCTTATT-----GGTAATGAGCTAAGAGTGTGGGATTTACCGGATGGC 3045
 Qy 12649 TCCGGGACAGATATTCAGTACTCTCGGACAAAGTGGCGGAAGGGGTCTGACGCTG 12708
 Db 3046 ACACGCAAGTATGCTTTTACTTACGATGCGCAACAGGTACCTGCTGATGGCTTAAATCTG 3105
 Qy 12709 GAACACCTGTGGCGCGCAAGCCTGCTCGGATAGTCAGGTCTCGGTACGCTGGCGGGT 12768
 Db 3106 GAAACCTGTGCTGAAATAGCCTGATTTCCGATGATAAACCTCGGAAATACCTCAAT 3165
 Qy 12769 CAGCAGCAAGTCTGGTATCTGGAATTCACAGAGCTTGGCCACCGTCTGCTCGGCCACTC 12828
 Db 3166 CAGCAACGAACGTTCTATACCGCAGCGGAAACCAAAACCGCTGAAACACCGCACACGA 3225
 Qy 12829 CCCCCAAGGTAGCTTTTATCGAAACGGCGGTCTGGATGAGGATGTTGTTCACTTCACTG 12888
 Db 3226 CAAGCGTTAATCGCTTTTACGAAACGGCGGTATTAACGGAATCTCTGTTATCCGCGTTT 3285
 Qy 12889 GCTGCTTACATTTGGAATG-----ACATCTCAGCAAGCCGTTTACCGGCA 12936
 Db 3286 GATGGCGGTATACGCCAGCAATTAACCGGAACTATGACACAGCGCGGATACCAACAA 3345
 Qy 12937 TCCGGATACCTTTTCCCTCAGGAGGGAAGCAGAACAGGCATTTGGACCCAGTGTGAC 12996
 Db 3346 GAGCCTTATCTGTTTCCACGACCGCGGAAACAA-----AGTTTGGTGGCGGCTCAA 3399
 Qy 12997 GGATATGTTACCTATGCGCGGAGAGCATTTCTGGCTACCGTATCTTCTTCCGGACAGT 13056
 Db 3400 GGCTATACCGATTACGGGAGGGAAGCAATTTTGGGCTCTGTGGCAACAGTAAACAGC 3459
 Qy 13057 ATGTTGACCGGCCAGTTTACCGTACCGGTGAGCGGTACGACTCGGTCACTACGAGTGG 13116
 Db 3460 CTGTTAACCGGGAAATGACGTTAAATGGTACTCACTATTTGTGTCACTACCCAAACC 3519
 Qy 13117 CAGGATCCGAGGATTTGACCAACGCGCATATGACTGCGGCTTCTGACGCGCCGCTC 13176
 Db 3520 CAAGATGCTCCCGGCTCACCGTCTCAGCAATTTATGACTGGCGGTTTTCTTCAACCAACG 3579

Qy 13177 CCGGTGACGGACCCCAATGATATCTGAGTCCGTCACCTCTGGATGCTCTGGCGGGTG 13236
 Db 3580 CAACTGACTGACATCAACGATAATGTGCATCTCATCCTTGGATGCTCTGGGACGCCCT 3639
 Qy 13237 ACCACCTTCGATCTCTGGGCAACGAGAAATGTTATTCACCGGTTACAGT----- 13287
 Db 3640 GTCACGCAACGTTTCTGGGGATCGAAAGCGGTGTTGGAACAGGTTACTCTTCATCAGAA 3699
 Qy 13288 GATGCCACGTTTTCGTTTCGGAACCGCGCAGCAGCGCTCTGCGGCTTGAACGCGGCCCTA 13347
 Db 3700 GAAAAACCATCTCTCCCAACCATATCGATACCGCTATTAATCTAAACCGGACCACTC 3759
 Qy 13348 CAGTAGACAGTCTGTTGTTATGTCAGGACACTTGG----- 13386
 Db 3760 CCTGTGCAAGTGTCTGTCTATGACCGGACAGTTGATGCCACTATTTAGTCAAGAA 3819
 Qy 13387 ----- 13386
 Db 3820 ACCTTCAACACATTAACGAGGAAGCAGGAGACGCTGCGTGATTCAGTATTATCAGC 3879
 Qy 13387 -----GGAGATGACGAAATGAGAAA----- 13408
 Db 3880 GAAAGATTGGCGTATTGCGCACTGACTCGCGCGCTGGCTACAAAGTCAAAAGATCATG 3939
 Qy 13409 -----TGCCCCCGCACGTCGTCGTCG 13431
 Db 3940 ACACCATTAGTTAAACTGTTAAACACAGCATTTGTTTACCTCCCAATACCTTACGCTG 3999
 Qy 13432 GCTACCGATCGCTATGACAGTGTATACCGGACAGCAGGTCGCGCAACAGGTGACATTCAGT 13491
 Db 4000 ACCACAGACCGTTATGACCGGACTCTGAGCAGCAAAATTCGCCAACAAAGTCGCAATTAGT 4059
 Qy 13492 GACGGTTTGGCGGTGAGTTGCAATCGGCAACCGCGACCGCGGCGGCAACGCTGGGCA 13551
 Db 4060 GATGGTTTGGCGGTCTGCTACAAGCGTCTGTACGACATGAGGCGAGGCGGAGCTGGCAA 4119
 Qy 13552 CAGGAGCGGACGCGCAAACTGTTGACGCGCACTGACGGATTGCGGTCACCTAGCAACG 13611
 Db 4120 CGTAACCAAGACGTTCTCTGTTGACAAAGTGA-----GAATACC 4161
 Qy 13612 AATTTCCGTCGCGGTACCGGAGGCGGATGATGACAAATAAAGGTCTGCTGTCGG 13671
 Db 4162 AAAACGCGTTGGCGGTACCGGACGCGACCGAATATGATAATAAAGGGCAACGATACGC 4221
 Qy 13672 GTTTATCAGCCCTATTTTGTGACAGTTGGCAATATGTCAGTATGACAGTCCCGCCAG 13731
 Db 4222 ACTTATCAGCCCTATTTCTCAACGACTGGCGATATGTCAGTATGACAGCGCCGAA 4281
 Qy 13732 GACCTGTATGCCGACACGCACTTTTACGATCCGAGCGGCAATGCGAGGTTATTCAG 13791
 Db 4282 GAAGCTATGCGGATCTCATATTTATGATCCAAATTTGGCGGAGAAATCCGGGTTATCT 4341
 Qy 13792 GCAAAAGGTGAACGCGGACAGGTCTGTATATACCCGTTGGTTGTGGTCAAGTGAACGAG 13851
 Db 4342 GCAAAAGGTGCTGCGGCAAGCAATATTTCCCGTGGTTTACCGTGTGAGGATGAG 4401
 Qy 13852 AATGATACCG 13861
 Db 4402 AATGATACCG 4411

RESULT 10
 US-10-754-115-22
 ; Sequence 22, Application US/10754115
 ; Publication No. US20040208907A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hev, Timothy
 ; APPLICANT: Schleper, Amanda
 ; APPLICANT: Bevan, Scott
 ; APPLICANT: Bintrim, Scott
 ; APPLICANT: Mitchell, Jon
 ; APPLICANT: Li, Ze Sheng

11395 GTGAATATCCCGGTTTACCGAGTCAGTACAGTTTAAACCTGACAGATATTGCTG 11454
1795 ATGATTTGCGGGATTCAGCAATCTGCCGCGAGTTTAACTCTGATCGAGTTCATCTG 1854
11455 GCCGATACCGAGCGGTTCCGGTACACCGAGCTGATTTATGCGATGAGTACCGGTTAGTC 11514
1855 GCCGATTTGATGGAGCGGCGCTGCGGATTTGATTTATGTTATGCTGACCGCTCGGAT 1914
11515 ATTTATTTCAACAGAGTGTATTTATTCGCGAGCGGATACGCTGCTCTTGGCGAAA 11574
1915 ATTTTCAGCAATGAAGTGGCAACGGTTTGGCAAAACCAATTCACATCTCTTTTCTGAC 1974
11575 GGTGTGCGCTATGATCGCACTGCACTGCTCAAGTGGCGATATCAAGGGGCTGGGGTG 11634
1975 GGCTGGGTTTGTATGATACCTGCGAGTTGCAAGTAGCGATGATACAGGGTTAGCGGT 2034
11635 CTTAGCGCTGTTACTGAGCGTCCCGCATGTGCGCCCTCATCATCTGGGTGTGCCATTTATCG 11694
2035 GTCAGCGCTGATCTTAAGCGTACCGCATATGGCGCCACATCATTTGGCGCTGCGATCTGACC 2094
11695 GCAGACAAACCTGTTGTTGAATGGCATGAACAAACATATGGGGCGCGGATGCACTG 11754
2095 AACGCGAAACCGGTTTACTCAGTGAACCGCAACAAATATGGGGCCCAATCACACCTTG 2154
11755 CACTATCGCAGTTCCGGTGCAGTTCTGGCTGGATGAGAAAGCCGAGCACTGGCGGAGGC 11814
2155 CATTAACGATGCTCTGTCAGTTCTGGCTGGATGAAAGCTGCGGATTTGGCTACCGGA 2214
11815 AGTTCCCGCTGCTACTACCTGCCATTTACATTCGATACCTGTGGGCTTGGGTGTCAG 11874
2215 CAAACACCGGCTCTGTTACCTGCCCTTCCCGGTCCTACACCTTTGGCAAAACAGAAACCGAG 2274
11875 GATGAGATCACCGGTAAACGCTCTGGTCAGGACGCTGCTTTATGCCACCGGCTCTGGAC 11934
2275 GATGAATACGCGCAATAGTTAGTGAACCAAGTATGCTTATGCTCACGGCGCTGGGAT 2334
11935 GGCAGAGAACCGAGTTTCGGGGGTTTGGTTTGGATCAGGATACCGATACCTTG 11994
2335 GGAAGTGAACGGAAATTCGTGGCTTTGGTTATGTTGAGCAGACAGACGCATCACTC 2394
11995 GCAAGCAGGGTACGGCAGCGAACTGAGTATGCCCTTCTGTGACCGGAACTGGTATGCC 12054
2395 GC---TCAAGGCAATGCGCGGAACGTACACACCGGCACTCAACCAAAAGCTGGTATGCC 2451
12055 ACCGGGTACCGGCACTAGACGAGCTCTGCCGAGCGTATGGCGAAACAGTACCGGCC 12114
2452 ACCGGATTAACCTCGGTAGATAATGCGTTATCCGCGGGTATTTGGCGTGGCGAAGCAA 2511
12115 GCTTTTGGCGATTTCCGACCCGTTTCACTGTGCTTCAAGGAGGATGAGCAGATAT 12174
2512 GCTTTTGGCGGTTTACGCCACGTTTACTCTCTGGAAAGAGGGCAAGATGTTCCACTG 2571
12175 ACTCG---GACGACAGCAAGAATCTGTGGTTCGACGAGCCCTGAAAGGCATCTGCTG 12231
2572 ACACCGGAAGATGACCAATATCTATATCTGTTAAACCGGCGCTAAAGGTGAGCCACTG 2631
12232 CGCAGTGAAGTTATACGTCGCGATGCGACGAGCCGCGGATATCCCTTACAGCTCACT 12291
2632 CGTAGTGAACTTACGGGCTGGATGGCAGCGCAACAGATCCCGCTATACAGTGACT 2691
12292 GAGTCTCGCCCGCAGGTACGGCTAGTTGAAGCGAATG---GAGACTACCGGTTGGTGG 12348
2692 GAATCCCGTCCAAGGTGGCCAAATTAAGAATGGCGCCACCGTTTCCCGGTGCTCTGG 2751
12349 CCGATGGGCGGAAAGCGGTACGTGATTTATGAACGGTATCAAAATGATCTCAATGC 12408
2752 GCCTAGTCGTGGAAAGCGGTATTTACTACAGCAAGTATATCAAGTATCCCAAGTGC 2811
12409 CAACAGCAGCGGTACTCTCTCAGTGTGATACGTTTCCCACTGCGTCAGTCACTGTC 12468
2812 AATCAGATATACGTTGTCAGTGACCTATTCCGGCAACCACTGAAACAGGTTTCCGTA 2871
12469 AATTATCCAGACGCCCTCGCTCGGCGGAACAATCCATATCCGGCGTCTTTACCGGCGAG 12528

2872 CAATATCCCGCGCAACAAACCAACCAATCCGTATCCGATACCTTACCGGATACG 2931
12529 CTGTTGCGCAACAGTTATGACGAGCAGCAGATATTAAGCTGGGGTTGCAACAGAGC 12588
2932 CTGTTGCGCAGCAGTTATGACGATCAACACAGCTATTCGATTAACCTTCCGCAATCC 2991
12589 AGTGACATCACTTGTGTTTCACTGTCTGAGGGGCATTGGTTGTTGGGGTTGGCGAGGCG 12648
2992 AGTTGGCACCATCTTATT-----GGTAATGAGCTAAAGATGTGGGATTTACCGGATGCC 3045
12649 TCGCGGAGCAGTATTCACGTACTCTGCGGACCAACGTCGCCGGAAGGGGTCTGACGCTG 12708
3046 ACACGAGTGAATGCTTTACTTACGATGCCAAACAGGTACTGTGATGGCTTAATCTG 3105
12709 GAACACCTGTTGGCGCCCGAAAGCCTGCTCGGATGATCAGGTGCGGTACGTTGGCGGT 12768
3106 GAACCCCTGTGCTGAAATAGCCTGATTCGCGATGATAAACCTCGCAATACCTCAAT 3165
12769 GACGACAGTCTGATCTGATTCAGATTCACAAAGCTTGCACCGTCCGCTGCTCGGCACCTC 12828
3166 CAGCAACGAAACGTTCTATACCGACGGGAAAAACCAACACCGCTGAAAAACCGCACCA 3225
12829 CCCCCAACAGGTAGCTTTTATCGAAACCGCGCTGCTGGATGAGGGTATGTCAGTTCACTG 12888
3226 CAACGCTTAATGCTTTTACCGAAACGGGGTATTAACCGAATCTCTGTTATCCGCGTTT 3285
12889 GCTGCTACTATTTGGATGA-----ACATCTCGAAGAACCGGTTTACCGGCAA 12936
3286 GATGGCGTATTAACGCGACAGAAATTAACGCGGAATACTGACACAGCGCGGATACCAACAA 3345
12937 TCGGATACCTTTTCCCTCGAGCGGAGGAGCAGAACAGGCAATTTGAGACCCAGTGTGAC 12996
3346 GAGCCTTATCTGTTTCCAGCACCGCGCGAAAAACAA-----AGTTTGGGTAGCGGTCAA 3399
12997 GGATATGTTACCTATGCGCGCAGACGATTTCTGGCTACCGCTATCTTTTGGGACAGT 13056
3400 GGCATATACGATTAACGAGCAGCAACATTTTGGCGCTCTGTCGACAAAGTAAACAGC 3459
13057 ATGTTGACCGGCGCAGTTACCGTGAACGGGTGACGGTACGACTGCGGTATACAGCATGG 13116
3460 CTGTTAAACCGGAAAAATGACGTTAAATGGGATCTCACTATGTTGTCATCAACCCAAAC 3519
13117 CAGGATCGCGAGGATTTGTCACACAGCGGATGACTGCGGCTTCTGACGCGCCGTC 13176
3520 CAAGATGCTGCGCGCTCACCTCTCAGCAATTAATGACTGGCGTTTCTCAACCAACG 3579
13177 CCGGTGACCGGACCCCAATGATTAATCTGCACTGCTGCTGATGCTCTGGGCGCGGTG 13236
3580 CAACGACTGACATCAACGATTAATGTCATCTCATCACCTTGGATGCTCTGGAGCGCCT 3639
13237 ACACCTGCGATTTCTGGGCGACGAGAAATGTTATTCGACCGGTTACAGT----- 13287
3640 GTACCGCAACGTTTCTGGGGATCGAAAGCGGTGGCAACAGTTTACTCTTTCATCAGAA 3699
13288 GATGCCAGTTCTGCTTCCGACCGCGCAGCAGCGCTCTGCGTTGACGCGGCCCTTA 13347
3700 GAAAAACCAATCTCTCCACCAACGATATCGATAACGCTATTAATCTAACCGGACCACTC 3759
13348 CCAGTAGCACTGCTGTTGTTATGTCACGCAAGTTGG----- 13386
3760 CCTGTGCGACAGTGTCTGCTTATGACCGGACAGTTGGATGCCACTATTTACGTCAAGAA 3819
13387 ----- 13386
3820 ACCTTCAACATTAACGAGGAAGCAGGAGACGCTGCTGATTCAGTATTATCAGC 3879
13387 -----GGAGATGACCAATGAGAAA----- 13408
3880 GAAGATTGGCGTATTTGGCACTGACTCGCCCGCTTGGTACAAAGTCAAAAGTCACT 3939
13409 -----TGCCCCCGACGTCGTGCTG----- 13431

Db 3940 ACACCATTAAGTTAACTGTTAAACACAGCATTTGGTTTACCTCCCAATACCTTACGCTG 3999
Qy 13432 GCTACCGATCGCTATGACAGTGATACCGGACAGCAGGTCCGCCAAACAGGTGACATTCAGT 13491
Db 4000 ACCACAGACGTTATGACCGGACTCTGAGCAGCAAAATTCGCCAAACAGTCGATTTAGT 4059
Qy 13492 GACGGTTTTGGGGTGAGTTGCAATCGGCAACCGCGCAGCGGCAACGCTGGCAA 13551
Db 4060 GATGGTTTTGGCGCTCTGCTACAGCGCTCTGTACGACATGAGGCGAGCGGAAGCTGGCAA 4119
Qy 13552 CGAGGACGCGACGCAAACTGGTTCAGCGCCAGTCAGCGATTGCGGTCAGTGTAGCAAG 13611
Db 4120 CGTAACCAAGCGGTTCTCTGGTGACAAAGTGA-----GAATACC 4161
Qy 13612 AATTTCCGCTGGGCGGTACCGGAGCGCGAGGTATGACAAATAAGTCTGCTGTTCCG 13671
Db 4162 AAAACGGTTGGGCGGTACCGGAGCGCACCGAATATGATATTAAGGGCAACGATACGC 4221
Qy 13672 GTTTATCAGCGGTATTTTCTGGACAGTTGGCAATATGTAGTGATGACAGTCCCGCCAG 13731
Db 4222 ACTTATCAGCCCTATTTCTCAACGACTGGCGATATGTAGTGATGACAGCGCCAGAAA 4281
Qy 13732 GACCTGTATCGGACAGCACTTTTACGATCCGACGCGGATGCGGATGCGAGTTATACG 13791
Db 4282 GAAGCCTATCGGATCTCATATTTATGATCCAAATTGGGCGAGAAATCCGGGTTATTA 4341
Qy 13792 GCAAAAGGTTGAACGCGGACAGGTGCTGTATACCCCGTGTGTTGGTTCAGTGAAGACGAG 13851
Db 4342 GCAAAAGGCTGGCTGCGCCAAAGCCAAATATTTCCGTTGGTTTACCGTGAGTGAGATGAG 4401
Qy 13852 AATGATACCG 13861
Db 4402 AATGATACCG 4411

RESULT 11
US-10-609-113-42
; Sequence 42, Application US/10609113
; Publication No. US20040110184A1
; GENERAL INFORMATION:
; APPLICANT: Bintrim, Scott
; APPLICANT: Bevan, Scott
; APPLICANT: Zhu, Baolong
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 4434
; TYPE: DNA
; ORGANISM: Photorhabdus strain w14
US-10-609-113-42

Query Match 5.9%; Score 1108.8; DB 17; Length 4434;
Best Local Similarity 56.0%; Pred. No. 2.4e-268;
Matches 2493; Conservative 0; Mismatches 1732; Indels 225; Gaps 12;

Qy 9598 ATGCAAAATCATCAAGCATGGCCATTACTGCCCCACAGTTGCTTCGGGGGCGGTGCG 9657
Db 4 ATGCAGAAATTCACAAACATTCAGTTTACCGAGCTGTCATTACCRAAAGGCGGCGGCT 63
Qy 9658 GTACCGGGCTCAAGGTTGATATCGCGGCGGCGAGGCGGATGTTGGCGGACCCCTGAGT 9717
Db 64 ATTACCGGTATGGTGAAGCATTAACACAGCGCGGCGGATGATGTCGCGCTTATCC 123

Qy 9718 ATTCCCTTCCGGTTAGCCCCCGGTCCGGGTTACGCCCCCACTGGGGCACATTAATATCAC 9777
Db 124 CTGCCATTACCCATTTCCCGCGGGCGTGGTTACGCACCCCTCGCTCACTCTGAAATTAACA 183
Qy 9778 AGCGGTTCGGGNAACGGCCCTTTTGGCATTTGGCTGGGTTATCGCGGTGCTGCTGTCCAG 9837
Db 184 AGTGAACCGGTAAACAGCCCATTTTGTCTCGTGGGACTTGGCGGCTCATGGAATTCGT 243
Qy 9838 CGTCTGTCGCGCAACCGAGCACCTACTACGATGATACATGATGAATTCACCGGTCCGGAC 9897
Db 244 CGTGCACCATGATACCGCGCTACCGAATTAAGATGAACCGATACTTTCTGGGGCCGAA 303
Qy 9898 GGTGAGGTCTGTGTCGGGCACTACCGGTCTGTGGCAACCAAGAGACGCGAGGCCACC 9957
Db 304 CGTGAAGTCTGTGTCGTAGCATTAATGAGCGAGTCAAGCTGATATCCGCACTGAATCC 363
Qy 9958 TCATCTACTGGGNAACCCAGCGGAAGTTTCAAGTTTCAAGTTTACGTTTACGTTTACGTA 10017
Db 364 TCATTCAGGGCATCAATTTGGGTGCGACCTTACCCTTACCTGTTATCGCTCCCGCTA 423
Qy 10018 GAGGGTAGTCTCAGCGCCCTTGAGCGTTGGCTGCCCGCGACGAGACAGAAACGGAATTT 10077
Db 424 GAAAGCCACTTTTAAACCGGTTGGAATACTGGCAACCCCAACACCGCGCAACGATTT 483
Qy 10078 TGGGTGTTATATACCCCTGACGACAGGTGGTCTCTGTGGGCCAAATGCGCAGGTTCG 10137
Db 484 TGGCTGATATACAGCCCCGAGGACAGGTCCATTTACTTGGCAAAAATCTCAGGACGT 543
Qy 10138 ATCAGCAACCCACAGCCCAACAGAGCGCGGTTTGGTGTATGAGTCTCTCGGTATCA 10197
Db 544 ATCAGCAATCCACTCAATGTTTAAACCAACAGCGCAATGGCTGTTGGAAGCTCGATATCA 603
Qy 10198 CTTTACCGGGAACAGATGATTTACCAATACCGTGCAGAGATGATGACGGTTGTAGCAG 10257
Db 604 TCCACAGCAACAGATTTATTAATATCGCGCTGAAGATGAGCAGGTTGTGAAC 663
Qy 10258 GCGAGCGGACGCGCACCCGCGCGCGCCCAACGTTTATCCGTTGGCGGTCTGTGAT 10317
Db 664 GACGAGCTAGCAGCCCAACCCAGCGCAACCGTTTACGGCTACCTGCAACAGTACATTAC 723
Qy 10318 GGTAAACGCTGACCGCGCAGCGAGCTTTCCTTACACTAAACGAGATGACCCACTTAAT 783
Qy 10375 AGCTGCTGTTTATCTGTTGTTTATGATGAGGTAGCTCGGTGCTGCTGAAGCG 10434
Db 784 GGCTGGATGTTCTGTTTATTTGACTACGTTGAGCGCAAAACAGCTTATCTGAATG 843
Qy 10435 CCGGCTGCGCAACACACAGGAAGTGGGAGTGGCTGTGTCGTCAGGATGTTTTCGCGG 10494
Db 844 CGGCTGTTTAAAGCCACAGGCA-----ATTGGCTTTCGCAAAAGACCGTTTTCGCGT 897
Qy 10495 TATGAGTTTGGTTTAACTCGGAGCTCGCGGCTGTGCGGTGAGTTTGTGTTTCCAT 10554
Db 898 TATGAGTACGGTTTGAATTTGCGTACTCGCGCTTATGCGCCCAAACTACTGATGTTT 957
Qy 10555 TACCTAGGTGTTCTGCGGGGAGTTTCGGGAGCAATGATGCGCGCAGCATTTTCTCGC 10614
Db 958 CGTCTACAAACCCCTATCTGTCAGGCAAAAGGGGATGATGAACCTGCGCTAGTGTCC 1017
Qy 10615 CTGTTCTGGACTACAGGGAAGTCTCTTCACTCAGTCTGCTCGAGAACGTCACAGGTG 10674
Db 1018 CTGATCTGATATTAACGAAACCGGATGGTTCAGTACGCTCTGTTCTGTCGCGGTA 1077
Qy 10675 GCTTATGAGTCGAGCGGAGCTCTTGTGCTTTCGCGCACTGTCATTTGGGGTGGCAAC 10734
Db 1078 GGCCATGAGGACAAACACCGGTTACCGGCTGCCACCACTGGAATCTGCGCTATCAGCCT 1137
Qy 10735 TTTTACCCCGGACATTTGCGCATGCGAGACGCTGACGATATGGCAGTTGAGTTG 10794
Db 1138 TTTGAGCCAGAACAAACCGCACTCTGGCAATCAATGATGATGCTGCAAAATTTCAACACC 1197
Qy 10795 CTTCAACCCCTATCAGCTTGTAGACCTTAAACGGGGAAGTGTGGTGGTATCTCTGTATCAG 10854

1198 ATTACGGCTGGCAACTGCTTGACCTGAAGGAGAGGGCGTGCCCGCACTCTCTATCAG 1257
10855 GACAGCGGTGCTGGTGTGATCCGTGAACCGGTGACCGAGTCGGGGGATGATCCGATGCT 10914
1258 GATAGAAATGGCTGGTGTGATCGATCTGCCCAACGTCAGCGCGGGGAGAGATGAATGCG 1317
10915 GTGACCTGGGGGCGGCTGGGCGCTGCCGACATGCCCGCTTGTGATACACGCGCATC 10974
1318 GTCACTGGGGGAAAATGCAACTCTTCCCATCACACCGAGCTGTGCAGGATAACGCCTCA 1377
10975 CTGGCGGACTTAATGGGATGTGCGCTGGAGTGGGTGGTTACCGCCCCCGGTGGCG 11034
1378 CTGATGGAATTAACCGGTGACGGGCAACTGGACTGGGTGATACCGGGCGGGGCTAAGG 1437
11035 GGGATGATGATCGCACCCCGCGCGGACTGGTTCGATTTTCAACCCCGCTGTGAGCCTTG 11094
1438 GGCATACACAGCCAACACCGGATGGCAGTTGGACGCGTTTACGCGCATTTACATGCCCTG 1497
11095 CCGGTAGATATCGGATCCAAAGCAGTGTCTCGGCTCTATTTCGGCAAAAACGATGTTGG 11154
1498 CCGATAGAAATTTCTCATCTCTCGCGCTCAACTTGGCGATTTAATGGGAGCCGGGCTGTCC 1557
11155 GACATGCTGCTATCGGCGCGCAGTGTTCGCTCTATTTCGGCAAAAACGATGTTGG 11214
1558 GATTAGTGTAAATGGTCCAAAAGTGTGGCTTATATGTCATTAACCGGTGATGTTT 1617
11215 AATAAAGGGAGACCTGCAGCAAAACGAAAGACTCACTCTGCGGTCCCGGGGTGAC 11274
1618 ACCGAAGGCGGATGTGTGCAATCCGGTGTATCACCTGCGCTACCGGCGCGCAT 1677
11275 CCAGCTACCTCGTGGCTTCAGTGATATGGCTGGCAGTGGACAGCAGATTTTGACGGAG 11334
1678 GCCGTGAAGTGTAGTGCAATTTAGTGACGTACTGGGTTCAAGGCCAAGCACTCTGGTTGAA 1737
11335 GTGCGTGTAAATGGAGTACGTTACTGGCCAAACCTGGGCAACGCTGTTTCGGTACGCG 11394
1738 GTTAGTGCACTCAAGTCACTGCTGGCGAATCTGGGCGATGGCGGTTTGGTCAGCCA 1797
11395 GTGAATATTCGGGTTTTAGCCAGTCAGTGACTACGTTTAAACCTGACCAAGATATTCGTG 11454
1798 ATCGTATTCGGGGATTCAGCCAACTCTGCGCCAGTTTTTAATCCTGATCGATTCATCTG 1857
11455 GCGGATACCGACGGTTCGGTACCAAGGACCTGATTTATGCGATGAGTACCGGTTAGTC 11514
1858 GCGGATTTGGATGGGAGCGCCCTGCGGATTTGATTTATGTTCAATGCTGACCGTCTGGAT 1917
11515 ATTTATTTCAACACAGATGGTAAATTTATTTGCGCGACCGCATACGCTGCTCTTGCAGAA 11574
1918 ATTTTCAGCAATGAAGTGGCAACGGTTTGGCAAAACCAATTCACTCTCTTTTCCGTGAC 1977
11575 GGTGCGGTATGATCGCACTGCACTGTCGCAAGTGGCGGATATCCAGGGGCTGGGGGTG 11634
1978 GGCCTCGGTTTGTATGATACCTGCCAGTTTGAAGTAGCCGATGTAACAAGGTTAGGCGTT 2037
11635 CCTAGCCTGTACTGAGGTCCCGATGTGCGGCTCATCATCTGGGTGTGCCATTTATCG 11694
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2098 AACGGAACCGTGGTTACTCAGTGAAAGCAACAAATATGGGGCCCAATCACACTTG 2157
11755 CACTATCGAGTTCGGTGCAGTTCTGGCTGGATGAGAAAGCCGAGCACTGGCGGAGGC 11814
2158 CATTACCGTAGTCTGTCCAGTCTGGCTGGATGAAAAGCTGCGGCAATGGCTACCGGA 2217
11815 AGTTCCTCCCTGCTTACCTGCCATTTAATTGCATACCTGTGGGTTTCGGTGTGCGAG 11874
2218 CAAACACCGGTCTGTTACCTGGCCCTTCCCGGTTCCATACCTTTGGCAAAACAGAAACCGAG 2277
11875 GATGAGATACCGGTAAACCGTCTGGTCAGCGAGTGTCTTTATCGCCACCGGCTCTGGGAC 11934

2278 GATGAATCAGCGGCAATAAGTTAGTGACCAAGCTTACGTTATGCTCACGCGCTTGGGAT 2337
11935 GGGCAGGAACCGGAGTTTCGGGGGTTTGGTTTGTGATCAGGGATACCGGATACCTTG 11994
2338 GGACGCTGAACCGGAATTTCTGGCTTTGTTTATGTTAGCAGACACAGACCATCAACTC 2397
11995 GCAAGCCAGGATACCGGACGGAACGTAGTATGCTTCTGTGAGCCGGAATGTTGATGCC 12054
2398 GC---TCAAGGCAATGCGCGCGAAGCTACACCAACCGGCACTCACCAAAAGCTGGTATGCC 2454
12055 ACCGGGTACCGGCAAGTACAGAGGCTCTGCCGGAGAGCTATTGGCAAAACGATGCCGCC 12114
2455 ACCGATTTACCTGCGGTAGATAATGGGTTATCCGCGGGTATTTGGGTGGCGATAGCAAA 2514
12115 GCTTTGCGGATTTCCGACCCGTTTCACTGTCCGTTTCAAGAGAGGATGAGAGACATAT 12174
2515 GCTTTCCGCGGTTTACGCCAGCTTTTACTCTCTGGAAAGAGGCAAGATGTTCCACTG 2574
12175 ACTCCG---GACGACAGCAAGACATTTCTGGTTGACAGAGCCCTGAAAAGGATCTGCTG 12231
2575 ACACCGGAAGATGACCATTAATCTATCTGTTTAAACCGGGCGCTAAAAGGTCAGCCACTG 2634
12232 CCGAGTGTGATTAACGGTCCGATGGCAGCAGCGAGCGATATCCCTTACAGCGTCACT 12291
2635 CGTAGTGAATCTTACGGGCTGATGGCAGCGCACAGCAACAGATCCCCTATACAGTACT 2694
12292 GAGTCTCGCCCGCAGGTACGGCTGTGTAAGCGAATG---GAGACTACCCGTTGTTGGT 12348
2695 GAATCCCGTCCACAGGTGCGCAATTAACAAGATGGCGCCACCGTTTCCCGGTTGCTCTGG 2754
12349 CCGATGGGCGGGAAGCGTACGTCAGTTTATGAAACGTACCAACAATGATCCTCAATCG 12408
2755 GCTCAGTCTGGAAGCGGTAGTTATCACTACGAACGTTATCAGTATCCCCAGTGC 2814
12409 CAACAGCAGCGGTACTCTCTCAGTGTGATGAATACGGTTTCCCACTGCGTCAGGTCAGTGC 12468
2815 AATCAGGATATCAGCTGTCTCAGTGACCTATTTCGGGCAACCACTGAAACAGGTTTCCGTA 2874
12469 AATTATCCACGACGCGCTCCGTCCGGGACAAATCCATATCCGCGGTCTTACCGGCGAG 12528
2875 CAATATCCCGCGCAACAAACCAACCAATCCGTATCCCGATACCCCTACCGGATAGG 2934
12529 CTTGTCGCCAACAGTTATGACGAGCAGCAGAGATATTACGCTGGGTTGCAACAGAGC 12588
2935 CTGTTTGCAGCAGTTATGACGATCAACAACAGCTATTGCGATTAACCTGCCGACAATCC 2994
12589 AGTCACATCACTCTGTTTCACTGTCTGAGGGGCATTTGGTTGTTGGGGTTGGCGAGGCG 12648
2995 AGTTGGCACCATCTTATT-----GGTAATGAGCTAAGAGTGTGGGATTTACCGGATGCG 3048
12649 TCGCGGAGCAGTGTATTCAGCTACTCTGCGGACAAAGTCGCCGGAAGGGGCTGTGACGCTG 12708
3049 ACACGAGTGATGCTTTTACTTTACGATGCCAAACAGTACCTGTGCGATGGCTTAAATCTG 3108
12709 GAAACCTGTTGGCGCCCGGAAAGCTGCTCGGATAGTACGCTCGGTACGTTGCGGGGT 12768
3109 GAAACCTGTTGCTGTAATAATAGCCTGATTCGCGATGATAAACCTCGCGAATCACTCAAT 3168
12769 CAGCAGCAAGTCTGGTATCTGATTTCAACAAGACGTTGCGCCGCTGCTCTCGCCGACATC 12828
3169 CAGCAACGAACTTCTATACCGACGGGAAAACCAACACCCCTGAAAACACCGACACGA 3228
12829 CCCCCCAAGGTAGCTTTTATCGAAACGCGCGTGTGCGATGAGGGGTATGTTGATGTTCACTG 12888
3229 CAAAGGTTAATCGCCTTTACCGAAACGCGGATTTAAACGGAATCTCTGTTATCCGCGTTT 3288
12889 GCTGCTCATGTTGATGA-----ACATCTCGAGCAAGCCGGTTTACCGCAAA 12936
3289 GATGGGTTTATTCGCCAGACGAATTAACGGGAATTAAGTACAGAGCCCGGATACCAACAA 3348
12937 TCCGGATACCTTTTCCCTCGAGGAGGAAAGCAGAACAGGCAATTTGGAGCCCAAGTGTCTAG 12996
3349 GAGCCTTATCTGTTTCCACGCAACCGCGGAAACAA-----AGTTTGGGTAGCGGTCAA 3402

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QY 12997 GGATATGTTACTATGCGGCGCAGAGCAATTTCTGGCTACCGCTATCCTTTCCGGACAGT 13056
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Db 3403 GGCATATACCGATTACGGGACGGAACACAAATTTTGGGCTCTCTGTCACAAAGTAAACAGC 3462
QY 13057 ATGTTGACCGGCGCCAGTTACCGTGACCGGTGACCGGTACGACTCGCTCATCAACGAGTGG 13116
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Db 3463 CTGTTAACCGGAAATGACGTTAAATGGGATACTCACTATTGTGTCATCACCCMAACC 3522
QY 13117 CAGGATCCGCGAGGATTTGACACACAGCGCACTATGACTGGCGCTTCTTGACGCCCGTC 13176
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Db 3523 CAGATGCTCGCGCCCTACCGTCTCAGCCAAATATGACTGCGGTTTCTCAACCAACG 3582
QY 13177 CGGATGACGACCCCAATGATAATCTGCAGTCCGCTCACTCTGATGCTCTGGGCGGGTG 13236
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Db 3583 CAACTGACTGACATCAACGATATGCTCATCTCATCACCTTGGATGCTCTGGGAGCGCCT 3642
QY 13237 ACACCCCTGGATTTCTGGGCGACGGAGATGGTATGCGCACCGGTTACAGT----- 13287
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Db 3643 GTCACGCAACGTTTCTGGGGGATCGAAAGCGGTGTGGCAACAGGTTACTCTTCATCAGAA 3702
QY 13288 GATGCCACGTTGTCGTTCCGGACGCGCAGCAGCGCTCTGGGTTGACGCGCCCTTA 13347
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Db 3703 GAAAMACATCTCTCCACCAAAACGATATCGATACCGCTATTAATCTAAACGCGACACTC 3762
QY 13348 CCAGTAGCACAGTCTCTGGGTATGTCAACGACAGATTGG----- 13386
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Db 3763 CCGTGCACAGTCTCTGGTCTATGACACGCGACAGATTGGATGCCACTATTTCAGTCAAGAA 3822
QY 13387 ----- 13386
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QY 13387 ----- 13408
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Db 3883 GAAGATTGGCGTATTTGGCGCACTACTCGCGCGGTTGGTACAAAGTCAAAAGATCAGT 3942
QY 13409 ----- 13431
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Db 3943 ACACATTAGTTAACTGTTAAACCAACAGCATTTGGTTTACTCTCCCATACCTTACGCTG 4002
QY 13432 GCTACCGATCGCTATGACAGTGATAACGGACAGCAGGTCCGCCAACAGGTGACATTCAGT 13491
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Db 4003 ACCACAGACGTTATGACCGCGACTCTGAGCAGCAAAATTCGCCAACAAAGTCGATTTAGT 4062
QY 13492 GACGTTTTGGCGGTGAGTTGCAATCGCAACCGGACGCGCGGCGCAAGCCTGSCAA 13551
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Db 4063 GATGGTTTGGCGGCTCTGCTACAGCGCTCTGTACGACATGAGCGAGCGCAAGCCTGSCAA 4122
QY 13552 CGAGGACGCGACGCGCAAACTGGTGACGCGCCAGTGACGGAATTCGCGGTCACTGTAGCAACG 13611
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Db 4165 AAAACGCGTTGGCGGTGACGCGGACGCGACCGAAATATGATAAAGGGCAACGATACGC 4224
QY 13672 GTTTATCAGCGGTATTTCTGGACAGTTGGCAATATGTCAGTATGACAGTGCCTGCGCCAG 13731
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QY 13732 GACCTGTATGCGACACGCACTTTTACGATCCGACGCGCAGCGGAAATGGCAGGTTTATTACG 13791
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Db 4285 GAAGCCTATGGGATCTCATATTTATGATCCAAATTTGGGCGAGAAATCCGGGTTTACT 4344
QY 13792 GCAAAAGGTGAAACGCGACAGGTGCTGTATACCCCGTGGTTTGTGTCAGTGAAGACGAG 13851
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Db 4345 GCAAAAGCGTGGCTGCGCCAAAGCCAAATATTTCCCGTGGTTTACCGTGAAGTATGAG 4404
QY 13852 AATGATACCG 13861
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Db 4405 AATGATACCG 4414
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RESULT 12
US-10-706-424-9
; Sequence 9, Application US/10706424
; Publication No. US20040103455A1
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA Sequences from tcd Genomic Region of Photorhabdus luminescens
; FILE REFERENCE: 62878
; CURRENT APPLICATION NUMBER: US/10/706,424
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 4425
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4422)
US-10-706-424-9
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Query Match 5.5%; Score 1046.4; DB 17; Length 4425;
Best Local Similarity 56.4%; Pred. No. 1.4e-252;
Matches 2166; Conservative 0; Mismatches 1606; Indels 66; Gaps 9;

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QY 9598 ATCCAAATCATCAAGACATGGCCATTAATGCTTACGGAATTTTCTACTGCCCAAGGGGGGGCGCT 60
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Db 1 ATCCAAATTTCACAAGATTTTCTACTGGAATTTTCTACTGCCCAAGGGGGGGGGCGCT 60
QY 9658 GTCACCGGGCTCAAGGCTGATATCGCGCGGCGAGGCGCGGATGTCGGCGGACCCCTCAGT 9717
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Db 61 ATCCCGGAATGGGTGAAGCATTAACCCCACTGACCGGATGATGCGCGGCTATCT 120
QY 9718 ATTCCTCTGCGGTTAGCCCCCGGTGCGGGTTAGCCCCCACTGCGGGCACTTAATATATCAC 9777
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Db 121 CTACCATTTGCTATTTCTGCGGGCGGTTATGCTCCCGCATTTCACTCTGAAATTACAAC 180
QY 9778 AGCGGTGCGGGAAACGGCCCCCTTTGGCATTTGGCTGCGGATGTCGGGTCGTGCTGTCAG 9837
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Db 181 AGCGGCGCGGTAAACAGTCCATTTGGTCTGGGTTGGGATTTGCAACGTTATGACTATCCGC 240
QY 9838 CGTCTGACGCGCAACCGAGCACCTACTACGATGATCTGATGAATTTCAACGCTCGGAC 9897
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Db 241 CGCGGACCCATTTTGGCGTCCCCATTTATGACGAAACCGATACCTTTTGGGGCCAGAA 300
QY 9898 GGTGAGGTGCTGTCGCGGCACTCACGGCTGTGCGCAACCAAGAACGACGCGAGGCCACC 9957
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Db 301 GCGGAAGTCTGCTGTG-----GTAGCGGATCAACCTCGCGAGCATCC 342
QY 9958 TCACTACTGGGATAAACCCAGCGGAAGCTTCAAGTTTCAAGTTTACCGTTACGTCAGTACG 10017
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Db 343 ACATTACAGGATATCAATTTAGCGCGCACCTTTACCGTTACCGGCTACCGTTCCCGTCTG 402
QY 10018 GAGGGTAGTCTCAGCGCCTTTGAGCGTTGGCTCCCGCGACGACAGAAACGGAATTT 10077
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Db 403 GAAAGCCATTTACGCGATTTGGAATATTGGCAACCCAAACACAGGTAACAGATTTT 462
QY 10078 TGGGTGTTATATACCCCTGACCGACAGGTGGCTCTGCTGGGCGGAAATGCGCAGGCTCGC 10137
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Db 463 TGGTTGATATATAGCCAGATGGGAGGTGCTACTTCTGTTAAATCACCGCAAGCGCGG 522
QY 10138 ATCAGCAACCCACAGCCCCAACACAGCGGCGGTTTGGCTGATGAGTCTCTCGGTATCA 10197
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Db 523 ATCAGCAACCCATTCCTCCCAACGACACAAACAGCACAATGGCTGTGGAAGCTCTGTATCA 582
QY 10198 CTTTACCGGCAACAGATGTTATTACCAATACCGTGGGAGAGATGATGACGCTGTGACGAG 10257
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Db 583 TCAGTGGCGAAACAAATTTTATTAATATTCGCGCGAGAGATGACACAGGTTCCGGAACA 642
QY 10258 GCGGAGCGGACGCGCACCGCGCGGCGGCGCAACGTTTATCCGCTGGCGGCTCTGTAT 10317
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Qy	12472	TATCCAGCAGCCCTCGTTCGGCGGCAATCCATATCCGGCGTCTTTACCGCGCAGCGTGTG	12531
Db	2854	TACCCGCGCGCCAGAGCCAGCAATCAATCTGTATCTCTGATACATTTGCTGATAAGTTG	2913
Qy	12532	TTCCGCAACAGTTTATGACGAGCAGCAGATATTACGCTTGGGTTGCAACAGAGCAGT	12591
Db	2914	TTAGCCAAACAGCTATGATGACAAACAGCCAAATTACGGCTCACCTATCAACATCCAGT	2973
Qy	12592	GCAATACACTTGTTTCACTGTCGTAGGGGCAATGGTTTGGGTTGGCGAGCGTCG	12651
Db	2974	TGGCATCACCTGACCAACAATACCG-----TTTCGAGTATTGGGATTACCGGATAGTACC	3027
Qy	12652	CGGGACGATGATTTCACTGTTCTCTCGGGACACAGTTCGCGAAGGGGTTGACCGTGGAA	12711
Db	3028	CGCAGTGATATCTTTACTTATGCGCGCTGAATAATGTCCTGCTGGTGGTTTAAATCTGAA	3087
Qy	12712	CACCTGTTGGCGCCGAAAGCCTGGTCTCGGATAGTCAGGTCCGTTACGCTGGCGGGTCCAG	12771
Db	3088	CTTCTGAGTGATAAAATAATAGCCTGATCGCGACGATAAACACAGTGAATACCTCGGTCCAG	3147
Qy	12772	CAGCAAGTCTGGTATCTGGAATTCACAAGACGTTTGGCCACCGTCTGCTCCGCGACTCCCC	12831
Db	3148	CAAAAAACCGCTTATACCGGATGGACAAAAATACAACGCCGTTTCCAACAACCAACACGGCAA	3207
Qy	12832	CCCAAGGTAGCTTTTATCGAAGCGCGCTGCTGGATGAGGGTATGGTCAGTTCTACTGGCT	12891
Db	3208	GCCTGATTGGCTTTTACCGAAACAAACGGTATTCAACACAGTCACATATTATCAGCGTTTAAAC	3267
Qy	12892	GCCTACATTGTGATGAACA-----TCTCGAGCAAGCGGTTTACCGCAATCC	12939
Db	3268	GGAAAGCATCCGTCGATAAATTATCAACGACGCTGGAGCAAGCTTGGATATCAGCAACA	3327
Qy	12940	GGATACCTTTTCCCTCGAGCGAGGGAAGCAGAACAGGCATTTGTGGACCCAGTGTCAAGGA	12999
Db	3328	AATTATCTATTTCCTCGCACTGGAGAAG-----ATAAAGTTTGGTAGCCCATCAACGCG	3381
Qy	13000	TATGTTTACCTATGCGCGCGCAGAGATTTCTGGCTACCGCTATCCTTTCTGGGACAGTATG	13059
Db	3382	TATACCGATTATGGTATACGCGGCACAGTTTCTGGCGCCGCAAAAAACAGAGCAACCCAA	3441
Qy	13060	TTGACCGGCCAGTTTACCGTGACGCGTGACGCGTACGACTGCGTCTATCACGCAGTGGCAG	13119
Db	3442	CTCACCGGTAANAATCACCTCATCTGGGATGCAAACTATTGGCTTGTGGTACAAACCCGG	3501
Qy	13120	GATGCGCGAGGATTTGTCAACACAGCCGACTATGACTGCGCTTCTCTGACGCGCGTCCGG	13179
Db	3502	GATGCTCTGGACTGACAACCTCAGCCAAATATGACTGGCGGTTTTCTGACCCCGGTGCAA	3561
Qy	13180	GTGACGAGCCCCAATGATTAATCTGCAAGTCCGTCACCTCTGGATGCTCTGGCGCGGTGACC	13239
Db	3562	CTCACCGATATCAATGACAATCAGCACTTATCACACTGGATGCAATTTGGGCGGACCAATC	3621
Qy	13240	ACCTTCGATTTCTGGGGCAGCGAATGTTATTTGCCACCGGTTA-----CAGTCAAT	13290
Db	3622	ACATTGGCTTTTGGGGAATGAAACGCGAAGATGACAGTTTATCTCTACCGGAANA	3681
Qy	13291	GCCACGTTGTCGTTCCGGACGGCGCAGCAGCCGCTCTGGCGTTTGACGCGCGCCCTACCA	13350
Db	3682	GCATCATTTTCTCCACCATTCCGATGTTAATGCGGCTATTGAGTTTAAAAAAACCGTCCCT	3741
Qy	13351	GTAGCACAGTGTCTGGTGTATGTACCGACAGTGTGGGAGATGACGACAATGAGAAAA	13408
Db	3742	GTAGCACAGTGTCAAGTCTACGCACACAGAAAGCTGGATGCCAGTATTAAAGTCAGAAAA	3799

RESULT 13

RESUL 13
US-10-609-113-43

US-10-003-113-43 ; Sequence 43, Application US/10609113

; Publication No. US20040110184A1

GENERAL INFORMATION:

; APPLICANT: Bintrim, Scott

APPLICANT: Bevan, Scott

APPLICANT: Zhu, Baolong


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Db 2914 TTAGCCAAAGCTATGATGACCAACACGCGCAATTTACGGCTCACTATCAACAATCCAGT 2973
QY 12592 GCACATCACCTGTTTCTACCTGCTGAGGGGCAATTTGTTGGGTTGGCGGAGGCGTCG 12651
Db 2974 TGGCATCACCTGACCAACAATACG-----TTGAGTATTTGGATTTACCGGATAGTACC 3027
QY 12652 CGGAGCATGATTTTACGTACTCTGCGGACAAAGTGCAGGAGGGGCTCTGACGCTGGAA 12711
Db 3028 CGCAGTGATATCTTTACTTTATGCGGCTGAAAATGTGCTGCTGTTGTTAAATCTGGAA 3087
QY 12712 CACTGTTGGCGCCGAAAGCTGCTCGGATAGTCAGTTCGGTACGCTGCGGCGGTCAG 12771
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QY 12772 CAGCAAGCTGTTGATCTGGAATTCACAAGACGTTGCGACCGTTCGCTCCGCGCACTCCC 12831
Db 3148 CAAAAAACCGCTTATACCGATGACAAAATACAAAGCGCTTGCAACACGCGTTCGCGGAA 3207
QY 12832 CCCAAGGTAGCTTTTATCGAAACGCGCTGCTGGATGAGGTATGTTCACTGGCT 12891
Db 3208 GCCCTGATTTGCTTTTACCGAAACAAACGCTTCAACCGATTCACATTTACGCGTTTAA 3267
QY 12892 GCCTACATTTGATGAAAC-----TCTCGAGCAAGCGGTTTACCGGCAATCC 12939
Db 3268 GGAAGCATCCCGTCCGATAAATATCAACGACGCTGAGCAAGCTGGATATCAGCAACAA 3327
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QY 13120 GATGCGCAGGAGTTGTCACACAGCGCACTATGACTGCGCTCTGACGCGCGTCCG 13179
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QY 13240 ACCCTGATTTCTGGGCGCAGGAAATGTTATTTGCCACCGTTA-----CAGTGAT 13290
Db 3622 ACATTGCGCTTTTGGGGAACGTGAAACCGCAAGATGACAGTTATTCTCACCAGGAAAA 3681
QY 13291 GCCACGTTGCTGCTGCGGAGCGGAGCAGCGCTCTGCGTTGACGCGCGCTTACCA 13350
Db 3682 GCATCATTTTCTCCACCATCCGATGTTTAAATGCGCTATTGAGTTAAAAAACCGCTCCCT 3741
QY 13351 GTAGCAGTGTCTGTTGTTATGTCACGACAGTTGGGAGATGACGCAATGAGAAAA 13408
Db 3742 GTAGCAGTGTGAGTTGCTAGCCAGCAAGAGCTGGATGCGATTTAAGTCAAGAAA 3799

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RESULT 14

US-10-754-115-44

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; Sequence 44, Application US/10754115
; Publication No. US20040208907A1
; GENERAL INFORMATION:
; APPLICANT: Hey, Timothy
; APPLICANT: Schleper, Amanda
; APPLICANT: Bevan, Scott
; APPLICANT: Bintrim, Scott
; APPLICANT: Mitchell, Jon
; APPLICANT: Li, Ze Sheng
; APPLICANT: Ni, Weiting
; APPLICANT: Zhu, Baolong

```

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; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 4425
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4422)
; US-10-754-115-44

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Query Match 5.5%; Score 1046.4; DB 18; Length 4425;
 Best Local Similarity 56.4%; Pred. No. 1.4e-252;
 Matches 2166; Conservative 0; Mismatches 1606; Indels 66; Gaps 9;

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RESULT 15
 US-10-242-056-31

; Sequence 31, Application US/10242056
 ; Publication No. US20030113323A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ensign, Gerald C
 ; APPLICANT: Bowen, David J
 ; APPLICANT: Petell, James
 ; APPLICANT: Fatig, Raymond
 ; APPLICANT: Schoonover, Sue
 ; APPLICANT: ffrench-Constant, Richard

; APPLICANT: Orr, Gregory L
 ; APPLICANT: Merlo, Donald J
 ; APPLICANT: Roberts, Jean L
 ; APPLICANT: Rocheleau, Thomas A
 ; TITLE OF INVENTION: Insecticidal Protein Toxins from
 ; TITLE OF INVENTION: Photorhabdus
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dowelanco
 ; STREET: 9330 Zionsville Road
 ; CITY: Indianapolis
 ; STATE: IN
 ; COUNTRY: US
 ; ZIP: 46268
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/242,056
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/063,615
 ; FILING DATE: 18-MAY-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/395,497
 ; FILING DATE: 28-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/007,255
 ; FILING DATE: 06-NOV-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/608,423
 ; FILING DATE: 28-FEB-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/705,484
 ; FILING DATE: 28-AUG-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/743,699
 ; FILING DATE: 06-NOV-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Borucki, Andrea T.
 ; REGISTRATION NUMBER: 33651
 ; REFERENCE/DOCKET NUMBER: 50301E
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 317-337-4846
 ; TELEFAX: 317-337-4847
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4458 base pairs
 ; TYPE: nucleic acid
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 ; TOPOLOGY: linear
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Query Match 5.1%; Score 969.8; DB 15; Length 4458;

Best Local Similarity 53.8%; Pred. No. 3.3e-233;
 Matches 2395; Conservative 0; Mismatches 1857; Indels 201; Gaps 11;

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Job time : 9352 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 06:08:43 ; Search time 50294 Seconds
(without alignments)
13720.507 Million cell updates/sec

Title: US-10-070-489A-1

Perfect score: 18937

Sequence: 1 ggatccgagtggaaggaatca.....cgtgccacggagcatggc 18937

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	385.6	2.0	1023	9	CNS01EVJ
C 2	296.	1.6	983	9	CNS01GGB
C 3	256.8	1.4	654	8	AQ991360 Rfc02280
C 4	241.4	1.3	672	8	AQ990989 Rfc01839
C 5	223.6	1.2	749	8	AQ991727 Rfc00357F
C 6	216.8	1.1	685	8	AQ990831 Rfc01661
C 7	216.6	1.1	748	8	AQ991760 Rfc00753F
C 8	214.6	1.1	605	8	AQ990411 Rfc01179
C 9	197.6	1.0	881	9	CNS01R9G
C 10	192	1.0	617	8	AQ990217 Rfc00949
C 11	188.6	1.0	602	8	AQ991038 Rfc01893
C 12	188.2	1.0	604	6	CB065346 EST645027
C 13	178	0.9	735	8	AQ991741 Rfc00508F
C 14	158	0.8	765	8	AQ991783 Rfc00869
C 15	154.8	0.8	594	8	AQ990688 Rfc01498
C 16	144.8	0.8	603	9	CNS01LYT
C 17	141.6	0.7	683	9	CNS01R60
C 18	139.6	0.7	693	9	CNS01KXV
C 19	133.2	0.7	733	2	AW901477 RCO-NN101
C 20	125.6	0.7	312	8	AQ990147 Rfc00869
C 21	125.6	0.7	547	8	AQ990013 Rfc00707
C 22	119.2	0.6	494	8	AQ991400 Rfc002327
C 23	118	0.6	548	8	AQ998949 Rfc00508
C 24	117.4	0.6	567	8	AQ990696 Rfc01508

25	105.8	0.6	660	8	AQ991527	AQ991527 Rfc02507
26	105.2	0.6	406	8	AQ990055	AQ990055 Rfc00763
27	100	0.5	460	8	AQ991476	AQ991476 Rfc02418
C 28	92.4	0.5	819	8	AQ991798	AQ991798 Rfc02474F
C 29	86.2	0.5	479	8	AF175370	AF175370 AF175370
C 30	85.4	0.5	710	8	AQ989937	AQ989937 Rfc00617
31	84	0.4	422	8	AQ991079	AQ991079 Rfc01939
32	81.6	0.4	1101	9	CNS00EVL	AL061936 Drosophil
C 33	81.4	0.4	1101	9	CNS0021J	AL061936 Drosophil
C 34	80.4	0.4	1139	8	AQ897537	AQ897537 HS_3153 A
C 35	79.2	0.4	1101	9	CNS0039G	AL063921 Drosophil
C 36	79	0.4	781	8	AQ991625	AQ991625 Rfc01183F
C 37	77.6	0.4	477	9	CNS07FW3	AL608997 Anopheles
C 38	76.8	0.4	1896	9	CG753083	CG753083 P048-1-C0
C 39	76.2	0.4	1127	9	CL128786	CL128786 ISB1-95C2
C 40	75.6	0.4	1101	9	CNS00EVL	AL061936 Drosophil
C 41	75.2	0.4	802	9	CNS01241	AL061936 Drosophil
42	75	0.4	1029	9	CNS01ZGM	AL101100 Drosophil
43	74.8	0.4	585	9	CNS01NVV	AL174271 Tetradon
44	72.8	0.4	720	8	AQ990621	AL152748 Anopheles
C 45	71.6	0.4	1592	9	CG750135	AQ990621 Rfc01421
						CG750135 P044-3-D0

ALIGNMENTS

RESULT 1
CNS01EVJ/c
LOCUS
DEFINITION
CNS01EVJ 1023 bp DNA linear GSS 30-MAY-2001
Anopheles gambiae GSS SP6 end of clone 03B12 of Notredame library
from strain PEST of Anopheles gambiae (African malaria mosquito),
genomic survey sequence.
ACCESSION
AL141056
VERSION
AL141056.1 GI:6999174
KEYWORDS
GSS.
ORGANISM
Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE
1 (bases 1 to 1023)
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
JOURNAL
BP 131 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
REFERENCE
2 (bases 1 to 1023)
Roth,C.W., Brey,P.T., Ke.Z., Collins,F.H. and Weissenbach,J.
TITLE
Direct Submission
JOURNAL
Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France
COMMENT
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.

FEATURES
source
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/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="03B12"
/clone_lib="Notredame1"
/note="end : SP6"

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Best Local Similarity 76.7%; Pred. No. 2.2e-90;
Matches 517; Conservative 4; Mismatches 123; Indels 30; Gaps 3;
QY 18268 ACTGGTACGATCGGTGCCAGGAACCTTTATCAGACCCGCGGCGTTTCG 18327
|||||
Db 1023 ACTGGTACGGTTCGTACGAGAACCCCTTTCATCAGACCCGCGGCGGACGTTTG 964
|||||

Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.		Location/Qualifiers	
FEATURES		source	
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		/organism="Anopheles gambiae"	
		/mol_type="genomic DNA"	
		/strain="PEST"	
		/db_xref="taxon:7165"	
		/clone="06L12"	
		/clone_lib="NotreDamel"	
		/note="end : T7"	
ORIGIN			
Query Match		1.6%; Score 296; DB 9; Length 983;	
Best Local Similarity		82.4%; Pred. No. 1.8e-66;	
Matches 397; Conservative 2; Mismatches 52; Indels 31; Gaps 4;			
QY	18327	GGTTTCTCCCGTACCGTCAATCTCCAGCGCGTGTAAACCTTCGGCAGCAGCGTG-CCCGT	18385
Db	983	GTTTTTTCCCGTACCKTCATCGCCAGTGCATCGTAAACCTTCGGCAGCAGCGTGC	924
QY	18386	TTGCGGTTGGCCAGAAAACCATAGTAACGACCACTTTTAAATTCGCCGTCAGGATATGG	18446
Db	923	TTACCGTTGGCCAGAAAACCKTAGTAGCAGCCCTTTTAGAATGCCGCGCGGAATATGG	864
QY	18446	CTGACGTAAACGCTGCAGCATCTCCTCTGGCTGATTTTCTGGCGTTTGTCTGCTGCGTA	18505
Db	863	CTGACGTAAACGCTGCAGCATCTCCTCTGGCTGATTTTCTGGCGTTTGTCTGCTG	804
QY	18506	CGGTGATCGTAATACTGATGCACACCGCCCGCGGTAGTGGCGTAGCTCAGAAAGCC	18565
Db	803	CGGTGATCGTAATAACCGATGCACACCGCCCGCGATAGTGGCGCAGCTCAGAAAGCG	744
QY	18566	GCCACCGCGCGCGCTTCAGGTACCGGGCCAGGTATTTTACGCTGCGCCAGGCGCGCGG	18625
Db	743	GCCACCGCGCGCGCTTCAGGTACCGGGCCAGGTATTTTGCACSTGCGCCAGGCGCGCGG	684
QY	18626	GTCTTTTGGCAAAATTCACATTTCCAGCGCGCGGTATTGCGCATGCG------	18677
Db	683	GTCTTTTGGCAAAATACATTTCCAGCGCGCGGTATTGCGCATGCGATACGATACCGTGC	624
QY	18676	-----GGTCTTCGTCGCGATATGCCAGACCCGCGAGCGCGCCAGGATGAT------	18725
Db	623	CACCGATCTTCAATACGGATATGACCGCGCGCGGACCGCGGCTTGAATTTGGGCG	564
QY	18725	-----GCCACGAGGTGAACGACCGCATTTGGCCAGATGCTTCCACTCTTTCTTT	18777
Db	563	TAGTTGTCGCGCAGCAGGTAAACAC-CCGTTGCGCCAGATCTGCCCTACCTCTTTCTTT	505
QY	18777	TT 18778	
Db	504	TT 503	
RESULT 3			
AQ991360			
LOCUS			
DEFINITION			
Rfco2280 Photorhabdus luminescens strain W14 M13 library			
Photorhabdus luminescens genomic clone PLG02280, genomic survey			
sequence.			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the			
Genoscope.			
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :			
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr			
- Web : www.genoscope.cns.fr)			
2 (bases 1 to 983)			
1 (bases 1 to 983)			
Genoscope.			
Direct Submission			
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :			
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr			
- Web : www.genoscope.cns.fr)			
2 (bases 1 to 983)			
1 (bases 1 to 983)			
Genoscope.			
Direct Submission			
Submitted (16-FEB-2000) BIMI, Institut Pasteur, 25, rue du Dr.			
Roux, Paris 75015, France			
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Roux, Paris 75015, France			
Submitted (16-FEB-2000)			

MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.

FEATURES
source
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/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG02280"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN
Query Match 1.4%; Score 256.8; DB 8; Length 654;
Best Local Similarity 63.2%; Pred. No. 4.3e-56;
Matches 407; Conservative 0; Mismatches 236; Indels 1; Gaps 1;
QY 8385 CCGTGTCTCGGCATCAACCGCGCTCTTTTGGCCGAGCGCGCGATATCTGTC 8444
DB 8 CCGGGCTTACACGGCAGTTTCAGCATCCCGTCTGGCCGCTGGCGGCTGATCTGTGTC 67
QY 8445 CCAATATTTACGGCTGCGCGCTCGCGCTATGGCGCACTATTTAAAGCCACCG 8504
DB 68 CTAACATCTTTCGGCTTTCGGCTGGCGCAGCGCTGGGGGGCTATCGCTGAGCGACAG 127
QY 8505 CCATCGGCATCCAGGTGCTCTCGATGCCACCGCATATCAGCGGACAAATCAGCGAGT 8564
DB 128 GTTATGTGATGGAATTCCTCGCGAATGTTATGAACACCGAAGCGGATAAATATAGCCAAT 187
QY 8565 CGGAGTGTACCGCGCTCGCGGAGGAGTGGGAATCCAGCGTGTAGTGGCGAGTCTG 8624
DB 188 CTGAAACCTACCGCTCGCGCTCAGGAGTGGGAGATCCAGCGGAATAATGCCGAAGCGG 247
QY 8625 ACCTGGCGCAGATTGATGCCAGTGGCGCCATGGCAGTGGCGGGAAGGGCTGAGC 8684
DB 248 AATTGAAGCAATCGATCTCAGCTCAATCAGTCTGCTGATCGCGCGGAAGCGCGGTAT 307
QY 8685 TGCAGAAACTTACCTTTGAGACCCAGACAGCCAGGACAGGGCGAGTTGGCAATTCCTGC 8744
DB 308 TGCAGAAACCAAGTCTGAAACCCCAACAGAACAGACCCCAATCTCAATTTGCGCTCTCTGC 367
QY 8745 AGAGTAAGTTCAACATACGGCTCTGTACAGTGGCTGGCGGCGAGGTTGTCGCGCAATTT 8804
DB 368 AACGTAAAGTTCAGCAATCAGGCGGTATACCACTGGCTGGCTGGCTGCGACTGGCGCGATTT 427
QY 8805 ATTACCAAGTTCTATGACTCGCAGTATCCCGCTGCTGATGGCGCAACAGCGCTGGCGAGT 8864
DB 428 ACTTTCAAGTTCTACGATTTGGCGGTTCGCGGTGTCCTGATGGC-AGCAAGCTTACGGTT 486
QY 8865 GGGATAAAATTCGAGACTAGTTCGTTTATCCAGCGCGGGGCGCTGATGGGGGCAAAATGCGG 8924
DB 487 GGGAACTCATGATGACNTGCGCTTATTAACCGGGCGCTTGGCAGGAACCTATGCGG 546
QY 8925 GTCTGCTGGCGGGGAAACCTGATGCTGAATCTGGCGCAGATGGAGCAGCGCTTGGCTGA 8984
DB 547 GTCTGCTTGCAGGTGAAACCTTGATGCTGAGTCTGGACAAATGGAGACGCTCATTTTGA 606

QY 8985 CGGGGGATGAGCGGGCAATAGAGGTGACCGGACGGTCTGCTGCTG 9028
DB 607 AACCGGATAAACCCCAATTANAGTTGAACGACAGTATCCTTG 650

RESULT 4
AQ990989/c
LOCUS
DEFINITION
Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01839, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE
AUTHORS
1 (bases 1 to 672)
ffrench-Constant R.H., Waterfield N., Burland V., Perna N.T.,
Daborn P.J., Bowen D. and Blattner F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shotgun.

FEATURES
source
1..672
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01839"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/notes="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN
Query Match 1.3%; Score 241.4; DB 8; Length 672;
Best Local Similarity 62.8%; Pred. No. 5.6e-52;
Matches 390; Conservative 0; Mismatches 228; Indels 3; Gaps 1;
QY 5309 TATCTGCTGTGATATCAGGTGTGAGCCAGGTAAACACCCCGCATTCGGAGGCC 5368
DB 672 TACTTNTTGTATGATATCAGGTTCCTGCGCAATAAACCACCCCGATCGCGAGGCC 613
QY 5369 ATCCCGCGCATCGGCTGTATATCAACCGGCGCTTAAACGGAATAGAACTCAGCGCCATG 5428
DB 612 ATTGCGAG---TATTAACGTACGTACCCCGNCATTTGGAAATGTGAAGAAATGCCAT 556
QY 5429 GCAGAGGTGAGGGGGCGGTTCAGTTTTTTTCACTGACTGGGATACGTTCAACAAACGTTACAGC 5488
DB 555 TCGGGGTTATCAGCGCCCAATTTCTTTATCGACTGGGACAAATACAAATAACGCTACAGC 496
QY 5489 ACCTGGGGCGGCTCTCAGAGCTGGTTTACTATCCGGAATAACTACCTCGACCCGACGGTC 5548
DB 495 ACTTGGCGGGTCTTTCTCAATTAGTTTACTACCCCGGAAACTATATTGATTCGACCATG 436

South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.

Seq primer: M13 Forward
Class: shotgun.

FEATURES

Location/Qualifiers

1..685
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01661"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 1.1%; Score 216.8; DB 8; Length 685;
Best Local Similarity 60.9%; Pred. No. 2.1e-45;
Matches 405; Conservative 0; Mismatches 253; Indels 7; Gaps 3;

QY 11522 TCACACAGAGTGTATTTATTCGCCGAGCGGCATAGCTGCTCTTCCGAAAGGTGTGC 11581
DB 3 TGAACAAAGTGGCAATGGCTTGGCTGAACACGATGACATTAACGCTTCCCGAAGGTGTGC 62

QY 11582 GCTATGATCCACCTGACGCTCTCAAGTGGCGGATATCCAGGGGCTGGGGTGCCTAGCC 11641
DB 63 GTTTGATCATCTGTGACGTACAAATGCGCGATGTACAGATTAAGGCTGCCAGCC 122

QY 11642 TGTACTGACGGTCCCGTCTGCGCTCATCATCTGGGTGTGCCATTTATCGGCAGACA 11701
DB 123 TGATACTGAGCGTCCGATATGCTCCCATCACTGCGCTGCGATCTGACCAACATGA 182

QY 11702 AACCTGGTTTGAATGGATGACACAAATATGGGGCCCGGCTGCACTGCACTATC 11761
DB 183 AGCGGTGGTTACTCAATGAAATGAACAAATATGGGGTCCATCACTACCGGACAAAC 242

QY 11762 GCAGTTCCGCTGAGTTCGCTGATGAGAAAGCCAGGACCTGGCGGAGGAGTCCC 11821
DB 243 GCAGTTCTCCCAATCTGCTGGATGAAAGCGCGGCTGACTACCGGACAAAC 302

QY 11822 CTGCTGCTACCTGCCATTTACATTTGATACCTGTGGCGTTCGGTGGTGACAGATGAGA 11881
DB 303 CGGTTTGCTATCTCCCTTCCGATCCACACCTATGGCAACCGAAACAGAAATGAAA 362

QY 11882 TCACCGGTACCGTCTGGTACGAGCGTGTATTCGCCAGCGGCTTGGGACGGGAGG 11941
DB 363 TCAGCGCAACAAATAGTACCAACACTTCGTTATGCTCTGCGCGATGGGACGGACGG 422

QY 11942 AACCGAGTTTCGGGGGTTGGTTTGTTCAGATCAGGATACCGATACCTTCGCAAGCC 12001
DB 423 AGCGGGAATTCGGGATTTGGTTATGTAGACAGACAGACAGCATCAACTGCG---TC 479

QY 12002 AGGGTACGGCGACGGAATCGAGTATGCTTCTGTGACCGGAACCTGATATGCA-CCGGG 12060
DB 480 AAGGCAACGCGCAGAACGTACGCCACCGCGCTGACCAAAACTGGTATGCCACCGGA 539

QY 12061 GTACCGGACGTACAGCGCTCTGCCGAGACGCTATTGGCAAAACGATCCGCGCTTTT 12120
DB 540 CTGCGGTGTATAGATAACGCAATTAACCGAGTATTGGC---GTGATGATCANGCTTTT 596

QY 12121 GCCGATTTCCGACCCGTTTCACTGTCGGTTACGAGAGATGATGACGACATATCTCCG 12180
DB 597 GCCGGTTTCTACCGCGCTTTACGACTTGGCAAGATAACAAAGATGTCCGTTAACCCCG 656

QY 12181 GACGA 12185

Db 657 GAAGA 661

RESULT 7

AQ991760/c
LOCUS

DEFINITION
Photorhabdus luminescens genomic clone PLG00753F, genomic survey

sequence.
AQ991760

VERSION
AQ991760.1 GI:9650256

KEYWORDS
GSS.

SOURCE
Photorhabdus luminescens

ORGANISM
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

REFERENCE
1 (bases 1 to 748)

AUTHORS
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence

JOURNAL
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE
20378633

PUBMED
10919786

COMMENT
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk

This is one of a selected subset of flipped clones from the M13
library. For annotation of identified clones (BLASTX, BLASTN and
mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.

Seq primer: M13 Reverse
Class: shotgun.

Location/Qualifiers

1..748
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"

/db_xref="taxon:29488"
/clone="PLG00753F"

/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"

/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN

Query Match 1.1%; Score 216.6; DB 8; Length 748;
Best Local Similarity 70.2%; Pred. No. 2.4e-45;
Matches 288; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 7301 ATGGACTCTCCGGAGCCCAATGCCCTCTATTTCTGGAGCTGTCTTATTACAGCCGATG 7360

DB 460 ATGGATTNCTGGCGCCCAATGCTCTATTTCTGGGAACTGTCTTATTACAGCCGATG 401

QY 7361 ATGGTGTCTTCAGCGGTTGTTGAGGAACAGCACTTCCCGAAGCCACCCGCTGGCTGCAG 7420

DB 400 ATGATGGCTCATCGTTTGTTCAGGACAGAAATTTNATCGCGGAGAACCAATTGGTTCGGT 341

QY 7421 TATGTCGTGAAACCCGCGCGGACCGTGGTAAACCGGGTCTCTGCAGAAATTACACCTGGAAT 7480

DB 340 TATGTCGTGAGTCCATCCCGTTATATCGTTGATGGTAAATTTGCTATCTACCNCTGGAAC 281

QY 7481 GTCCGTCCTCGCTGAGGAGACACCCGCTGGAACGACTCCCGCTGCACTCCATTGACCCC 7540

DB 280 GTGCGAGCCCTGGAAGAGACACCAAGTTGGATGCAACAACTGGACTCCACCGATCCA 221

QY 7541 GATGCAATGACCCAGTACGACCCCATGCAATTAAGGTGCGCCACCTTTATGTCGTACCTC 7600

Db 220 GATGCTGATGCCCAAGATGATCCGATCGACTCAAGGTGGCTACCTTTAATGGCAGCTTG 161
 QY 7601 GACCTGCTGATGCCCGCGGTGATGCCGCTACCGCTGCTCGAGCGGACACCCCTTAAC 7660
 Db 160 GATCTGCTAATGATGCCCGGTGATGCTGCTTACCGCCAGTTAGAGCGTGATACGTTGGCT 101
 QY 7661 GAGCGCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7710
 Db 100 GAAGCTAAATGTTGGTATATACAGGCGCTTAATCTGTTGGGTGATGAGCC 51

RESULT 8
 LOCUS A0990411
 DEFINITION Rf001179 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG01179, genomic survey
 sequence.
 ACCESSION A0990411 GI:9649005
 VERSION A0990411.1
 KEYWORDS Photorhabdus luminescens
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 REFERENCE 1 (bases 1 to 605)
 AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 MEDLINE 20378633
 PUBMED 10919786

COMMENT Contact: ffrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssr@bath.ac.uk
 This is one of 2,122 random reads from the M13 library. For
 annotation of identified clones (BLASTX, BLASTN and mapping to E.
 coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
 Acids Res.
 Seq primer: M13 Forward
 Class: shotgun.

FEATURES
 source
 1..605
 /organism="Photorhabdus luminescens"
 /mol_type="genomic DNA"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG01179"
 /dev_stage="primary phase variant"
 /clone_lib="Photorhabdus luminescens strain W14 M13
 library"
 /notes="Genomic DNA from strain W14 was size selected (1-2
 kb) and then cloned into M13 Janus."

ORIGIN
 Query Match 1..11; Score 214.6; DB 8; Length 605;
 Best Local Similarity 62.3%; Pred. No. 7,6e-45;
 Matches 351; Conservative 0; Mismatches 211; Indels 1; Gaps 1;

QY 14967 TTACGGACCGCTTGTGATCGCTGGCAATACGATCGCGAGAGATTTCTCAATCTGGCTG 15026
 Db 1 TGACAGAGCGCTTATCTGCGCTGGCAATACAACTCGGAGAAAGATTAACCTCTCG 60
 QY 15027 GCCAGTGTCTAGCTATTACGATACCGCGGACTGTGAGAGGACGACATCGCCCTGA 15086
 Db 61 GTCTGTGTATAGCCCACTACGACACAGCGGAGTGACCCGGTTGATGAGTCACTGCG 120
 QY 15087 GCGCGCTGCGCTGCGCGCTCACGCGGAGTTGCTGCCCGGCGGGGCGCAACTGGA 15146

Db 121 CGGCGCCATGCTATCCCAATCTCACCATTCTGCGGGAAGGCGAGGAGTAACTGGA 180
 QY 15147 TGGGTGAGGATCGCTCGGCTTGAATGACCTCTCTGATGGGAGAGCTTTCTTCCACCAGA 15206
 Db 181 GCGGTGACGACGAAACTGTCTGGCAGGGAATCTGSCAAGTGAAGTCTATACGACACAAA 240
 QY 15207 CCACGCTGATCGACCGGCGGCTCTGAGCATCACGATGCAAAAGTATATCTGCAGC 15266
 Db 241 GTACCACCTAATCCATCGGGGCTTTACTGACCCAAACCGATCGAAAGCAATATTTCAGC 300
 QY 15267 GTGTGSCATATGATGTGGCTGGCTGCTATCGGCGAGTTGTTGACGCTGAAGGACGGA 15326
 Db 301 GTCTGGCTTATGACATTCGCGTCAAGTTAAAGGAGATTTGGTTGACGGTGAAGGCCAGA 360
 QY 15327 CGGAGCAGGTATCTGTCGGCTCCCTCGAGCTACTCGGCGCGCGGAAAAAGTTGCGTGAAG 15386
 Db 361 GTGAACAGGTGATTGTTAAGTCCCTGAGCTGCTGAGCCGAGTCTATAAATTGCGTGAAG 420
 QY 15387 AACACGGCAACGCGCTGTGTAACCTCGTATATTATTCAG-CGGAACACAGCGCTGACG 15445
 Db 421 AGCAGCGTAAACGCGCTGTTACCGAGTACAGTTATGAGCCCGGAACTCAACGCTCTGATA 480
 QY 15446 GGGATTAAACGGAACGCTCGCTCGGCACGTTGCCGGAGCAAAAGTGTGCGAGACCTG 15505
 Db 481 GGTATACACCCCGCGTGCCTCAANGAGTCAATCANGAGCCAGAAAGTATTGCGAGTCTA 540
 QY 15506 CGCTATACGTATGACCCGCTAGG 15528
 Db 541 CGCTATAAGTATGATCCCGTGG 563

RESULT 9
 LOCUS CNS01R9G/c
 DEFINITION CNS01R9G 881 bp DNA linear GSS 14-JUN-2001
 Anopheles gambiae GSS T7 end of clone 32J18 of NotreDamel library
 from strain PEST of Anopheles gambiae (African malaria mosquito),
 genomic survey sequence.

ACCESSION AL157124
 VERSION AL157124.1 GI:7018043
 KEYWORDS GSS.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.

REFERENCE 1 (bases 1 to 881)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)

REFERENCE 2 (bases 1 to 881)
 AUTHORS Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J.
 TITLE Direct Submission
 JOURNAL Submitted (16-FEB-2000) BMI, Institut Pasteur, 25, rue du Dr.
 Roux, Paris 75015, France
 COMMENT This clone is from an A. gambiae BAC library provided by F.H.
 Collins and sequenced by Genoscope in collaboration with the
 Laboratory of Biochem. and Biol. Molec. of Insects, Institut
 Pasteur.

FEATURES
 source
 1..881
 /organism="Anopheles gambiae"
 /mol_type="genomic DNA"
 /strain="PEST"
 /db_xref="taxon:7165"
 /clone="32J18"
 /clone_lib="NotreDamel"
 /note="end : T7"

ORIGIN
 Query Match 1.0%; Score 197.6; DB 9; Length 881;

Best Local Similarity 83.0%; Pred. No. 3e-40;
Matches 244; Conservative 8; Mismatches 27; Indels 15; Gaps 2;

QY 18446 CTGACGTAAAGCTGACGATCTCTCTGCTGCTATTTCTGCGGTTTGCTGCTCGTA 18505
DB 881 CTGACGTAAAGCTGACGATCTCTCTGCTGCTATTTCTGCGGTTTGCTGCTG 822

QY 18506 CGGTGATCGTAATCTGATGACACACCGCCCGCGGTAGTGGCTAGCTGAGAAGCC 18565
DB 821 CGGTGATCGTAATCTGATGACACACCGCCCGCGGTAGTGGCTAGCTGAGAAGCG 762

QY 18566 GCACCGCGCGGCTTTCAGGTACCGCGGCGAGGTATTTCAAGCTGCGCCACGCGCGCG 18625
DB 761 GCACCGCGCGGCTTTCAGGTACCGCGGCGAGGTATTTCCACSTGCGCCACGCGCGCG 702

QY 18626 GTCTTTTGGCAAAATTCATTTTC-CAGGCGCGCGGTATTTGCGCATGCG- 18675
DB 701 GTCTTTTGGMAAAATATACATTTTCAGGCGCGCGGTATTTGCGCATGMAAATAAGGTG 642

QY 18676 -----GGTCTTTCGTTGCGGATATGCGGACCGCGCGGCGCGCGGCGCGGTTGAT 18724
DB 641 MMACAGATMTTATTAGGATATGACMGAGCGCGCGCGCGCGGCGGTTGAT 588

RESULT 10
AQ990217
LOCUS
DEFINITION
Photobacterium luminescens strain W14 M13 library
Photobacterium luminescens genomic clone PLG00949, genomic survey
sequence.

ACCESSION
AQ990217
VERSION
AQ990217.1
KEYWORDS
GSS.
SOURCE
Photobacterium luminescens
ORGANISM
Photobacterium luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photobacterium.

REFERENCE
AUTHORS
1 (bases 1 to 617)
french-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photobacterium luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL
MEDLINE
PUBMED
20378633

COMMENT
10919786
Contact: french-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsaric@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see french-Constant et al. 2000, Nucleic
Acids Res.

Seq primer: M13 Forward
Class: shotgun
Location/Qualifiers
1. .617
/organism="Photobacterium luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29408"
/clone="PLG00949"
/dev_stage="primary phase variant"
/clone_lib="Photobacterium luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2
kb) and then cloned into M13 Janus."

ORIGIN

Query Match

1.0%; Score 192; DB 8; Length 617;

Best Local Similarity 60.8%; Pred. No. 8.1e-39;
Matches 355; Conservative 0; Mismatches 225; Indels 4; Gaps 3;

QY 8410 GCTCTTTTGGCGGCGCGCGGATATGCTGCCAATATTTAGCGGCTGCCGTCGG 8469
DB 18 GNCOCGTATGGGCGCGCGGTGATATGNNCCAAATATCTTCGGCTGGCTGATGG 77

QY 8470 GGGCTCCCCCTATGGGGCACTATTTAAAGCCACCGCATCGGATGTCCTCCGA 8529
DB 78 CGGNATGCANTATGGNGCTATTGNCATATGCCATCGCTGACGGTATTTGAGTTGAGTCTTC 137

QY 8530 TGCCACCCGCATATACGCGGACAAATACAGCCAGTTCGGAAGTGTACCGCGTCCCGGGA 8589
DB 138 TGCAAGATGTTGATGCGCGGAGAAAGTTGCTCAGTCGGAATATATATCGCGCTCGCTCA 137

QY 8590 GAGGTGGGAAATCCAGCGGTAGTGGCGAGTCTGAGTGGCGGAGATTGATGCCAGCT 8649
DB 198 AGAATGGAAATTCAGCGGTGACACGCAACGCGGAGATTAAACAGTTAAACGCGCAACT 257

QY 8650 GCGCGCATGCGCGCGCGGAGGGCTGAGCTGCGAGAAATCTTACCTTGAGACCCA 8709
DB 258 GGAATCACTGTCTATTTCGCGGTGAGCCGCTGAAATGCAAAAGAGTACTCTGAAACCCA 317

QY 8710 GCAGACCCAGGACAGCGCGAGTTGGCATTTCTGCGAGAGTAAGTTCAA-CAATACGGCTC 8768
DB 318 GCAAGCTCAGCGCGAGGCAAACTTACTTTCTTAAGAAGCAAAATTCAGTAAATCAAGCGT 377

QY 8769 TGTACAGCTGCTGCGCGGCGAGGTTGTCGCCCATTTATTACAGTTCTATGACCTCG-CA 8827
DB 378 TATATAGTTGGTTTACCGGGCGTTGTGTCAGGTATTTATTTCCAGTTCTATGATCTGGCCC 437

QY 8828 GTATCCCGCTGCTGATGCGCAACAGCGCTGCGAGTGGAGTAAATTCGAGACTAGGTGCG 8887
DB 438 GTATCAGTTGCTGATGCGAGNACAATCTTCAATGGAAGCTAATGATAATTNCATT 497

QY 8888 TTTATCCAGCGCGGCGCTTGGATGCGGGCAATATGCGGCTCTGCTGCGCGGGGAAACCTTG 8947
DB 498 ACTTTGCAACCGGTGATGCGCAAGGAACCTTA--CCGGCTTATTGTGTGAGAGAGCTTTG 555

QY 8948 ATGCTGAATCTGCGCGAGATGAGCAGCGCTGCTGACGGGGA 8991
DB 556 ATACAAATCTGGCAAAATGGAAGCATATCTGAAATGGGA 599

RESULT 11
AQ991038
LOCUS
DEFINITION

AQ991038 602 bp DNA linear GSS 14-AUG-2000
Rf01893 Photobacterium luminescens strain W14 M13 library
Photobacterium luminescens genomic clone PLG01893, genomic survey
sequence.

ACCESSION
AQ991038
VERSION
AQ991038.1
KEYWORDS
GSS.
SOURCE
Photobacterium luminescens
ORGANISM
Photobacterium luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photobacterium.

REFERENCE
AUTHORS
1 (bases 1 to 602)
french-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photobacterium luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL
MEDLINE
PUBMED
20378633

COMMENT
10919786
Contact: french-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsaric@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For

annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
Seq primer: M13 Forward
Class: shotgun.

FEATURES

source
1..602
Location/Qualifiers
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01893"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/notes="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 1.0%; Score 188.6; DB 8; Length 602;
Best Local Similarity 62.1%; Pred. No. 6.5e-38;
Matches 332; Conservative 0; Mismatches 199; Indels 4; Gaps 2;
QY 8509 CGGCATCCAGGTGCTCCGATGCCACCCGATATCAGCGGCACAAAATCAGCCAGTCGGA 8568
Db |||||
QY 48 CGGTATTGAGTTGAGTGTCTTCCCAAGATGTTGATGCGGAGAAATGTTCTCAGTCGA 107
Db |||||
QY 8569 AGTGTACGCCGTCGCGGAGAGAGTGGGAAATCCAGCGTGTATGATGCGCAGTCTGACGT 8628
Db |||||
QY 108 AATATATCGCGTCGCGCTCAGAAATGGAATTCAGCGTGACACGACCAACGCGGAGAT 167
QY 8629 GCGCGAGATTGATGCCAGTCGCGGCATGCGAGTGGCGGAGGGGCTGAGCTGCA 8688
Db |||||
QY 168 TAACCACTTAACCGCCAACTGGAATCACTGTCTATTCGCGGTGAAGCGCTGAAATGCA 227
QY 8689 GAAACCTTACCTTTGAGACCCAGCAGACCCAGGCGCAGTTGGCACTTCTCTGACAG 8748
Db |||||
QY 228 AAAAGAGTACCTGAAACCCAGCAAGCTCAGGCGCAGGCACACTTACTTCTTAAGAAG 287
QY 8749 TAAGTTCAACATACACGCTCTGTACAGCTGCTGCGGGGAGGTTGTCGCCATTATTA 8808
Db |||||
QY 288 CAAATTCAGTAATCAACGCTTATATAGTTGGTTTACGAGGCGGTTGTCAGGTATTTATTT 347
QY 8809 CAGATTCTATGACCTGCGAGTATCCCGCTGCTGATGCGGCAACAGGCTGCGAGTGGCA 8868
Db |||||
QY 348 CCAATTCTATGATCTTGCCGATATCACGTTGCTGTATGGCAGAGCAATCTCTCAATGGGA 407
QY 8869 ---TAAATTCGAGACTAGGTGCTTTATCCAGCGGGGGCTGTGATGGGGGCAAAATGCCGG 8925
Db |||||
QY 408 AGCTAATGATAATTCATTAGCTTTGTCAACCGGGTGATGGCAAGGAATTCAGCCGG 467
QY 8926 TCTGCTGGCGGGGAAACCTGTATGTGATCTGGCGCAGATGAGCAGGCTGGCTGAC 8985
Db |||||
QY 468 CTTATTGTGTGGAGAACTTTGATACAAAATCTGGC-CAAAATGGAAGAGCATATCTGAA 526
QY 8986 GGGGGATGAGCGGCAATAGAGTGTGACGCGAGCTCTGCTGTCGGAGGTCTAT 9040
Db |||||
QY 527 ATGGGAATCTCGCGCTTTTGAAGTAGAACGACGCGGTTTCAATTGCGAGTGGTTAT 581

RESULT 12

CB065346

LOCUS

DEFINITION EST645027 HOGA Medicago truncatula CDNA clone HOGA-2E7, mRNA

sequence.

ACCESSION CB065346

VERSION CB065346.1

KEYWORDS GI:27810924

SOURCE Medicago truncatula (barrel medic)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

REFERENCE

AUTHORS Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
Utterback,T., Cho,J. and Fraser,C.M.

TITLE

ESTs from roots of Medicago truncatula treated with
oligogalacturonides of Dp 6-20

JOURNAL

Unpublished (2001)

COMMENT

Contact: Michael G. Hahn

Complex Carbohydrate Research Center

University of Georgia

220 Riverbend Road, Athens, GA 30602-4712, USA

Tel: 706-542-4457

Fax: 706-542-4412

Email: hahn@ccrc.uga.edu

TIGR sequence name: MTMAE28TK

More information is available at: www.medicago.org

Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

FEATURES

Location/Qualifiers

source

1..604

/organism="Medicago truncatula"

/mol_type="mRNA"

/cultivar="A17"

/db_xref="taxon:3880"

/clone="HOGA-2E7"

/tissue_type="3 day old seedling roots"

/dev_stage="24 hours after treatment in the dark at 26 C

with 0.5 mg/ml oligogalacturonides (DP 6-20) in the

presence of 100 ug/ml Gentamicin"

/lab_host="XLOLR"

/clone_lib="HOGA"

/note="Vector: pBluescript SK-; Site1: EcoRI; Site2:

XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA

was directionally ligated into the Unizap XR vector from

Stratagene and packaged using Gigapack III Gold packaging

extracts. Plasmids containing cDNA inserts were excised

from the recombinant lambda-Zap phage using Ex-assist

helper phage and propagated in SOLR cells."

ORIGIN

Query Match 1.0%; Score 188.2; DB 6; Length 604;
Best Local Similarity 61.6%; Pred. No. 8.3e-38;
Matches 301; Conservative 0; Mismatches 188; Indels 0; Gaps 0;
QY 7274 GCCCTGGAGAGGGAGTGATGTGTTTATGACCTTCGCGAGCCAAATGCCCTCTATTTC 7333
Db |||||
QY 12 GTCATGCCACGCGAGGCGCGGTGCCGATGGACTTCACCGCGCGAACCGCGTGTATTTC 71
QY 7334 TGGGAGCTGTTCTATTACACGCCGATGATGTGTTCCAGCGGTTGTCGAGGAAACAGCAC 7393
Db |||||
QY 72 TGGGAGCTGTTCTACTACGCCCGATGATGTGATGCGAGCGTTCTCCAGGAAAGCGC 131
QY 7394 TTCGCGGAAGCACCCGCTGGCTGCAGTATGTCTGGAAACCCGCGCGGGACGCTGGTAAAC 7453
Db |||||
QY 132 TACGACCAACGCTGAACAATGGCTCGGTTATATCTTCAACCCCTTTGGGGTATGGCGATGG 191
QY 7454 GGGGTGCTGCAGAAATACACCTGGATCTCGTCCGCTGGAGGAGACACCGGCTGGAAAC 7513
Db |||||
QY 192 GCTGGGACGCTTCGCGCTTGTGGAACGTCACGCCCTCTGGAAGAGGACAGTTCTGGGAAAC 251
QY 7514 GACTCGCGCTGGACTCCATTGACCCCGATGCAATAGCCCACTAGACCCCATGCAATTAC 7573
Db |||||
QY 252 GATGAGCGCTGCGTTCGCTGACCCCGATGCCGTGGGCCAGAACGCCCATGCACTAC 311
QY 7574 AAGTGTGCGACCTTTATGTCTGATCTCGACCTGTGATTGCGCGCGGTGATGCGCGCTAC 7633
Db |||||
QY 312 AAGCTCAATGCAATTCATGCGGCTGTTGGATATCAACATCGGTGCTGGCGATGCCGCTTAT 371
QY 7634 CGGCTGTGCGAGCGGACACCTTAAACGAGGCCCGGATGTGTACGTCCAGGCCCTGAAAC 7693
Db |||||
QY 372 CGCAACTGGACGAGATAGCTTGGCGAGGCAAGATGTGGTATCAGCGCGCCCTGGAG 431
QY 7694 CTTCTGGCGCAGACGACCCCTATATTTCTTTTGACGCGGACTGTGTCGGCGTTGACCCCTGGGT 7753
Db |||||


```

Db      432 CTGTTGGGGAGCGGCCCTGGACTCCCGCGGCAACCGGTTGGAAAGAGCACCCTGCTGGGG 491
QY      7754 GAGCAGCC 7762
Db      492 CAACCTGGCC 500

RESULT 13
LOCUS   AQ991741
DEFINITION Rf00508F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00508F, genomic survey
sequence.
ACCESSION AQ991741
VERSION   AQ991741.1 GI:9650237
KEYWORDS  GSS.
SOURCE    Photorhabdus luminescens
ORGANISM  Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 735)
AUTHORS   ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE     A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL   Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE   20378633
PUBMED    10919786
COMMENT   Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bsrfc@bath.ac.uk
This is one of a selected subset of flipped clones from the M13
library. For annotation of identified clones (BLASTX, BLASTN and
mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.
Seq primer: M13 Reverse
Class: shotgun.
Location/Qualifiers
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kb) and then cloned into M13 Janus."

ORIGIN
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Best Local Similarity 62.7%; Pred. No. 4.7e-35;
Matches 277; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY      7370 CAGCGGTGTTGCAGGAACAGCACTCCCGGAAGCCACCGCTGGCTGCAGTATGTCGG 7429
Db      32 CAGCGCTGCTACACGAACAACACTTCGATGAAGCAACCGTTGGTTGAAATATATCTGG 91

QY      7430 AACCGCGCGGCGACGTGGTAAACGGGGTCTGCGAGAAATTACACCTGGAATGCGGTCG 7489
Db      92 AATCCATCTGTTATATTAGACATGGTTCAGATTTCAGCACTACCGCTGGAATGCGGCCA 151

QY      7490 CTGAGGAGGACACCGCTGGAACGACTCGCGCTGACTCCATTGACCCCGATGCAATA 7549
Db      152 TTATTGGAAGATATCAGTTGGAACAGATGATCCACTGAAATTCAGTCGATCCCGATGCCATA 211

QY      7550 GCCCAGTACGACCCCATTCGATTTACAGGTGCGCACCTTTATGTCGTAACCTCGACCTGCTG 7609

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Db      212 GCACAATATGATCCAATGCACTATATAAGTCGTTACTTTTATGCGCACCCCTTGATCTGTTG 271
QY      7610 ATTGCCCGGGTGATGCCCGCTACCGCTCGAGCGGGACACCCCTTTAACGAGGCCCGG 7669
Db      272 CTGGACCGTGGAGATTACCGCTATCGTCAGTTAGAACGGGACACGCTTATGAGCTAAG 331
QY      7670 ATGTGTACGTCCAGGCCCTGAACCTTCTGGGCGACGAGCCCTATATTTCTTTTACGCC 7729
Db      332 ATGTGTATATGCAACGACTGCATCTGTTAGGCGATAAACCTCATCTATCTTTCAAGTTCA 391
QY      7730 GACTGTGCGGCTGTACCGCTGGTGACGACGAGCGAGGTGACGCGGATTCACG 7789
Db      392 ACGTGGCGTAAACCGAGTTTGGTGACCTGCGCAACCGGAAAAACAGGAGGAACAAGCC 451
QY      7790 GAGGCCCTGCTGCGCGCTGGGCC 7811
Db      452 CATGCAATGACTGCCCTCGGAC 473

RESULT 14
LOCUS   AQ991783/c
DEFINITION Rf02280F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02280F, genomic survey
sequence.
ACCESSION AQ991783
VERSION   AQ991783.1 GI:9650377
KEYWORDS  GSS.
SOURCE    Photorhabdus luminescens
ORGANISM  Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE 1 (bases 1 to 765)
AUTHORS   ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE     A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL   Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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library. For annotation of identified clones (BLASTX, BLASTN and
mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.
Seq primer: M13 Reverse
Class: shotgun.
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kb) and then cloned into M13 Janus."

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Best Local Similarity 56.8%; Pred. No. 1e-29;
Matches 366; Conservative 0; Mismatches 260; Indels 18; Gaps 4;

QY      9343 GCGCGTCTCACCGGAATGAACACAGCGGCCCAATTCCAACTGGATTTCAATGACCCGCG 9402

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Db 657 GGCAGTTTCTCCGGTATGAATAAAGCGNCCAAATTCACGTNGATTTCACCATGGCAA 598
 QY 9403 TTACCTGCGCTTTGAAGGACTCCAGTTGATGACAGGAGCCCTGACATGAGCTTCCC 9462
 Db 597 ATTCTNCCATTGGAAGGATCGCCATTGAT---CAAAGGACGCTGACATGAGCTTCCC 541
 QY 9463 GGATGCTG-----ACGGCAAAACACAGCGATGCTCTCAGTCTGAGCGACATC 9511
 Db 540 AATGATNTATCGCGAGAAAGGTACCAAGCACCATATGTTAAACCCCTGACCGATATC 481
 QY 9512 ATCTGCAATACGTTACACCATATACAGCTGATAGGTATCAACATAGCGGAGCCGCCG 9571
 Db 480 ATTCTGATATTCGCTACACCATTAATAACCGTCCCAAGCTACTAA--AACAGGCTCCG 423
 QY 9572 AACGAGGCTCGGAGGAGACTGAGATGCARATCATCAAGACATGSCCATTTACTGCC 9631
 Db 422 AATCGGGGCTGTAAGAG--TTTTATGAGAAATTCACAAACATTCAGTGTTCACGAGC 365
 QY 9632 CCACGTTTGCCTTCGGGGCGGTGCGGTCAACGGGCTCAAGGGTGATATCGCGCGGAG 9691
 Db 364 TGTCATTACCAAGCGCGGNGCTATTACCGTATGGGTGAGCATTAACACCANCCG 305
 QY 9692 GCGCGATGTCGGCGACCCCTGAGTATTCCTTTCGGGTTAGCCCGGTCGGGGTTACG 9751
 Db 304 GCGCGATGTCGGCGGCTTATCCCTGCTCCATTACCCATTTCCGCGGNGTGGTTACG 245
 QY 9752 CCCCCACTGGGCACTTAATATACAGCGGTCGGGGAACGGCCCTTTGGCATTTGGCT 9811
 Db 244 CACCTCTGCTCACTTGAATATACACAGTGAACCGGTAAACGCCCATTTGGTCTCGGT 185
 QY 9812 GGGGTATCGCGGTGCTGTCTCGAGTCGTACGCGCAACGGAGCACCTTACTACGATG 9871
 Db 184 GGAAGTCGGCGCTGTCGCAATTTGTCGACCAAGTACCGCGGTACCGAATTACGATG 125
 QY 9872 ATACTGATGAATTCACCGTTCGGAAGTGTGCTGTCGGCGGCACTACGCGTGTCTG 9931
 Db 124 AAACCGATATCTTCTCGGGCGGAAAGTCAAGTGTGTCGTAGCATTAATAGGCAG 65
 QY 9932 GCACCCAGAGCAGCGGAGCCACTCACTACTGGGGATAAC 9975
 Db 64 GTCAAGCTGATATCCCGAGTGAATCTCATTTGAGGGGAGGAGC 21

RESULT 15
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 Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG01498, genomic survey
 sequence.
 ACCESSION
 AQ990688
 VERSION
 AQ990688.1 GI:9649282
 KEYWORDS
 GSS.
 SOURCE
 ORGANISM
 Photorhabdus luminescens
 Photorhabdus luminescens
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Photorhabdus.
 REFERENCE
 1 (bases 1 to 594)
 Authors
 French-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.
 TITLE
 A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: potential implications for virulence
 JOURNAL
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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 Email: bssr@bath.ac.uk
 This is one of 2,122 random reads from the M13 library. For
 annotation of identified clones (BLASTX, BLASTN and mapping to E.

coli K12 genome) please see french-constant et al. 2000, Nucleic
 Acids Res
 Seq primer: M13 Forward
 Class: shotgun.
 Location/Qualifiers
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 library"
 /note="Genomic DNA from strain W14 was size selected (1-2
 Kb) and then cloned into M13 Janus."

ORIGIN

Query Match 0.8%; Score 154.8; DB 8; Length 594;
 Best Local Similarity 63.1%; Pred. No. 6.7e-29;
 Matches 236; Conservative 0; Mismatches 137; Indels 1; Gaps 1;
 QY 16086 TTCAACACAGCGGGTAGTGTACTCCGGGGCTGGAGTTACGTATCATGGCAATGGCG 16145
 Db 374 TCAACAAACAGCGAGTCTTACTTCCAGGGTTGGAATTACANACCACTCAAGCGCG 315
 QY 16146 TCACGAAAAAAGAACCTGACAGTTATTA-CGGTGGGCGAGCTGGGGCGGACAGTG 16204
 Db 314 CCAATATCACCGAAGACTTGCAGTATTGTCTGTCGGAACAAGCAGGNAGACACAAGTA 255
 QY 16205 CCGCTATTGCACTGGGAGATCGCAAGCGGATGACCTCGATGAGACTCGGTGCGTTAC 16264
 Db 254 CCGCTTCTACANTGNNAAAAGGCCANCCNCTGNNATAGATNATNATNATNATNATNAT 195
 QY 16265 AGTTACGATAACCTCGTGGGCGAGCCAGCTGGAGCTGGACAGAGAGGGTTACCTTATC 16324
 Db 194 AGCTAGCATANTCTTNCACACAGCAGCGAATTTAGAACTGNATATGCACGGGTAAATATC 135
 QY 16325 AGTGAGGAGGAGTTCTACCCGTATGCGGAGACGGCTGTTCTGACCGCGCGAAGTGAGTT 16384
 Db 134 AGTTCGNAAGAGTATTACCCCTATGCGGCAACCGCAATATGNNCGNCAAGAAATCAGGTT 75
 QY 16385 GAGGCTGACTACAAAATATCGATCTCAGGCAAGGAGCGTGCACGACGGGCTGGAT 16444
 Db 74 GAGCTGGTNACAAACCATTCGTTATTCAGNCAAGAGCGGTGATGCAACAGACTGTAC 15
 QY 16445 TATTACGGTTATCG 16458
 Db 14 TATTACGGTACCG.1

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